

(2) INFORMATION POUR LA SEQ ID NO: 83:

(A) LONGUEUR: 304 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(78154..79065)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 83:

Met	Ser	Tyr	Arg	Gly	Leu	Thr	Ile	Leu	Gly	Cys	Ser	Ser	Gln	Gln	Pro
1				5					10					15	
Thr	Arg	His	Arg	Asn	His	Gly	Ala	Tyr	Leu	Leu	Arg	Trp	Asn	Gly	Glu
			20					25					30		
Gly	Leu	Leu	Phe	Asp	Pro	Gly	Glu	Gly	Thr	Gln	Arg	Gln	Phe	Ile	Tyr
		35					40					45			
Ala	Asn	Ile	Ala	Pro	Thr	Val	Val	Ser	Arg	Ile	Phe	Ile	Ser	His	Phe
	50					55					60				
His	Gly	Asp	His	Cys	Leu	Gly	Leu	Gly	Ser	Met	Leu	Met	Arg	Leu	Asn
65				70						75				80	
Leu	Asp	Arg	Val	Ser	His	Pro	Ile	His	Cys	Tyr	Tyr	Pro	Ala	Ser	Gly
			85						90					95	
Lys	Lys	Tyr	Phe	Asp	Arg	Leu	Arg	Tyr	Ser	Thr	Ile	Tyr	His	Glu	Thr
			100					105					110		
Ile	Lys	Val	Ile	Glu	His	Pro	Ile	Asp	Arg	Glu	Gly	Ile	Val	Glu	Asp
		115					120					125			

Phe Gly Asn Phe Arg Ile Glu Ser Arg Gln Leu Asp His Leu Val Asp
 130 135 140
 Thr Leu Gly Trp Arg Ile Thr Glu Pro Asp Thr Thr Lys Phe Ile Pro
 145 150 155 160
 Glu Lys Ile Lys Ala Ala Gly Leu Lys Gly Pro Ile Met Gln Glu Leu
 165 170 175
 Ile Asn Lys Gly Arg Val Lys Val Asn Asp Thr Ile Val His Leu Asp
 180 185 190
 Asp Val Ser Tyr Thr Arg Lys Gly Asp Ser Ile Ala Val Val Ala Asp
 195 200 205
 Ser Leu Pro Cys Gln Ala Ile Val Asp Leu Ala Arg Asn Ala Arg Ile
 210 215 220
 Leu Leu Cys Glu Ser Thr Tyr Leu Glu Glu His Ser His Leu Ala Lys
 225 230 235 240
 Ser His Tyr His Met Thr Ala Lys Gln Ala Ala Glu Gln Ala Lys Arg
 245 250 255
 Ala Glu Val Gln Gln Leu Ile Leu Thr His Phe Ser Ala Arg Tyr Asn
 260 265 270
 Thr Thr Glu Glu Phe Val Gln Glu Ala Gly Glu Ile Phe Pro Asn Val
 275 280 285
 Phe Ala Ala Glu Glu Phe Cys Ser Tyr Glu Phe Pro Lys Asn Pro Ser
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 84:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 698 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(79878..81971)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 84:

Ala Gln Val Leu Leu Ser Ile Glu Asp Arg Ile Arg Ile Val Lys Pro
 1 5 10 15
 Ile Gln Asp Lys Tyr Leu Lys Ala Lys Val Ser Tyr His Lys Glu Asn
 20 25 30
 Lys Glu Leu Thr Glu Glu Leu Lys Ala Tyr Ser Ile Ser Ile Val Ser
 35 40 45
 Ile Ile Lys Asp Leu Leu Lys Leu Asn Pro Leu Phe Lys Glu Glu Leu
 50 55 60
 Gln Ile Phe Leu Gly His Ser Asp Phe Thr Glu Pro Gly Lys Leu Ala
 65 70 75 80
 Asp Phe Ser Val Ala Leu Thr Thr Ala Thr Arg Glu Glu Leu Gln Glu
 85 90 95
 Ile Leu Glu Thr Thr Asp Met His Asp Arg Ile Asp Lys Ala Leu Val
 100 105 110
 Leu Leu Lys Lys Glu Leu Asp Leu Ser Arg Leu Gln Ser Ser Ile Asn
 115 120 125
 Gln Lys Ile Glu Ala Thr Ile Thr Lys Ser Gln Lys Glu Phe Phe Leu
 130 135 140
 Lys Glu Gln Leu Lys Thr Ile Lys Lys Glu Leu Gly Leu Glu Lys Asp
 145 150 155 160
 Asp His Ala Val Asp Leu Glu Lys Phe Met Glu Arg Phe Asn Lys Arg

165															170															175														
Asp	Val	Pro	Gln	Tyr	Ala	Met	Asp	Val	Ile	Gln	Asp	Glu	Met	Asp	Lys	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
180															185															190														
Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn	Tyr	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn												
195															200															205														
Tyr	Leu	Asp	Trp	Leu	Thr	Ile	Val	Pro	Trp	Gly	Ile	Gln	Thr	Lys	Glu	Tyr	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn												
210															215															220														
Tyr	His	Asp	Leu	Lys	Lys	Ala	Glu	Ser	Ile	Leu	Asn	Lys	Asp	His	Tyr	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
225															230															235														
Gly	Leu	Glu	Asp	Ile	Lys	Gln	Arg	Ile	Leu	Glu	Leu	Ile	Ser	Val	Gly	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
245															250															255														
Lys	Leu	Ala	Asn	Gly	Met	Lys	Gly	Ser	Ile	Ile	Cys	Leu	Val	Gly	Pro	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
260															265															270														
Pro	Gly	Val	Gly	Lys	Thr	Ser	Ile	Gly	Arg	Ser	Ile	Ala	Lys	Val	Leu	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
275															280															285														
His	Arg	Lys	Phe	Phe	Arg	Phe	Ser	Val	Gly	Gly	Met	Arg	Asp	Glu	Ala	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
290															295															300														
Glu	Ile	Lys	Gly	His	Arg	Arg	Thr	Tyr	Ile	Gly	Ala	Met	Pro	Gly	Lys	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
305															310															315														
Leu	Val	Gln	Ala	Leu	Lys	Gln	Ser	Gln	Ile	Met	Asn	Pro	Val	Ile	Met	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
325															330															335														
Ile	Asp	Glu	Val	Asp	Lys	Ile	Gly	Ser	Ser	Tyr	His	Gly	Asp	Pro	Ala	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
340															345															350														
Ser	Ala	Leu	Leu	Glu	Val	Leu	Asp	Pro	Glu	Gln	Asn	Lys	Asp	Phe	Leu	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
355															360															365														
Asp	His	Tyr	Leu	Asp	Val	Arg	Val	Asp	Leu	Ser	Asn	Val	Leu	Phe	Ile	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
370															375															380														
Leu	Thr	Ala	Asn	Val	Leu	Asp	Ser	Ile	Pro	Asp	Pro	Leu	Leu	Asp	Arg	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
385															390															395														
Met	Glu	Val	Leu	Arg	Leu	Ser	Gly	Tyr	Ile	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
405															410															415														
Ile	Ala	Thr	Lys	Tyr	Leu	Val	Pro	Arg	Ala	Arg	Lys	Glu	Met	Gly	Leu	Leu	Gln	Thr	Leu	Glu	Thr	Ser	Ser	Ala	Glu	Tyr	Ala	Val	Cys	Arg	Asn													
420															425															430														
Ser	Ala	Gln	Asn	Val	Thr	Phe	Gln	Pro	Glu	Ala	Ile	Lys	His	Met	Ile	Leu	Gln</																											

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 83792..84850

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 86:

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Ser Gly Gly Arg Phe Lys Glu Val Ser Glu Ala Tyr Glu Val Leu Gly
1      5      10      15
Asp Ala Gln Lys Arg Glu Ser Tyr Asp Arg Tyr Gly Lys Asp Gly Pro
20      25      30
Phe Ala Gly Ala Gly Gly Phe Gly Ala Gly Met Gly Asn Met Glu
35      40      45
Asp Ala Leu Arg Thr Phe Met Gly Ala Phe Gly Gly Asp Phe Gly Gly
50      55      60
Asn Gly Gly Gly Phe Phe Glu Gly Leu Phe Gly Gly Leu Gly Glu Ala
65      70      75      80
Phe Gly Met Arg Gly Gly Ser Glu Ser Ser Arg Gln Gly Ala Ser Lys
85      90      95
Lys Val His Ile Thr Leu Ser Phe Glu Ala Ala Lys Gly Val Glu
100     105     110
Lys Glu Leu Val Ser Gly Tyr Lys Ser Cys Asp Ala Cys Ser Gly
115     120     125
Ser Gly Ala Asn Thr Ala Lys Gly Val Lys Val Cys Asp Arg Cys Lys
130     135     140
Gly Ser Gly Gln Val Val Gln Ser Arg Gly Phe Phe Ser Met Ala Ser
145     150     155     160
Thr Cys Pro Asp Cys Ser Gly Glu Gly Arg Val Ile Thr Asp Pro Cys
165     170     175
Ser Val Cys Arg Gly Gln Gly Arg Ile Lys Asp Lys Arg Ser Val His
180     185     190
Val Asn Ile Pro Ala Gly Val Asp Ser Gly Met Arg Leu Lys Met Glu
195     200     205
Gly Tyr Gly Asp Ala Gly Gln Asn Gly Ala Pro Ala Gly Asp Leu Tyr
210     215     220
Val Phe Ile Asp Val Glu Pro His Pro Val Phe Glu Arg His Gly Asp
225     230     235     240
Asp Leu Val Leu Glu Leu Pro Ile Gly Phe Val Asp Ala Ala Leu Gly
245     250     255
Ile Lys Lys Glu Ile Pro Thr Leu Leu Lys Glu Gly Thr Cys Arg Leu
260     265     270
Ser Ile Pro Glu Gly Ile Gln Ser Gly Thr Val Leu Lys Val Arg Gly
275     280     285
Gln Gly Phe Pro Asn Val His Gly Lys Ser Arg Gly Asp Leu Leu Val
290     295     300
Arg Val Ser Val Glu Thr Pro Gln His Leu Ser Asn Glu Gln Lys Asp
305     310     315     320
Leu Leu Arg Gln Phe Ala Ala Thr Glu Lys Ala Glu Asn Phe Pro Lys
325     330     335
Lys Arg Ser Phe Leu Asp Lys Ile Lys Gly Phe Phe Ser Asp Phe Ala
340     345     350
Val

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(2) INFORMATIONS POUR LA SEQ ID NO: 87:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 682 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 84876..86921

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 87:

```

Glu Gly Ala Ala Val Arg His Ser Val Tyr Gln Leu Asp Ser Ala Val
1      5      10      15
Glu Asn Val Phe Arg Leu Ala Trp Thr Leu Arg Phe Ser Glu Arg Lys
20     25     30
Met Leu Leu Leu Ser Arg Gln Ser Gly Ser Gly Gly Ser Phe Gln Leu
35     40     45
Ser Cys Ala Gly His Glu Leu Ala Gly Val Val Ala Ala Lys Ser Leu
50     55     60
Ile Pro Gly Lys Asp Trp Ala Phe Pro Tyr Tyr Arg Asp Gln Gly Phe
65     70     75     80
Pro Leu Gly Leu Gly Cys Asp Leu Ser Glu Ile Phe Ala Ser Phe Leu
85     90     95
Ala Arg Thr Thr Gln Asn His Ser Ala Gly Arg Met Met Pro Tyr His
100    105    110
Tyr Ser His Lys Lys Leu Arg Ile Cys Cys Gln Ser Ser Val Val Gly
115    120    125
Thr Gln Phe Leu Gln Ala Ala Gly Arg Ala Trp Gly Val Lys Asn Ser
130    135    140
Gly Lys Ser Glu Val Val Tyr Val Ser Gly Gly Asp Gly Ser Thr Ser
145    150    155    160
Gln Gly Glu Phe His Glu Met Leu Asn Phe Ala Ser Leu His Gln Leu
165    170    175
Pro Leu Val Ile Ala Ile Gln Asn Asn Gln Trp Ala Ile Ser Val Pro
180    185    190
Phe Ala Asp Gln Cys Gly Ala Asp Leu Val Ala Leu Gly Asn Ser Tyr
195    200    205
Ser Gly Leu Ala Thr Tyr Glu Val Asp Gly Gly Asp Val Ser Val Leu
210    215    220
Thr Gln Thr Phe Glu Arg Ala Val Ser Asp Ala Arg His Arg His Ile
225    230    235    240
Pro Ala Leu Val Ile Val Asn Val Val Arg Leu Glu Ser His Ser Asn
245    250    255
Ser Asp Asn Gln Ala Lys Tyr Arg Ser Glu Glu Asp Leu Ser Cys Cys
260    265    270
Gln Ala Gln Asp Pro Leu Val Arg Leu Glu Lys Ser Leu Leu Asp Asp
275    280    285
Phe Gly Val Ala His Glu Val Ile Glu Gln Ile Lys Ala Glu Leu Gln
290    295    300
Glu Thr Val Asn Gln Ala Cys Glu Leu Ala Glu Ser Ala Pro Phe Pro
305    310    315    320
Cys Lys Gly Ala Thr Lys His Glu Val Phe Ala Pro Tyr Asn Ile Ser
325    330    335
Leu Ile Asp Tyr Glu Asn Ala Leu Glu Thr Ala Ser Leu Gln Lys Leu
340    345    350
Glu Pro Arg Val Met Arg Asp Ala Ile Thr Glu Ala Leu Val Glu Glu
355    360    365
Met Gln Arg Asp Pro Gly Val Val Val Phe Gly Glu Asp Val Ala Gly

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          370          375          380
Asn Lys Gly Gly Val Phe Gly Val Thr Arg Thr Leu Thr Glu Gln Phe
385          390          395          400
Gly Glu Asn Arg Cys Phe Asn Thr Pro Leu Ala Glu Ala Thr Ile Ile
          405          410          415
Gly Ala Ala Val Gly Met Ala Phe Asp Gly Phe Tyr Lys Pro Val Ala
          420          425          430
Glu Ile Gln Phe Ala Asp Tyr Ile Trp Pro Gly Ile Asn Gln Leu Phe
          435          440          445
Ser Glu Ala Ala Ser Ile Tyr Tyr Arg Ser Ala Gly Glu Trp Glu Met
          450          455          460
Pro Ile Val Ile Arg Thr Pro Cys Gly Gly Tyr Ile Gln Gly Gly Pro
465          470          475          480
Tyr His Ser Gln Asn Ile Glu Ala Phe Leu Ala His Cys Pro Gly Leu
          485          490          495
Lys Val Val Tyr Pro Ser Asn Ala Ala Asp Ala Lys Ala Leu Leu Lys
          500          505          510
Ala Ala Ile Arg Asp Pro Asn Pro Val Val Phe Leu Glu His Lys Ala
          515          520          525
Leu Tyr Gln Arg Arg Leu Phe Ser Thr Thr Pro Val Phe Ser Ser Asp
          530          535          540
Tyr Val Leu Pro Phe Gly Gln Ala Arg Ile Val His Pro Gly Thr Asp
545          550          555          560
Leu Thr Ile Val Ser Trp Gly Met Ser Leu Val Met Ser Val Glu Val
          565          570          575
Ala Arg Asp Leu Leu Glu Leu Gly Ile Ser Val Glu Val Ile Asp Leu
          580          585          590
Arg Thr Ile Val Pro Cys Asp Phe Ala Thr Val Cys Glu Ser Val Lys
          595          600          605
Lys Thr Gly Lys Leu Leu Val His Glu Ala Ser Glu Phe Cys Gly
          610          615          620
Phe Gly Ser Glu Leu Val Ala Leu Val Ala Glu Arg Ala Tyr Arg Tyr
625          630          635          640
Leu Asp Ala Pro Ile Lys Arg Ile Gly Ala Leu His Ala Pro Val Pro
          645          650          655
Tyr Ser Lys Val Leu Glu Asn Glu Val Leu Pro Gln Lys Glu Lys Ile
          660          665          670
Phe Gln Glu Ala Lys Leu Leu Ala Glu Phe
          675          680

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(2) INFORMATIONS POUR LA SEQ ID NO: 88:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 446 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(87313..88650)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 88:

```

Asp Arg Pro Thr Asn Ser Asn His Pro Leu Gly Asn Arg Gly Thr Leu
1      5      10      15
Ala Asn Thr Ser Ser Gln Glu Ser Val Leu Arg Ile Cys Ser Arg Glu
20      25      30

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Ser Thr Ser Thr Gly Cys Leu Glu Gln Ala Asp Val Thr Leu Ser Leu
   35           40           45
Tyr His Cys Ile Pro Asn Leu Ile Thr Ser Pro Ile Cys Leu Arg Ile
   50           55           60
Arg Leu Phe Ser Ser Cys Ser Val Phe Gln Lys Gln His Pro Ile Phe
   65           70           75           80
Ile Gly Ser Ala Tyr Trp Leu Ala Gly Met Leu Ala His Gln Ala Pro
           85           90           95
Ile Cys Cys Ala Leu Leu Ile Val Ala Leu His Pro Phe Ile Pro Lys
           100           105           110
Arg Cys Leu Lys Thr Leu Phe Ser Leu Ser Ile Cys Phe Gly Val Pro
           115           120           125
Leu Leu Phe Ser Pro Leu Ile Ser Pro Ser Asn Ala Ser Arg Ser Val
           130           135           140
Ala Asn Ser Lys Ile Gln Val Thr Lys Gly Ser Ala Ser Gly Tyr Phe
   145           150           155           160
Leu Ile Lys Lys Lys Leu Thr His Arg Tyr Ser Gly Thr Ala Leu Ser
           165           170           175
Leu Glu Thr Glu Asp Lys Gln Ser Tyr Gln Asn Leu Pro Cys Ser Ile
           180           185           190
Ile Ser Thr Ile Pro Leu Ser Glu His Thr Val Tyr His Leu Glu Gly
           195           200           205
Cys Val Ser Lys Ser Ser Cys Pro Ile Thr Phe Arg Ser Ser Lys Leu
           210           215           220
Ile Asn Thr Pro Thr Gln Ser Ser Ile Phe Leu Arg Asn Ser Ser Asn
   225           230           235           240
Tyr Ser Leu Pro Ile Leu Lys Glu Asn Phe Arg Phe Phe Leu His Gln
           245           250           255
Arg Ile Leu Asn Leu Phe Ser Asp Lys Asp Ile Gly Arg Phe Ser Ser
           260           265           270
Ser Leu Ile Leu Gly Thr Pro Leu Ser Tyr Lys His Lys Glu Leu Phe
           275           280           285
Lys Ser Lys Gly Leu Ser His Leu Phe Ser Val Ser Gly Trp His Phe
           290           295           300
Ser Leu Phe Ala Asn Thr Phe Phe Phe Leu Leu Gly Thr Leu Ser Pro
   305           310           315           320
Lys Lys Arg Gly Leu Trp Val Leu Phe Leu Leu Ser Leu Leu Asn Phe
           325           330           335
Val Phe Pro Thr Ser Pro Ser Val Phe Arg Thr Trp Phe Ser Ser Ile
           340           345           350
Leu Phe Cys Leu Ala Pro Phe Ser Ile Gly His Cys Ser Ser Leu Asn
           355           360           365
Arg Leu Gly Ile Ser Phe Ile Phe Cys Ser Leu Phe Phe Pro Ile Ser
           370           375           380
Ser Pro Ala Leu Ile Leu Ser Phe Leu Ala Thr Leu Gly Ile Leu Phe
   385           390           395           400
Ser Leu Tyr Arg Tyr Val Ser Phe Thr Leu Pro Gly Asn His Tyr
           405           410           415
Ser Ala Leu Val Gly Phe Ser Ser Leu Phe Gly Leu Tyr Ser Gln Pro
           420           425           430
Tyr Gln Ser Leu Leu Leu Pro Ser Phe Leu Ser Phe Ser Gln
           435           440           445

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(2) INFORMATIONS POUR LA SEQ ID NO: 89:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 87440..87805

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 89:

```

Arg Tyr Lys Glu Asn Lys Met Pro Lys Val Ala Lys Lys Leu Ser Ile
1          5          10          15
Ser Ala Gly Asp Asp Ile Gly Lys Lys Ser Glu Gln Lys Ile Lys Leu
20          25          30
Ile Pro Ser Arg Phe Arg Leu Glu Gln Cys Pro Ile Glu Lys Gly Ala
35          40          45
Arg Gln Asn Arg Ile Leu Glu Asn Gln Val Leu Asn Thr Glu Gly Glu
50          55          60
Val Gly Asn Thr Lys Leu Arg Arg Glu Ser Arg Lys Arg Thr Gln Arg
65          70          75          80
Pro Arg Phe Leu Gly Glu Ser Val Pro Asn Lys Lys Lys Val Leu
85          90          95
Ala Asn Ser Glu Lys Cys His Pro Asp Thr Glu Lys Arg Trp Asp Asn
100          105          110
Pro Leu Leu Leu Asn Ser Ser Leu Cys Leu
115          120

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(2) INFORMATIONS POUR LA SEQ ID NO: 90:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 116 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 88400..88747

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 90:

```

Ala Leu Pro Met Lys Ile Gly Cys Cys Phe Trp Lys Thr Glu Gln Glu
1          5          10          15
Leu Asn Ser Leu Ile Arg Lys Gln Ile Gly Asp Val Met Arg Leu Gly
20          25          30
Met Gln Trp Tyr Lys Asp Ser Val Thr Ser Ala Cys Ser Lys Gln Pro
35          40          45
Val Glu Val Leu Ser Leu Glu Gln Met Arg Arg Thr Leu Ser Trp Glu
50          55          60
Glu Val Phe Ala Lys Val Pro Arg Leu Pro Arg Gly Trp Phe Glu Leu
65          70          75          80
Val Gly Leu Ser Gln Ala Asp Arg Ile Glu Leu Phe Arg Asp Phe Trp
85          90          95
Phe Ser Ala Leu Gly Val Glu Asn Thr Asp Phe Pro Gly Ile Cys His
100          105          110
Phe Phe Pro Leu
115

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(2) INFORMATIONS POUR LA SEQ ID NO: 91:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 88717..89265

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 91:

```

Phe Pro Trp Tyr Leu Ser Phe Phe Ser Ser Leu Ser His Leu Asp Val
1      5      10      15
Arg Ile Thr Arg Asn Ser Leu Ser Ala Pro Tyr Asp Val Gln Met Val
      20      25      30
Tyr Ser Tyr Lys Gly Ile Val Tyr Leu Gly Ala Pro Pro Phe Glu Thr
      35      40      45
Val Gly Val Val Phe Pro Lys Leu Gly Asp Glu Thr Tyr Arg His Phe
      50      55      60
Phe Ser Ile His Asn Gly Phe Ser Arg Glu Gly Glu Ile Gly Ile Phe
      65      70      75      80
Pro Tyr Arg Tyr Leu Ala Gln Ala Gln Tyr Leu Leu Arg Glu Asp Leu
      85      90      95
Leu Ser Arg Gly Lys Ile Ser Leu Glu Asp Asn Cys Ser Ser Leu Gly
      100      105      110
Ile Phe Pro Phe Tyr Ala Gln Tyr Asp Ile Ala Asp Ser Arg Cys Phe
      115      120      125
Ile Ile Asp Ala Lys Ile Arg Gln Tyr Phe Pro Ser Tyr Asn Val Arg
      130      135      140
Leu Asp Asn Gln Ser Leu Phe Pro His Gly Lys Ile Ala Ile Ser Glu
      145      150      155      160
Met Leu Ser Asp Ser His Tyr His Thr Phe Leu Leu Trp Leu Glu Gln
      165      170      175
Tyr Leu Leu Ser Gln Lys Pro
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 92:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 89457..89732

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 92:

```

Met Glu Asp Gly Glu Leu Ser Ala Val Phe Thr Ile Arg Asn Pro Ser
1      5      10      15
Gly Ile His Val Arg Pro Ala Gly Thr Ile Val Lys Leu Phe Glu Gly
      20      25      30
Glu Glu Cys Glu Ala Thr Leu Thr Tyr Leu Gly Lys Thr Val Asn Ala

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          35          40          45
Arg Ser Val Met Ser Ile Leu Met Leu Gly Ala Ser Tyr Asn Gly Glu
  50          55          60
Val Ala Val His Ile Lys Gly Pro Ser Ala Ser Arg Val Met Gln Lys
  65          70          75          80
Leu Ser Glu Val Phe Asn Ser Gly Phe Gly Glu Leu
          85          90

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(2) INFORMATIONS POUR LA SEQ ID NO: 93:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 562 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 89762..91447

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 93:

```

Glu Leu Gln Gln Glu Phe Val Ile Val Gly Glu Pro Ile Val Pro Gly
1          5          10          15
Ile Gly Leu Gly Lys Ala Leu Leu Leu Gly Lys Ser Ser Leu Arg Ile
  20          25          30
Arg Glu Leu Thr Leu Pro Gln Glu Val Glu His Glu Ile Ser Arg
  35          40          45
Tyr Tyr Lys Ala Leu Lys Arg Ser Arg Ser Asp Leu Ala Ala Leu Glu
  50          55          60
Lys Glu Ala Lys Gly Lys Gln Gly Tyr Gln Glu Ile Ala Ser Ile Leu
  65          70          75          80
Gln Ala His Leu Glu Ile Ile Lys Asp Pro Leu Leu Thr Glu Glu Val
  85          90          95
Val Lys Thr Ile Arg Lys Asp Arg Lys Asn Ala Glu Phe Val Phe Ser
  100          105          110
Ser Val Met Gly Glu Ile Glu Lys Ser Leu Cys Ala Val Gln Lys Thr
  115          120          125
Thr Ala Thr Thr Val Asp Arg Val Gln Asp Ile His Asp Ile Ser Asn
  130          135          140
Arg Val Ile Gly His Leu Cys Cys Gln His Lys Ser Ser Leu Gly Glu
  145          150          155          160
Phe Asp Gln Asn Leu Ile Val Phe Ser Glu Glu Leu Thr Pro Ser Glu
  165          170          175
Ala Ala Asn Ala Asn Pro Glu Tyr Ile Arg Gly Phe Val Ser Leu Glu
  180          185          190
Gly Ala Lys Thr Ser His Thr Ala Ile Val Ser Leu Ala Lys Asn Ile
  195          200          205
Pro Tyr Val Ala Asn Phe Thr Thr Glu Leu Trp Asp Thr Ile Asn Glu
  210          215          220
Phe Ser Gly Thr Leu Val Leu Ile Asn Gly Asp Lys Gly Glu Ile Thr
  225          230          235          240
Phe Asn Pro Gln Leu Ser Thr Ile Gln Thr Tyr Tyr Arg Lys Gln Ala
  245          250          255
Ser Val Ser Val Thr Val Pro Val Gln Val Gln Thr Gly Lys Asn Leu
  260          265          270
Pro Leu Ile Ser Leu Ser Ala Gln Ile Val Ser Thr Glu Glu Leu Pro
  275          280          285

```



```

Met Ile Glu Arg Glu Ser Pro Gly Thr Ser Val Gly Leu Phe Arg Ser
290 295 300
Glu Phe Met Ala Phe Ser Leu Gly Arg Leu Pro Cys Val Glu Glu Gln
305 310 315 320
Ala Asp Gln Tyr Ala Gln Leu Val Gln Phe Gln Cys Ser Asp Ile His
325 330 335
Val Leu Arg Leu Phe Asp Phe Gly Glu Asp Lys Glu Cys Pro Cys Ile
340 345 350
Ser Ser Ser His Arg Ser Val Arg Trp Leu Leu Glu Gln Glu Lys Val
355 360 365
Leu Lys Glu Gln Leu Gln Ala Ile Ala Ile Val Ser Arg Ile Gly Arg
370 375 380
Leu Lys Val Leu Ile Pro Gly Val Ile Asp Ala Ser Glu Ile Ala Leu
385 390 395 400
Val Lys Arg Leu Phe Gln Glu Glu Ile Arg Leu Leu Lys Gly Ile Ser
405 410 415
Glu Asn Ile Leu Trp Gly Ser Met Ile Glu Ile Pro Ser Ala Val Trp
420 425 430
Met Ile Glu Glu Ile Leu Gln Glu Ser Ser Phe Val Ala Leu Gly Thr
435 440 445
Asn Asp Leu Ala Gln Tyr Thr Leu Gly Thr Ser Arg Glu Arg Ser Leu
450 455 460
Leu Gly Glu Arg Ser Arg Val Pro His Pro Ser Val Ile Arg Met Ile
465 470 475 480
His His Val Val Glu Gln Ala Lys Gln Lys Asn Val Pro Val Ser Val
485 490 495
Cys Gly Glu Met Ala Gly Asp Pro Ala Leu Leu Pro Met Phe Leu Gly
500 505 510
Leu Gly Val Lys Glu Leu Ser Ala Val Ile Pro Ala Ile Asn Ser Leu
515 520 525
Lys Met Arg Leu Leu Asp Leu Asn Ser Arg Glu Cys Ser Arg Leu Thr
530 535 540
Lys Gln Leu Leu Arg Ala Lys Thr Tyr Glu Glu Val His Gln Leu Leu
545 550 555 560
Tyr Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 94:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(91435..91749)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 94:

```

Met Gly Ser Gly Tyr Ala Lys Lys Lys Lys Glu Ala Lys Leu Met Glu
1 5 10 15
Arg Gln Phe Met Glu Met Glu Ala Ser Leu Glu Gln Lys Arg Phe Ser
20 25 30
Gly Glu Ala Gly Asn Gly Leu Val Ser Val Thr Ile Asn Gly Lys Cys
35 40 45
Asp Leu Val Asp Val Arg Ile Lys Pro Asp Cys Leu Asp Pro Glu Asp

```

50		55		60											
Pro	Glu	Val	Val	Ala	Asp	Leu	Phe	Arg	Ala	Asp	Leu	Lys	Gln	Leu	Lys
65				70						75					80
Gln	Leu	Trp	Ile	Val	Lys	Cys	Pro	Leu	Cys	Lys	Trp	Glu	Cys	Arg	Ser
			85						90					95	
Asn	Phe	Phe	Arg	Tyr	Thr	Tyr	Arg	Ser							
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 95:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(91745..92392)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 95:

Pro	Ile	Ser	Thr	Cys	Arg	Ser	His	Tyr	Tyr	Pro	Lys	Leu	Arg	Thr	Ser
1				5					10					15	
Val	Thr	Pro	Val	Ser	Asp	Ala	Met	Gln	Met	Gly	Val	Ala	Pro	Ala	His
			20					25					30		
Phe	Leu	Gln	Asp	Val	Thr	Leu	Leu	Phe	Arg	Ser	Phe	Leu	Leu	Lys	Gln
		35					40					45			
Tyr	Ser	Lys	Gln	Phe	His	Ser	Val	Ala	Thr	Lys	Tyr	Ser	Ser	Glu	Ile
	50					55					60				
Leu	Leu	Glu	Ile	Leu	Asp	Phe	Leu	Gly	Glu	Ser	Ala	Arg	His	Ile	Asn
65					70				75					80	
Leu	Ala	Leu	Phe	Glu	Lys	Thr	Phe	Leu	Glu	Thr	Val	Ile	Ile	Arg	Leu
				85					90					95	
Leu	Arg	Ile	Tyr	Ser	Arg	Pro	Thr	Phe	Ser	Gln	Leu	Val	Ser	Gln	Ile
			100					105					110		
Arg	Gln	Pro	Ala	Pro	Thr	Gln	Ile	Arg	Pro	Ile	Pro	Thr	Ala	Ser	Glu
		115					120						125		
Leu	Glu	Ser	Cys	Pro	Pro	Gln	Ile	Lys	Ser	Ser	Asn	Thr	Glu	Glu	Thr
	130					135					140				
Lys	Ser	Ser	Pro	Gln	Pro	Thr	Ala	Val	Ala	Lys	Leu	Ser	Gln	Gly	Ser
145					150					155				160	
Leu	Leu	Thr	Ala	Ala	Ser	Ser	Gln	Thr	Lys	Lys	Glu	Thr	Ile	His	Gln
				165					170					175	
Glu	Thr	Pro	Pro	Pro	Ser	Leu	Asp	Lys	Ile	Ser	Pro	Ser	Glu	Ser	Ala
			180					185					190		
Ala	Ile	Asp	Thr	Leu	Leu	Gln	Phe	Ala	Val	Val	Glu	Phe	Ser	Gly	Val
		195					200						205		
Leu	Thr	Lys	Glu	Pro	Lys	His	Gly								
			210				215								

(2) INFORMATIONS POUR LA SEQ ID NO: 96:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 265 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(92344..93138)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 96:

```

Asp Leu Leu Ser Ser Phe Phe Lys Lys Val Pro Pro Glu Gln Phe Phe
1          5          10          15
Arg Asp Ser Trp Pro Gly Tyr Ser Arg Val Tyr Thr Gln Glu Phe Pro
          20          25          30
Ala Ser Glu Ser Arg Arg His Ala Tyr Ile Phe Ser Gly Ile Arg Gly
          35          40          45
Thr Gly Lys Thr Thr Leu Ala Arg Val Phe Ala Lys Ala Leu Asn Cys
          50          55          60
Gln Asn Pro Thr Gln Asp Gln Glu Pro Cys Asn Gln Cys Ala Ile Cys
          65          70          75          80
Lys Glu Ile Ser Leu Gly Thr Ser Met Asp Val Ile Glu Ile Asp Gly
          85          90          95
Ala Ser His Arg Gly Ile Glu Asp Ile Arg Gln Ile Asn Glu Thr Val
          100          105          110
Leu Phe Val Pro Ser Lys Ser Arg Tyr Lys Ile Tyr Ile Ile Asp Glu
          115          120          125
Val His Met Leu Thr Lys Glu Ala Phe Asn Ser Leu Leu Lys Thr Leu
          130          135          140
Glu Glu Pro Pro Ala His Val Lys Phe Phe Leu Ala Thr Thr Glu Ile
          145          150          155          160
Ala Lys Ile Pro Asn Thr Ile Ser Ser Arg Cys Gln Lys Met Leu Leu
          165          170          175
Lys Arg Ile Ser Glu Glu Thr Ile Ile Asp Lys Leu Ala Thr Ile Ala
          180          185          190
Lys Gln Glu Gly Thr Glu Thr Ser Arg Glu Ala Leu Leu Pro Ile Ala
          195          200          205
Lys Ala Ala Gln Gly Ser Leu Arg Asp Ala Glu Ser Leu Tyr Asp Tyr
          210          215          220
Val Val Gly Leu Phe Pro Glu Ser Leu Asp Pro Asp Ser Thr Ala Lys
          225          230          235          240
Ala Leu Gly Ile Leu Ser Glu Asp Ser Leu Tyr Gln Leu Ala Glu Ala
          245          250          255
Ile Thr Thr Gln Asn Tyr Glu Gln Ala
          260          265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 97:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 258 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(93361..94134)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 97:

```

His Leu Arg Thr Cys Cys Ala Ile Leu Glu Lys Asp Pro Ser Val Phe

```

```

1           5           10           15
Ser Glu Ile Ile Phe Leu Asp Ser Tyr Pro Gln Ile Ala Ser Ser Arg
                20           25           30
Ser Asp Ile Ser Thr Tyr Phe Asp Ile Ala Pro Ser Leu Arg Asn Phe
                35           40           45
Tyr Ala Ser Leu Thr Gln Ala Lys Ala Leu Asn Ile Ser Val Ser Met
                50           55           60
Phe Ser Pro Asn Thr Lys Gln Gly Gln Cys Ser Asp Cys Trp Gly Leu
65           70           75           80
Gly Tyr Gln Trp Ile Asp Arg Ala Phe Tyr Ala Met Glu Lys Arg Pro
                85           90           95
Cys Pro Thr Cys Gly Gly Phe Arg Val Gln Pro Leu Ile Gln Glu Val
                100           105           110
Val Tyr Glu Gly Lys His Phe Gly Gln Leu Leu Gln Ala Ser Leu Asn
                115           120           125
Glu Val Ala Glu Thr Phe Ser Phe Leu Lys Lys Ile Gln Lys Pro Leu
                130           135           140
His Thr Leu Ile Thr Asn Gly Leu Gly Tyr Leu Ser Leu Gly Gln Asn
145           150           155           160
Met Ala Ser Leu Ser Leu Ser Glu Lys Ile Ala Ile Lys Leu Thr Lys
                165           170           175
His Leu Phe Leu Pro Pro Lys His Pro Thr Leu Phe Leu Leu Asp Glu
                180           185           190
Ile Ala Thr Ser Leu Asp Asn Gln Gln Gln Ser Ala Leu Leu Val Gln
                195           200           205
Leu Asn Thr Leu Val Ser Leu Gly His Thr Val Val Ile Ile Glu Asn
                210           215           220
His Pro Ala Phe Ser Gln Gln Ala Asp Phe Trp Ile Gln Met Gly Arg
225           230           235           240
Lys Thr Asp Asn His Ile Leu Phe Ala Gly Pro Asn Pro Asn Leu Ser
                245           250           255
Phe Thr

```

(2) INFORMATIONS POUR LA SEQ ID NO: 98:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 189 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(94071..94637)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 98:

```

Ile Gly Leu Leu Asp Arg Val Gly Leu Gly Tyr Val Ile Leu Gly Gln
1           5           10           15
Glu Gln Gln Ser Leu Ser Asp Gly Glu His Tyr Arg Leu Leu Leu Ala
                20           25           30
Lys Ala Phe Ser Ser Gly Leu Thr Asp Val Ile Tyr Leu Leu Glu Asp
                35           40           45
Pro Leu Ala Gly Ile His Pro Glu Asp Ala Pro Cys Leu Leu Ala Val
                50           55           60
Ile Lys Lys Leu Val Thr Asn His Asn Thr Val Ile Val Thr Asp Arg
65           70           75           80

```

```

Glu Gly Ser Leu Ala Glu His Ala Asp Tyr Leu Leu His Leu Gly Pro
      85          90          95
Glu Pro Gly Pro Asn Gly Gly Tyr Leu Leu Ser Thr Ser Ala Leu Lys
      100          105          110
Gln Ser Gln Pro Val Leu Cys Asn Thr Arg Ser Ser Glu Glu Thr Pro
      115          120          125
Gln Leu Ser Val Ser Val Ser Thr Ser Met Ile Gln Ile Glu Asn Leu
      130          135          140
Ala Phe Pro Leu Gln Arg Leu Ser Thr Ile Ser Gly Val Ser Gly Ser
      145          150          155          160
Gly Lys Thr Thr Leu Leu Asn Ser Ile Tyr Glu His Ala Ala Leu Phe
      165          170          175
Leu Lys Arg Ile Leu Leu Tyr Ser Gln Lys Leu Phe Phe
      180          185

```

(2) INFORMATIONS POUR LA SEQ ID NO: 99:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1224 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(94628..98299)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 99:

```

Asn Ser Cys His Ser Arg Trp Asn Ser Thr Asp Phe Ala Arg Ser Ser
1      5      10      15
Ser Arg Gln Asp Val Leu Thr Val Arg Glu Cys Leu Arg Gln Gly Phe
      20      25      30
Thr Lys Val Leu Ile Asp Glu Glu Val Val Pro Ile His Lys Phe Leu
      35      40      45
Thr Thr Gly Ile Pro Val Pro Gly Gln Leu Ile Val Asp Thr Leu Ile
      50      55      60
Lys Asn Thr Ser Asn Thr Pro Arg Leu Lys Val Ser Leu Phe Thr Thr
      65      70      75      80
Leu Asp Ile Gly His Gly Glu Cys Ser Leu His Phe Asp Asn Gln Lys
      85      90      95
Arg Val Phe Ser Thr Gln Ala Thr Leu Pro Glu Thr Gln Gln Thr Tyr
      100      105      110
Ala Pro Leu Ser Pro Asp Leu Phe Ser Ser His Ser His Lys Asp Arg
      115      120      125
Cys Pro Gln Cys Gln Gly Ser Gly Ile Phe Ile Ser Ile Asp Asp Pro
      130      135      140
Cys Ile Ile Gln Gln Thr Leu Ser Ile Glu Asp Asn Cys Cys Pro Phe
      145      150      155      160
Ala Gly Asn Cys Ser Thr Phe Leu Tyr Arg Thr Ile Tyr Gln Ser Leu
      165      170      175
Ala Asp Ser Leu Gly Phe Ser Leu Ser Thr Pro Trp Gln Asn Leu Ser
      180      185      190
Pro Glu Ile Gln His Ile Phe Leu Tyr Gly Lys Glu Gly Leu Ser Ile
      195      200      205
Pro Val Lys Leu Phe Asp Gly Thr Leu Gly Lys Lys Thr Gln Thr His
      210      215      220
Lys Gln Trp Lys Gly Val Leu Asn Glu Ile Gly Glu Lys Ile Arg Phe

```

225					230					235						240
Ser	Asn	Lys	Pro	Ala	Arg	Tyr	Leu	Pro	Lys	Gly	Thr	Ser	Tyr	Thr	Val	
				245					250						255	
Cys	Pro	Arg	Cys	Asn	Lys	Thr	Gly	Leu	Ser	Asp	Tyr	Ala	Asn	Ala	Thr	
			260					265						270		
Arg	Trp	His	Gly	Lys	Ser	Phe	Ala	Asp	Phe	Gln	Gln	Met	Ser	Leu	Gln	
		275					280					285				
Glu	Leu	Phe	Ile	Phe	Leu	Asn	Gln	Leu	Pro	Lys	Lys	Glu	Leu	Ala	Ile	
	290					295					300					
Glu	Glu	Val	Ile	Gln	Gly	Phe	Lys	Ser	Arg	Leu	Ala	Ile	Leu	Ile	Asp	
305					310					315					320	
Leu	Gly	Leu	Pro	Tyr	Leu	Ser	Pro	Glu	Arg	Ala	Ile	Asp	Thr	Leu	Ser	
				325					330					335		
Gly	Gly	Glu	Arg	Glu	Arg	Thr	Ala	Leu	Ala	Lys	His	Leu	Gly	Ala	Glu	
			340				345						350			
Leu	Ile	Gly	Val	Met	Tyr	Ile	Leu	Asp	Glu	Pro	Ser	Ile	Gly	Leu	His	
	355						360					365				
Pro	Gln	Asp	Thr	His	Lys	Leu	Met	Asn	Val	Ile	Arg	Arg	Leu	Arg	Asp	
	370					375					380					
Gln	Gly	Asn	Thr	Val	Leu	Leu	Val	Glu	His	Asp	Glu	Gln	Met	Ile	Ser	
385					390					395					400	
Leu	Ala	Asp	Arg	Val	Ile	Asp	Ile	Gly	Pro	Gly	Ala	Gly	Ile	Phe	Gly	
				405					410					415		
Gly	Glu	Val	Val	Phe	Asn	Gly	Ser	Pro	Arg	Glu	Phe	Leu	Ala	Lys	Ser	
			420					425					430			
Asp	Ser	Leu	Thr	Ala	Gln	Tyr	Leu	Arg	Gln	Glu	Gln	His	Ile	Ser	Val	
	435						440					445				
Pro	Ala	Lys	Arg	Thr	Asn	Ser	Leu	Gly	Thr	Ile	Thr	Leu	Ser	Lys	Ala	
	450					455					460					
Asn	Lys	His	Asn	Leu	Lys	Asp	Leu	Thr	Val	Ser	Ile	Pro	Leu	Gly	Gln	
465					470					475					480	
Met	Thr	Val	Val	Thr	Gly	Val	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Ile	
				485					490					495		
Asn	Asp	Thr	Leu	Val	Pro	Cys	Val	Glu	Glu	Phe	Ile	Glu	Gln	Gly	Phe	
			500					505					510			
Cys	Ser	Thr	Leu	Ser	Ile	Gln	Gly	Ala	Leu	Ser	Arg	Leu	Val	His	Ile	
		515					520					525				
Asn	Arg	Asp	Leu	Pro	Gly	Arg	Ser	Gln	Arg	Ser	Ile	Pro	Leu	Thr	Tyr	
	530					535					540					
Ile	Lys	Ala	Phe	Asp	Glu	Val	Arg	Gln	Leu	Phe	Ala	Glu	Gln	Pro	Arg	
545					550					555					560	
Cys	Lys	Thr	Leu	Gly	Leu	Thr	Lys	Ser								

Val	Lys	Gln	Leu	Ile	Tyr	Val	Val	Gln	Ser	Leu	Ile	His	Gln	Gly	His
705					710					715					720
Ser	Val	Ile	Ile	Ile	Glu	His	Asn	Met	His	Val	Val	Lys	Val	Ala	Asp
				725					730					735	
Tyr	Ile	Leu	Glu	Leu	Gly	Pro	Glu	Gly	Gly	Asn	Lys	Gly	Gly	Tyr	Leu
			740					745					750		
Ile	Ala	Ser	Cys	Ser	Pro	Glu	Glu	Leu	Ile	His	Lys	His	Thr	Pro	Thr
		755					760					765			
Ala	Ile	Ala	Leu	Arg	Pro	Phe	Leu	Ser	Ser	Pro	Gln	Glu	Leu	Pro	Tyr
	770					775					780				
Leu	Pro	Asp	Pro	Ser	Pro	Lys	Pro	Pro	Val	Pro	Ala	Ala	Ile	Thr	Ile
785					790					795					800
Ala	Asn	Ala	His	Gln	Tyr	Asn	Leu	Lys	His	Ile	Asp	Leu	Ser	Ile	Pro
				805					810					815	
Arg	Tyr	Ala	Leu	Thr	Ala	Val	Thr	Gly	Pro	Ser	Ala	Ser	Gly	Lys	His
			820					825					830		
Ser	Leu	Val	Phe	Asp	Ile	Leu	His	Ala	Ala	Gly	Asn	Ile	Ala	Tyr	Ala
		835					840					845			
Glu	Leu	Phe	Pro	Pro	Tyr	Ile	Arg	Gln	Ala	Leu	Ile	Lys	Lys	Thr	Pro
	850					855					860				
Leu	Pro	Ala	Val	Asp	Lys	Val	Thr	Gly	Leu	Ser	Pro	Val	Ile	Ala	Ile
865					870					875					880
Glu	Lys	Thr	Ser	Ala	Ser	Arg	Asn	Ser	Asn	His	Ser	Val	Ala	Ser	Ala
				885					890					895	
Leu	Glu	Ile	Ser	Glu	Met	Leu	Glu	Ser	Leu	Phe	Thr	Arg	Ile	Gly	His
			900					905					910		
Pro	Tyr	Ser	Pro	Ile	Ser	Gly	Asp	Ala	Leu	Arg	Thr	Ile	Ser	Pro	Glu
		915					920					925			
Thr	Ile	Ala	Glu	Glu	Leu	Leu	Thr	His	Tyr	Thr	Lys	Gly	Tyr	Val	Thr
		930				935					940				
Ile	Thr	Val	Pro	Phe	Pro	Lys	Glu	Glu	Glu	Phe	Phe	Ser	Tyr	Thr	Gln
945					950					955					960
Glu	Met	Leu	Gln	Glu	Gly	Phe	Leu	Lys	Leu	Tyr	Ala	Asn	Glu	Gln	Phe
				965					970					975	
Tyr	Asp	Leu	Asp	Gly	Pro	Phe	Pro	Thr	Ser	Leu	Glu	Asn	Pro	Ala	Leu
			980					985					990		
Val	Ile	His	Val	Lys	Ile	Leu	Glu	Lys	Asn	Leu	Pro	Ser	Leu	Leu	
		995				1000					1005				
Ala	Ser	Leu	Thr	Leu	Ala	Phe	Ser	Lys	Ala	Ser	Ser	Val	Cys	Leu	His
		1010				1015					1020				
Ile	Glu	Tyr	Ala	Gly	Thr	Ser	Leu	Ser	Lys	Thr	Tyr	Arg	Gln	Gly	Leu
1025					1030					1035					1040
Gln	Asp	Ala	Ser	Gly	Asn	Leu	Phe	Pro	Asn	Ile	Glu	Thr	Pro	Ser	Ile
				1045					1050					1055	
Leu	Asn	His	Glu	Ser	Tyr	Leu	Cys	Pro	Leu	Cys	His	Gly	Lys	Gly	Phe
			1060					1065					1070		
Leu	Ser	Thr	Cys	Ser	Ile	Leu	Pro	His	Lys	Lys	Arg	Phe	Ala	Gln	His
			1075				1080					1085			
Thr	Pro	Ile	Ser	Leu	Phe	Thr	Ser	Leu	Phe	Pro	Asn	Gln	Asp	Pro	Ser
		1090				1095					1100				
Pro	Ile	Tyr	Pro	Leu	Leu	Asn	Glu	Leu	Gly	Ile	Pro	Ser	Ile	Ala	Leu
1105					1110					1115					1120
Phe	Gln	Glu	Ile	Asp	Val	Leu	Ser	Phe	Glu	Ser	Leu	Cys	Leu	Gly	Thr
				1125					1130					1135	
Gln	Gln	His	Leu	Gly	Leu	Asn	Ala	Leu	Cys	Thr	Lys	Ala	Met	Leu	Met
			1140					1145					1150		
Glu	Ser	Glu	Glu	Asp	Phe	Pro	Pro	Asp	Leu	Ile	Ser	Lys	Thr	Pro	Cys
			1155				1160					1165			
Asn	Gln	Cys	Gln	Gly	Leu	Gly	Val	Tyr	Thr	Tyr	Lys	His	Cys	Ile	Arg

1170 1175 1180
 Ile His Ser Ile Ser Leu Ser Glu Ile Tyr Gln Ser Asn Val Ala Phe
 1185 1190 1195 1200
 Leu Lys Lys Leu Leu Leu Ser Val Glu Glu Glu Pro Ser Leu Val Gln
 1205 1210 1215
 Asp Ile Leu Ser Arg Leu Ala Phe
 1220

(2) INFORMATIONS POUR LA SEQ ID NO: 100:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 201 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(98113..98715)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 100:

Met Ser Ser Ile Val Arg Leu Ser Gly Ile Thr Val Arg Asn Leu Lys
 1 5 10 15
 Asn Ile Thr Val Glu Phe Cys Pro Arg Glu Ile Val Leu Phe Thr Gly
 20 25 30
 Val Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe Asn Thr Ile Tyr Ala
 35 40 45
 Ala Gly Arg Lys Arg Tyr Leu Ala Thr Leu Pro Ser Phe Phe Ala Thr
 50 55 60
 Lys Leu Asp Ser Leu Pro Asp Pro Ser Val Lys Lys Ile Glu Gly Leu
 65 70 75 80
 Ser Pro Thr Val Ala Val Lys Gln Asn Phe Phe Glu Gln His Val His
 85 90 95
 Ala Thr Val Gly Ser Thr Thr Glu Ile Asn Ser Tyr Leu Ala Leu Leu
 100 105 110
 Phe Ser Leu Glu Gly Gln Ala Tyr Asp Pro Val Thr Leu His Pro Leu
 115 120 125
 Thr Leu Tyr Ser Lys Glu Lys Ile Leu Ser Glu Ile Ala Ala Ile Pro
 130 135 140
 Asp Gly Thr Gln Leu Thr Leu Leu Ala Pro Leu Pro Ala Arg Met Phe
 145 150 155 160
 Leu Pro Phe Glu Asn Val Ser Val Lys Gly Leu Pro Lys Ser Ser Leu
 165 170 175
 Met Lys Arg Leu Phe Leu Phe Ile Ser Phe Leu Gln Gln Ala Phe Leu
 180 185 190
 Phe Pro Val Asn Ser Leu Ser Ile Arg
 195 200

(2) INFORMATIONS POUR LA SEQ ID NO: 101:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 496 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(98741..100228)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 101:

Ile	Phe	Tyr	Ser	Leu	Ile	Pro	Val	Ser	Arg	Phe	Met	Ile	Ala	Arg	Thr	1	5	10	15
Lys	Ile	Ile	Cys	Thr	Ile	Gly	Pro	Ala	Thr	Asn	Thr	Pro	Glu	Met	Leu	20	25	30	
Glu	Lys	Leu	Leu	Asp	Ala	Gly	Met	Asn	Val	Ala	Arg	Leu	Asn	Phe	Ser	35	40	45	
His	Gly	Thr	His	Glu	Ser	His	Gly	Arg	Thr	Ile	Ala	Ile	Leu	Lys	Glu	50	55	60	
Leu	Arg	Glu	Lys	Arg	Gln	Val	Pro	Leu	Ala	Ile	Met	Leu	Asp	Thr	Lys	65	70	75	80
Gly	Pro	Glu	Ile	Arg	Leu	Gly	Gln	Val	Glu	Ser	Pro	Ile	Lys	Val	Gln	85	90	95	
Pro	Gly	Asp	Arg	Leu	Thr	Leu	Val	Ser	Lys	Glu	Ile	Leu	Gly	Ser	Lys	100	105	110	
Glu	Ser	Gly	Val	Thr	Leu	Tyr	Pro	Ser	Cys	Val	Phe	Pro	Tyr	Val	Arg	115	120	125	
Glu	Arg	Ala	Pro	Val	Leu	Ile	Asp	Asp	Gly	Tyr	Ile	Gln	Ala	Val	Val	130	135	140	
Val	Asn	Ala	Gln	Glu	His	Met	Val	Glu	Ile	Glu	Phe	Gln	Asn	Ser	Gly	145	150	155	160
Glu	Ile	Lys	Ser	Asn	Lys	Ser	Leu	Ser	Ile	Lys	Asp	Ile	Asp	Val	Ala	165	170	175	
Leu	Pro	Phe	Met	Thr	Glu	Lys	Asp	Ile	Ala	Asp	Leu	Lys	Phe	Gly	Val	180	185	190	
Glu	Gln	Glu	Leu	Asp	Leu	Ile	Ala	Ala	Ser	Phe	Val	Arg	Cys	Asn	Glu	195	200	205	
Asp	Ile	Asp	Ser	Met	Arg	Lys	Val	Leu	Glu	Ser	Phe	Gly	Arg	Pro	Asn	210	215	220	
Met	Pro	Ile	Ile	Ala	Lys	Ile	Glu	Asn	His	Leu	Gly	Val	Gln	Asn	Phe	225	230	235	240
Gln	Glu	Ile	Ala	Arg	Ala	Ala	Asp	Gly	Ile	Met	Ile	Ala	Arg	Gly	Asp	245	250	255	
Leu	Gly	Ile	Glu	Leu	Ser	Ile	Val	Glu	Val	Pro	Gly	Leu	Gln	Lys	Phe	260	265	270	
Met	Ala	Arg	Ala	Ser	Arg	Glu	Thr	Gly	Arg	Phe	Cys	Ile	Thr	Ala	Thr	275	280	285	
Gln	Met	Leu	Glu	Ser	Met	Ile	Arg	Asn	Pro	Leu	Pro	Thr	Arg	Ala	Glu	290	295	300	
Val	Ser	Asp	Val	Ala	Asn	Ala	Ile	Tyr	Asp	Gly	Thr	Ser	Ala	Val	Met	305	310	315	320
Leu	Ser	Gly	Glu	Thr	Ala	Ser	Gly	Ala	His	Pro	Val	His	Ala	Val	Lys	325	330	335	
Thr	Met	Arg	Ser	Ile	Ile	Gln	Glu	Thr	Glu	Lys	Thr	Phe	Asp	Tyr	His	340	345	350	
Ala	Phe	Phe	Gln	Leu	Asn	Asp	Lys	Asn	Ser	Ala	Leu	Lys	Val	Ser	Pro	355	360	365	
Tyr	Leu	Glu	Ala	Ile	Gly	Phe	Ser	Gly	Ile	Gln	Ile	Ala	Glu	Lys	Ala	370	375	380	
Ser	Ala	Lys	Ala	Ile	Ile	Val	Tyr	Thr	Gln	Thr	Gly	Gly	Ser	Pro	Met	385	390	395	400
Phe	Leu	Ser	Lys	Tyr	Arg	Pro	Tyr	Leu	Pro	Ile	Ile	Ala	Val	Thr	Pro	405	410	415	
Asn	Arg	Asn	Val	Tyr	Tyr	Arg	Leu	Ala	Val	Glu	Trp	Gly	Val	Tyr	Pro				

```

          420          425          430
Met Leu Thr Leu Glu Ser Asn Arg Thr Val Trp Arg His Gln Ala Cys
          435          440          445
Val Tyr Gly Val Glu Lys Gly Ile Leu Ser Asn Tyr Asp Lys Ile Leu
          450          455          460
Val Phe Ser Arg Gly Ala Gly Met Gln Asp Thr Asn Asn Leu Thr Leu
465          470          475          480
Thr Thr Val His Asp Ala Leu Ser Pro Ser Leu Asp Glu Ile Val Pro
          485          490          495

```

(2) INFORMATIONS POUR LA SEQ ID NO: 102:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(100337..101347)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 102:

```

Lys Arg Pro Ile Arg Tyr His Gly Val Lys Ala His Phe Gln Asn Thr
1          5          10          15
Ser Leu Lys Lys Thr Ser Gly Asn Val Glu Leu Gln Thr Pro Ile Ser
          20          25          30
Phe Pro Gln His Ala Gly Asn Ile Leu Cys Arg Leu Gly Lys Lys Tyr
          35          40          45
Pro Gln Leu Gln Val Val Thr Pro Ala Met Ser Leu Gly Ser Cys Leu
          50          55          60
Glu Asp Phe Arg Lys Gln Phe Pro Asp Arg Phe Thr Asp Val Gly Ile
65          70          75          80
Ala Glu Gly His Ala Val Thr Phe Ser Ala Gly Ile Ala Arg Ser Gly
          85          90          95
Thr Pro Val Cys Cys Ser Ile Tyr Ser Thr Phe Leu His Arg Ala Met
          100          105          110
Asp Asn Val Phe His Asp Val Cys Met Gln Glu Leu Pro Val Ile Phe
          115          120          125
Ala Ile Asp Arg Ala Gly Leu Ala Phe His Asp Gly Arg Ser His His
          130          135          140
Gly Ile Tyr Asp Leu Gly Phe Leu Cys Ser Met Pro Asn Met Val Ile
145          150          155          160
Cys Gln Pro Arg Asn Ala Leu Val Leu Glu Arg Leu Phe Phe Ser Ser
          165          170          175
Leu Leu Trp Lys Ser Pro Cys Ala Ile Arg Tyr Pro Asn Ile Pro Ala
          180          185          190
Asn Glu Lys Ala Ser Asn Ser Ser Phe Pro Phe Ser Pro Ile Leu Pro
          195          200          205
Gly Glu Ala Glu Ile Leu Cys Gln Gly Asp Asp Leu Leu Leu Ile Ala
          210          215          220
Leu Gly His Met Cys Asn Thr Ala Leu Thr Val Lys Glu His Leu Leu
225          230          235          240
Asp Tyr Gly Ile Ser Thr Thr Val Val Asp Pro Ile Phe Ile Lys Pro
          245          250          255
Leu Asp Arg Lys Leu Leu Gln Ser Leu Leu Thr His His Ser Lys Val
          260          265          270

```

```

Ile Ile Leu Glu Glu His Ser Ile His Gly Gly Leu Gly Ser Glu Phe
      275                      280                      285
Leu Leu Phe Leu Asn Gln His Asn Ile Lys Ala Asp Val Leu Ser Leu
      290                      295                      300
Gly Val Pro Asp Met Xaa Ile Pro His Gly Asn Pro Glu Leu Phe Lys
      305                      310                      315                      320
Phe Asp Trp Thr His Gln Arg Ser His His Ser Thr Asn Pro Phe Ser
      325                      330                      335
Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 103:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 296 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(101323..102210)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 103:

```

Met Thr Tyr Ser Leu Leu Pro His Ile His Ser Pro Gln Asp Leu His
1      5      10      15
Ala Leu Ser Leu Asp Lys Leu Pro Val Leu Cys Asp Glu Ile Arg Asn
      20      25      30
Lys Ile Ile Glu Ser Leu Ser Leu Thr Gly Gly His Leu Ala Ser Asn
      35      40      45
Leu Gly Gly Val Glu Leu Thr Val Ala Leu His Tyr Val Phe Ser Ser
      50      55      60
Pro Asp Asp Gln Phe Ile Phe Asp Val Gly His Gln Ser Tyr Val His
      65      70      75      80
Lys Leu Leu Thr Gly Arg Asn Thr Glu Ala Phe Ser Asn Ile Arg His
      85      90      95
Asp Asn Gly Leu Ser Gly Phe Thr Thr Pro Gln Glu Ser Asn His Asp
      100     105     110
Ile Phe Phe Ser Gly His Ala Gly Asn Ala Leu Ser Leu Ala Leu Gly
      115     120     125
Leu Ala Lys Gly Ser Ser Asn Ser Ser Ser His Ile Leu Pro Ile Leu
      130     135     140
Gly Asp Ala Ala Phe Ser Cys Gly Leu Thr Leu Glu Ala Leu Asn Asn
      145     150     155     160
Ile Pro Ala Asp Leu Ser Lys Phe Ile Ile Val Leu Asn Asp Asn Gln
      165     170     175
Met Ser Ile Ser Glu Asn Val Gly Asn Ile Pro Gln Gly Ile Ser Gln
      180     185     190
Trp Ile Tyr Pro Gln Lys Ile Ser Lys Leu Ser Gln Lys Ile His Ser
      195     200     205
Trp Ile Gln Asn Leu Pro Ser Phe Leu His Lys Lys Lys Thr Leu Ser
      210     215     220
His Lys Val Asp Ile Ala Leu Lys Ser Leu Ser His Pro Leu Phe Glu
      225     230     235     240
Gln Phe Gly Leu His Tyr Val Gly Pro Ile Asp Gly His Asn Val Lys
      245     250     255
Lys Leu Val Gln Ala Leu Gln Met Ile Lys Asp Gln Pro Gln Pro Ile

```

(2) INFORMATION POUR LA SEQ ID NO: 104:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(102210..102485)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 104:

Pro	Val	Met	Gln	Glu	Ile	Ser	Val	Pro	Glu	Ala	Ser	His	Leu	Asp	Thr
1				5					10					15	
Val	Ile	Gln	Arg	Leu	Leu	Val	Leu	Gln	Lys	Ala	Leu	Glu	Asp	Cys	His
			20					25					30		
Ser	Val	Glu	Ala	Ile	Leu	Ala	Ile	Tyr	Glu	Glu	Met	Phe	Ser	Leu	Ile
		35					40					45			
Gln	Glu	Gly	Glu	Thr	Asn	Leu	Asn	His	Val	Glu	Gln	Leu	Ser	Phe	Gln
		50				55					60				
Leu	Gln	Leu	Asn	Pro	Asp	Gly	Ser	Val	Ala	Val	Asp	Thr	Ser	Gly	Asn
65					70					75					80
Pro	Ile	Lys	His	Pro	Phe	Ile	Pro	Gly	Glu	Ser	Val				
				85					90						

(2) INFORMATION POUR LA SEQ ID NO: 105:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 504 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(102726..104237)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 105:

Met	Ser	Ile	Thr	Ser	Pro	Pro	Ile	Glu	Val	Ser	Val	Leu	Thr	Asp	Ser
1				5					10					15	
Ile	Lys	Asn	Leu	Leu	Glu	Lys	Asn	Phe	Leu	Arg	Val	Val	Val	Lys	Gly
		20						25					30		
Glu	Leu	Ser	Asn	Val	Ser	Leu	Gln	Thr	Ser	Gly	His	Leu	Tyr	Phe	Ala
		35					40					45			
Ile	Lys	Asp	Ser	Lys	Ala	Val	Leu	Asn	Gly	Ala	Phe	Phe	His	Phe	Arg
	50					55					60				
Ser	Lys	Tyr	Phe	Asp	Arg	Lys	Pro	Lys	Asp	Gly	Asp	Tyr	Val	Ile	Leu
65				70					75						80

His Gly Lys Leu Thr Val Tyr Ala Pro Arg Gly Gln Tyr Gln Ile Val
 85 90 95
 Ala Tyr Ala Leu Thr Phe Ser Gly Glu Gly Asn Leu Leu Gln Gln Phe
 100 105 110
 Glu Glu Arg Lys Gln Arg Leu Ala Glu Gly Tyr Phe Asp Pro Lys
 115 120 125
 Arg Lys Lys Pro Leu Pro Ser Gly Ala Arg Val Ile Gly Val Ile Thr
 130 135 140
 Ser Pro Thr Gly Ala Val Ile Gln Asp Ile Leu Arg Val Leu Ser Arg
 145 150 155 160
 Arg Cys His Gln Phe Gln Val Ile Leu Tyr Pro Val Thr Val Gln Gly
 165 170 175
 Ala Thr Ala Ala Gln Glu Ile Ser Gln Ala Ile Gln Phe Phe Asn Gln
 180 185 190
 Asn Ser Met Arg Val His Ala Leu Ile Ile Ala Arg Gly Gly Gly Ser
 195 200 205
 Ile Glu Asp Leu Trp Ala Phe Asn Glu Glu Glu Leu Val Lys Ser Ile
 210 215 220
 Val Ala Ser Ser Ile Pro Ile Ile Ser Ala Val Gly His Glu Thr Asp
 225 230 235 240
 Phe Thr Leu Cys Asp Phe Ala Ser Asp Val Arg Ala Pro Thr Pro Ser
 245 250 255
 Ala Ala Ala Glu Ile Val Cys Lys Ser Ser Asp Gln Tyr Arg Gln Glu
 260 265 270
 Leu Gln Asn Leu Arg Arg Tyr Val Ser Ser His Ala Arg Gln Phe Ile
 275 280 285
 Ala Ala Lys Lys Asn Leu Leu Thr His Trp Gln Arg His Leu Ala Ser
 290 295 300
 Val Asp Phe Tyr His Thr Ala Gln Gln Thr Leu Asp Tyr Thr Arg Ala
 305 310 315 320
 Ala Leu Glu Arg Gly Ile Glu Thr Lys Leu Glu Tyr Tyr Lys Gln Arg
 325 330 335
 Phe Ala Gln Tyr Arg Arg Trp Leu Lys Ser Asp Val Leu Ile Arg Ile
 340 345 350
 Glu Lys His Leu Ala Asp Leu Asn Gln Ser Leu Met Leu Ser Ile Lys
 355 360 365
 Asn Lys Ile Tyr Thr Lys Lys Thr Ser Leu Asn Gln Leu Tyr Thr Ser
 370 375 380
 Cys Leu Lys Asn Glu Leu Leu Asn Leu Gln His Arg Thr Gln His Ser
 385 390 395 400
 Arg Asn Ile Leu Ser Gln Leu Ser Arg Arg Leu His Ile Ala Ile Ala
 405 410 415
 Ser Ser Gln Gln Thr His Gln Glu Cys Leu Val Arg Leu Gln Asn Glu
 420 425 430
 Leu Ser Phe Thr Ile Gln His Leu Leu Thr Lys Ala Lys Glu Arg Cys
 435 440 445
 Gln Ala Ile Gln Glu Gln Ala Ser Ser Leu Asn Pro Lys Asn Val Leu
 450 455 460
 Lys Arg Gly Phe Ala Gln Leu Phe Asp Phe Asn Lys His Phe Val Ile
 465 470 475 480
 Ile Ser Ala Glu Ser Leu Lys Gln Ser Asp Leu Val Arg Ser Ala Ser
 485 490 495
 Lys Thr Val Lys Gln Leu Tyr Gln
 500

(2) INFORMATIONS POUR LA SEQ ID NO: 106:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 252 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(104254..105009)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 106:

```

Pro Ser Lys Gln Phe Val Phe Gly Asn Trp Lys Met Asn Lys Thr Leu
1      5      10      15
Thr Glu Ala Gln Thr Phe Leu Lys Ser Phe Leu Ser Ser Asp Ile Leu
20      25      30
Ser Asn Pro Gln Ile Ile Thr Gly Ile Ile Pro Pro Phe Thr Leu Leu
35      40      45
Ser Ala Cys Gln Gln Ala Val Ser Asp Ser Pro Ile Phe Leu Gly Ala
50      55      60
Gln Thr Thr His Glu Ala Asp Ser Gly Ala Phe Thr Gly Glu Ile Ser
65      70      75      80
Ala Pro Met Leu Lys Asp Ile Gly Val Asp Phe Val Leu Ile Gly His
85      90      95
Ser Glu Arg Arg His Ile Phe His Glu Gln Asn Pro Val Leu Ala Glu
100      105      110
Lys Ala Ala Ala Ala Ile His Ser Gly Met Ile Pro Val Leu Cys Ile
115      120      125
Gly Glu Thr Leu Glu Glu Gln Glu Ser Gly Ala Thr Gln Asp Ile Leu
130      135      140
Leu Asn Gln Leu Thr Ile Gly Leu Ser Lys Leu Pro Glu Gln Ala Ser
145      150      155      160
Phe Ile Leu Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys Val
165      170      175
Ala His Pro Asp Leu Val Gln Glu Thr His Ala Phe Cys Arg Lys Thr
180      185      190
Ile Ala Ser Leu Phe Ser Lys Asp Ile Ala Glu Arg Thr Pro Ile Leu
195      200      205
Tyr Gly Gly Ser Val Lys Ala Asp Asn Ala Arg Ser Leu Ser Leu Cys
210      215      220
Pro Asp Val Asn Gly Leu Leu Val Gly Gly Ala Ser Leu Ser Ser Glu
225      230      235      240
Asn Phe Leu Ser Ile Ile Gln Gln Ile Asp Ile Pro
245      250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 107:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 212 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 105259..105894

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 107:

```

Pro Leu Cys Cys Met Lys Val Lys Ile Cys Gly Ile Thr His Pro Asp
1      5      10      15
Asp Ala Arg Glu Ala Ala Lys Ala Gly Ala Asp Tyr Ile Gly Met Ile
20      25      30
Phe Ala Lys Asp Ser Arg Arg Cys Val Ser Glu Glu Lys Ala Lys Tyr
35      40      45
Ile Val Glu Ala Ile Gln Glu Gly Asn Ser Glu Pro Val Gly Val Phe
50      55      60
Pro Glu His Ser Val Glu Glu Ile Leu Ala Ile Thr Glu Ala Thr Gly
65      70      75      80
Ile Thr Ser Ile Gln Leu Ser Gly Glu Asp Ile Leu Phe Lys Phe Ser
85      90      95
Gln Leu Arg Glu His Phe Ser Ile Phe Tyr Val Val Ser Val Tyr Ser
100     105     110
Asn Gly Gln Pro Ser Ala Ala Leu Pro Pro Met Asn Asp Ala Val Thr
115     120     125
Val Val Tyr Asp His Ile Gly Gly Glu Arg Gly Ser Pro Phe Asp Trp
130     135     140
Lys Ala Phe Ser Pro Phe Gln His Asn Asn Trp Met Leu Gly Gly Gly
145     150     155     160
Val Asn Leu Trp Asn Ile Lys Glu Gly Ile Ser Leu Leu Asn Pro Arg
165     170     175
Gly Ile Asp Val Ser Ser Gly Val Glu Arg Pro Gly Ile Leu Arg Lys
180     185     190
Asp Ile Phe Leu Met Gln Ala Leu Ile Asn Ser Ala Lys Glu Leu Ser
195     200     205
Ser Ser Thr Leu
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 108:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 344 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 107429..108460

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 108:

```

Arg Thr Arg Gly Gly Gly Leu Phe Ser Asn Phe Cys Ser Ser Pro Thr
1      5      10      15
Val Gln Ala Leu Leu Arg Ala Trp Asp Arg Phe Phe Ser Arg Val Ser
20      25      30
Asp Gly Arg Phe Leu Gln Ile Tyr Tyr Gly Asp Gly Gly Leu Phe Val
35      40      45
Glu Arg Ala Leu Gln Leu Ile Ser Cys Pro Leu Gln Arg Ala Arg Ile
50      55      60
Arg Val Val Gly Ile Asn Pro Ser Phe Phe Val Thr Val Ser Asp Asn
65      70      75      80
Arg His Phe Tyr Thr Ser Pro Gly Ser Cys Gly Arg Ile Leu Asp Met
85      90      95
Ser Gly Tyr Leu Ser Ala Arg Arg Asp Gly Cys Val Ser His Val Pro
100     105     110
Phe Ser Pro His Ser Gln Ser Ile Thr Pro Gly Val Gly Asp Ala Cys

```

115 120 125
 Phe Glu Leu Gly Leu Arg Met Glu Phe Met Arg Leu Ala Gly Leu Ser
 130 135 140
 Ser Leu Ser Ala Ala Ser Ser Pro Thr Ser Glu Asp Ser Asp Ser Ser
 145 150 155
 Arg Leu Gln Leu Val Arg Val Val Ser Ser Glu Asp Ser Val Ala Phe
 165 170 175
 Ala Arg Leu Tyr Ala Ala Leu Asn Glu Asp Ile Thr Ser Ser Val Arg
 180 185 190
 Ala Ala Asn Pro Phe Pro Phe Ser Tyr Val Arg Leu Ile Leu Leu Leu
 195 200 205
 Thr Thr Leu Cys Arg His Thr Leu Thr Thr Thr Lys Ala Ala Tyr Ser
 210 215 220
 Tyr Thr Pro Ala Ser Trp Glu Ala Leu Asp Met Leu Asp Ser Gly Phe
 225 230 235 240
 Thr Ala Ser Tyr Val Gly Gly Val Leu Ser Glu Ile Phe Leu Leu Cys
 245 250 255
 Thr His Ser Pro Arg Arg Ala Gln Arg Ser Arg Met Leu Arg Met Leu
 260 265 270
 Ala Lys Leu Phe Ser Ser Trp Ala Trp Leu Val Gly Val Met Glu Leu
 275 280 285
 Ser Cys Gly Tyr Gly Val Thr Ile Gln Leu Leu Leu Gln Asn Asp Pro
 290 295 300
 Arg Gln Ser Cys Leu Arg Asn Leu Phe Phe Trp Met Glu Ser Thr Leu
 305 310 315 320
 Thr Pro Val Ile Leu Asp Ile Ala Glu Arg Ile Gly Leu Pro Tyr
 325 330 335
 Gly Ile Glu Leu Leu Asp Trp Ala
 340

(2) INFORMATIONS POUR LA SEQ ID NO: 109:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 108665..108955

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 109:

Leu Lys Ile Ala Arg Asp Met Ser Arg Ser Ser Leu Gln Gln Tyr Leu
 1 5 10 15
 Tyr Thr Lys Ser Thr Val Ile Ala Asn Ser Thr Thr Pro Ser Leu Asn
 20 25 30
 Asn Thr Ser Thr Cys Ser Gly Asn Ser Thr Thr Arg Pro Val Leu Pro
 35 40 45
 Ser Ile Thr Gly Ile Tyr Glu Thr Asp Val Gln Thr Thr Gly Val Ala
 50 55 60
 Arg Thr Leu Asn Val Ile Arg Met Ile Trp Cys Gly Val Met Leu Leu
 65 70 75 80
 Tyr Phe Leu Tyr Thr Ala Phe Arg Leu Val Arg Asn Ala Arg Arg Arg
 85 90 95
 Asn

(2) INFORMATIONS POUR LA SEQ ID NO: 110:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 149 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(109013..109459)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 110:

```

Thr Met Ile Leu Thr Thr Pro Ser Glu His Lys Ala Cys Leu Glu Lys
1           5           10           15
Gln Glu Lys Ala Val Ala Leu Leu Phe Pro Glu Asn Phe Val Lys Asp
          20           25           30
Thr Phe Tyr Lys Gln Leu Leu Gln Ile Gly Arg Thr Ala Lys Pro Phe
          35           40           45
Pro Lys Glu Phe Leu Thr Lys Glu Asn Leu Val Leu Gly Cys Gln Ser
          50           55           60
Asp Leu Tyr Leu His Gly Glu Phe Lys Asn Asn Ala Val Phe Phe Phe
65           70           75           80
Thr Tyr Thr Glu Ala Leu Ile Ser Ser Gly Val Ala Val Leu Phe Ser
          85           90           95
Asp Ile Tyr Ser Gly Glu Thr Pro Glu Thr Ile Leu Thr Cys Lys Pro
          100          105          110
Leu Phe Phe Glu Lys Leu Ser Arg His Leu Ser Met Gly Arg Ser Arg
          115          120          125
Gly Gly Glu Ser Leu Phe Leu Asn Met Gln Arg Ile Ala Val Gln Tyr
          130          135          140
Leu Ala Arg Lys Thr
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 111:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 221 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(109704..110366)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 111:

```

Ala Met Val Lys Ala Ala His Pro Leu His Ser Ser Ile Ser Gly Ala
1           5           10           15
Leu Pro Leu His Ser Ser Arg Gly Gly Ala Tyr His Asp Ser Leu Gly
          20           25           30
Asp Leu His Ser Pro Ile Ser Leu Thr Pro Pro Ala Leu Ser Val Leu
          35           40           45
Thr Pro Glu Pro Ala Gln Ser Lys Ser Arg Val Gln Ala Val Ala Asn

```

```

      50      55      60
Thr Ile Gly Asp Phe Leu Gln Arg Asn Trp Lys His Leu Leu Leu Tyr
65      70      75      80
Ile Leu Ala Trp Ser Leu Ile Leu Ile Cys His Ser Ser Val Ala Leu
      85      90      95
Val Leu Ser Ile Trp Leu Gly Ile Gly Phe Gly Ala Gly Val Val Leu
      100      105      110
Gly Ile Ile Ser Ala Asn Phe Leu Asp Lys Glu Asn Lys Tyr Pro His
      115      120      125
Leu Asn Ser Leu Trp Asn Ile Thr Asn His Gly Leu Gln Gln Leu Asp
      130      135      140
Pro Asn Gly Thr Arg Gln Val Leu Leu Ala Thr Val Ile Ala Ser Ile
145      150      155      160
Ser Ala Leu Ile Tyr Ala Ser Pro Gln Ala Ile Gly Phe Ile Ile Gly
      165      170      175
Ala Phe Leu Gly His Gln Thr Ser Ser Leu Ala Val Tyr Gly Tyr Arg
      180      185      190
Phe Lys Ser Gly Gln Asp Ile Leu Gln Ile Arg Asn Cys Leu Ile Asn
      195      200      205
Lys Lys Asn Glu Phe Asp Lys Pro Ser Cys Ser Val Gly
      210      215      220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 112:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 392 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 111345..112520

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 112:

```

Met Ser Lys Glu Thr Phe Gln Arg Asn Lys Pro His Ile Asn Ile Gly
1      5      10      15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
      20      25      30
Thr Arg Thr Leu Ser Gly Asp Gly Leu Ala Asp Phe Arg Asp Tyr Ser
      35      40      45
Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
      50      55      60
Ala Ser His Val Glu Tyr Glu Thr Ala Asn Arg His Tyr Ala His Val
65      70      75      80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
      85      90      95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala
      100      105      110
Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val
      115      120      125
Pro Tyr Ile Val Val Phe Leu Asn Lys Ile Asp Met Ile Ser Glu Glu
      130      135      140
Asp Ala Glu Leu Val Asp Leu Val Glu Met Glu Leu Ala Glu Leu Leu
145      150      155      160
Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu
      165      170      175

```

Lys Ala Leu Glu Gly Asp Ala Ala Tyr Ile Glu Lys Val Arg Glu Leu
 180 185 190
 Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp
 195 200 205
 Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
 210 215 220
 Gly Thr Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser Asp
 225 230 235 240
 Lys Val Gln Leu Val Gly Arg Asp Thr Lys Glu Thr Ile Val Thr Gly
 245 250 255
 Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly Glu Asn
 260 265 270
 Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu Arg Gly
 275 280 285
 Met Val Val Cys Leu Pro Asn Ser Val Lys Pro His Thr Arg Phe Lys
 290 295 300
 Cys Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His Lys Pro
 305 310 315 320
 Phe Phe Thr Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr Asp Val
 325 330 335
 Thr Gly Val Val Thr Leu Pro Glu Gly Val Glu Met Val Met Pro Gly
 340 345 350
 Asp Asn Val Glu Phe Glu Val Gln Leu Ile Ser Pro Val Ala Leu Glu
 355 360 365
 Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile Gly Ala
 370 375 380
 Gly Thr Ile Ser Lys Ile Ile Ala
 385 390

(2) INFORMATIONS POUR LA SEQ ID NO: 113:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 112915..113463

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 113:

Phe Met Phe Lys Trp Tyr Val Val Gln Val Phe Thr Ala Gln Glu Lys
 1 5 10 15
 Lys Val Lys Lys Ser Leu Glu Asp Phe Lys Glu Ala Ser Gly Met Ser
 20 25 30
 Asp Phe Ile Gln Gln Ile Ile Leu Pro Ser Glu Asn Val Met Glu Val
 35 40 45
 Lys Lys Gly Glu His Lys Ile Val Glu Lys Tyr Ile Trp Pro Gly Tyr
 50 55 60
 Leu Leu Val Lys Met His Leu Thr Asp Glu Ser Trp Ser Tyr Val Lys
 65 70 75 80
 Lys Thr Gln Gly Val Val Glu Phe Leu Gly Gly Gly Ala Pro Val Ala
 85 90 95
 Leu Ser Glu Glu Glu Ile Lys Asn Ile Leu Ala Asp Leu Glu Glu Lys
 100 105 110
 Lys Ser Gly Val Val Gln Lys His Lys Phe Glu Val Gly Ser Gln Val

```

          115          120          125
Lys Ile Asn Asp Gly Val Phe Val Asn Phe Val Gly Val Val Ser Glu
      130          135          140
Val Phe His Asp Lys Gly Arg Leu Ser Val Met Val Ser Ile Phe Gly
145          150          155          160
Arg Glu Thr Arg Val Asp Asp Leu Glu Phe Trp Gln Val Glu Glu Val
          165          170          175
Val Pro Gly Gln Glu Ser Glu
          180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 114:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 141 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 113572..113994

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 114:

```

Met Ser Asn Lys Lys Ile Ile Lys Ile Ile Lys Leu Gln Ile Pro Gly
1          5          10          15
Gly Lys Ala Asn Pro Ala Pro Pro Ile Gly Pro Ala Leu Gly Ala Ala
      20          25          30
Gly Val Asn Ile Met Gly Phe Cys Lys Glu Phe Asn Ala Ala Thr Gln
      35          40          45
Asp Arg Pro Gly Asp Leu Leu Pro Val Val Ile Thr Val Tyr Ser Asp
      50          55          60
Lys Thr Xaa Ser Phe Val Met Lys Gln Ser Pro Val Ser Ser Leu Ile
      65          70          75          80
Lys Lys Ala Leu Gly Leu Glu Ser Gly Ser Lys Ile Pro Asn Arg Asn
      85          90          95
Lys Val Gly Lys Leu Thr Arg Ala Gln Ile Thr Ala Ile Ala Glu Gln
      100          105          110
Lys Met Lys Asp Met Asp Val Val Leu Leu Glu Ser Ala Glu Arg Met
      115          120          125
Val Glu Gly Thr Ala Arg Ser Met Gly Val Asp Val Glu
      130          135          140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 115:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 195 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 114020..114604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 115:

```

Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
1      5      10      15
Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
20      25      30
Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
35      40      45
Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
50      55      60
Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
65      70      75      80
Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
85      90      95
Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
100     105     110
Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
115     120     125
Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
130     135     140
Val Thr Thr Asp Val Val Lys Thr Ile Ala Glu Leu Arg Lys Gly Lys
145     150     155     160
Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
165     170     175
Asn Phe Leu Ser Ile Val Arg Lys Ser Lys Lys Met Leu Lys Arg Cys
180     185     190
Val Gln Pro
195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 116:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 178 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 114720..115253

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 116:

```

Leu Ser Leu Lys Arg Lys Asn Glu Arg Arg Glu Lys Val Ala Leu Arg
1      5      10      15
Glu Val Glu Glu Lys Ile Thr Ala Ser Gln Gly Phe Ile Leu Leu Arg
20      25      30
Tyr Leu Gly Phe Thr Ala Thr His Ser Arg Ser Phe Arg Asn Asn Leu
35      40      45
Ser Gly Val Ser Ala Glu Phe Glu Val Leu Lys Lys Lys Ile Phe Phe
50      55      60
Lys Ala Leu Glu Thr Ser Gly Val Glu Met Asp Pro Glu Asp Ser Glu
65      70      75      80
Gly His Leu Gly Val Val Phe Ala Tyr Gly Asp Pro Val Ser Ala Ala
85      90      95
Lys Gln Val Leu Asp Phe Asn Lys Gln His Asn Asp Ser Leu Val Phe
100     105     110
Leu Ala Gly Arg Ile Asp Asn Ala Ser Leu Ser Gly Arg Glu Val Glu
115     120     125
Ala Val Ala Lys Leu Pro Ser Met Lys Glu Leu Arg Gln Gln Val Val

```

```

      130              135              140
Gly Leu Ile Ala Ala Pro Met Ser Gln Val Val Gly Ile Met Asn Ser
145              150              155              160
Val Leu Ser Gly Val Val Ser Cys Val Asp Gln Lys Ala Glu Lys Thr
      165              170              175
Gln Glu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 117:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 115362..115676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 117:

```

Lys Ile Ile Gly Arg Lys Val Gly Arg Tyr Ala Ala Ala Pro Val Val
1      5      10      15
Ala Val Ala Gly Ala Ala Ala Ala Gly Asp Ala Pro Ala Ser Ala Glu
      20      25      30
Pro Thr Glu Phe Ala Val Ile Leu Glu Asp Val Pro Ser Asp Lys Lys
      35      40      45
Ile Gly Val Leu Lys Val Val Arg Glu Val Thr Gly Leu Ala Leu Lys
      50      55      60
Glu Ala Lys Glu Met Thr Glu Gly Leu Pro Lys Thr Val Lys Glu Lys
      65      70      75      80
Thr Ser Lys Ser Asp Ala Glu Asp Thr Val Lys Lys Leu Gln Glu Ala
      85      90      95
Gly Ala Lys Ala Val Ala Lys Gly Leu
      100      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 118:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1258 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 116022..119795

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 118:

```

Ser Leu Arg Arg Ala Arg Met Phe Lys Cys Pro Glu Arg Val Ser Val
1      5      10      15
Lys Lys Lys Glu Asp Ile Leu Asp Leu Pro Asn Leu Val Glu Val Gln
      20      25      30
Ile Lys Ser Tyr Lys Gln Phe Leu Gln Ile Gly Lys Leu Ala Glu Glu
      35      40      45

```

Arg	Glu	Asn	Ile	Gly	Leu	Glu	Glu	Val	Phe	Arg	Glu	Ile	Phe	Pro	Ile
50						55					60				
Lys	Ser	Tyr	Asn	Glu	Ala	Thr	Ile	Leu	Glu	Tyr	Leu	Ser	Tyr	Asn	Leu
65					70					75					80
Gly	Val	Pro	Lys	Tyr	Ser	Pro	Glu	Glu	Cys	Ile	Arg	Arg	Gly	Ile	Thr
				85					90					95	
Tyr	Ser	Val	Thr	Leu	Lys	Val	Arg	Phe	Arg	Leu	Thr	Asp	Glu	Thr	Gly
			100					105					110		
Ile	Lys	Glu	Glu	Glu	Val	Tyr	Met	Gly	Thr	Ile	Pro	Ile	Met	Thr	Asp
			115					120					125		
Lys	Gly	Thr	Phe	Ile	Ile	Asn	Gly	Ala	Glu	Arg	Val	Val	Val	Ser	Gln
			130				135					140			
Val	His	Arg	Ser	Pro	Gly	Ile	Asn	Phe	Glu	Gln	Glu	Lys	His	Ser	Lys
145						150				155					160
Gly	Asn	Val	Leu	Phe	Ser	Phe	Arg	Ile	Ile	Pro	Tyr	Arg	Gly	Ser	Trp
				165					170					175	
Leu	Glu	Ala	Val	Phe	Asp	Ile	Asn	Asp	Leu	Ile	Tyr	Ile	His	Ile	Asp
			180					185					190		
Arg	Lys	Lys	Arg	Arg	Arg	Lys	Ile	Leu	Ala	Met	Thr	Phe	Ile	Arg	Ala
			195					200					205		
Leu	Gly	Tyr	Ser	Thr	Asp	Ala	Asp	Ile	Ile	Glu	Glu	Phe	Phe	Ser	Val
			210				215				220				
Glu	Glu	Arg	Ser	Leu	Arg	Ser	Glu	Lys	Asp	Phe	Val	Ala	Leu	Val	Gly
225						230				235					240
Lys	Val	Leu	Ala	Asp	Asn	Val	Val	Asp	Ala	Asp	Ser	Ser	Leu	Val	Tyr
				245					250					255	
Gly	Lys	Ala	Gly	Glu	Lys	Leu	Ser	Thr	Ala	Met	Leu	Lys	Arg	Ile	Leu
			260					265					270		
Asp	Thr	Gly	Val	Gln	Ser	Leu	Lys	Ile	Ala	Val	Gly	Ala	Asp	Glu	Asn
			275					280					285		
His	Pro	Ile	Ile	Lys	Met	Leu	Ala	Lys	Asp	Pro	Thr	Asp	Ser	Tyr	Glu
			290				295				300				
Ala	Ala	Leu	Lys	Asp	Phe	Tyr	Arg	Arg	Leu	Arg	Pro	Gly	Glu	Pro	Ala
305					310					315					320
Thr	Leu	Ala	Asn	Ala	Arg	Ser	Thr	Ile	Met	Arg	Leu	Phe	Phe	Asp	Ala
				325					330					335	
Lys	Arg	Tyr	Asn	Leu	Gly	Arg	Val	Gly	Arg	Tyr	Lys	Leu	Asn	Lys	Lys
			340					345					350		
Leu	Gly	Phe	Pro	Leu	Asp	Asp	Glu	Thr	Leu	Ser	Gln	Val	Thr	Leu	Arg
			355				360					365			
Lys	Glu	Asp	Val	Ile	Gly	Ala	Leu	Lys	Tyr	Leu	Ile	Arg	Leu	Arg	Met
			370				375				380				
Gly	Asp	Glu	Lys	Thr	Ser	Ile	Asp	Asp	Ile	Asp	His	Leu	Ala	Asn	Arg
385						390				395					400
Arg	Val	Arg	Ser	Val	Gly	Glu	Leu	Ile	Gln	Asn	His	Cys	Arg	Ser	Gly
				405					410					415	
Leu	Ala	Arg	Met	Glu	Lys	Ile	Val	Arg	Glu	Arg	Met	Asn	Leu	Phe	Asp
			420					425					430		
Phe	Ser	Ser	Asp	Thr	Leu	Thr	Pro	Gly	Lys	Ile	Ile	Ser	Ala	Lys	Gly
			435				440					445			
Leu	Val	Ser	Val	Leu	Lys	Asp	Phe	Phe	Ser	Arg	Ser	Gln	Leu	Ser	Gln
			450				455				460				
Phe	Met	Asp	Gln	Thr	Asn	Pro	Val	Ala	Glu	Leu	Thr	His	Lys	Arg	Arg
465						470				475					480
Leu	Ser	Ala	Leu	Gly	Pro	Gly	Gly	Leu	Asn	Arg	Glu	Arg	Ala	Gly	Phe
				485					490					495	
Glu	Val	Arg	Asp	Val	His	Ala	Ser	His	Tyr	Gly	Arg	Ile	Cys	Pro	Ile
				500				505					510		
Glu	Thr	Pro	Glu	Gly	Pro	Asn	Ile	Gly	Leu	Ile	Thr	Ser	Leu	Ser	Ser

515 520 525
 Phe Ala Lys Ile Asn Glu Phe Gly Phe Ile Glu Thr Pro Tyr Arg Val
 530 535 540
 Val Arg Asp Gly Ile Val Thr Asp Glu Ile Glu Tyr Met Thr Ala Asp
 545 550 555 560
 Val Glu Glu Glu Cys Val Ile Ala Gln Ala Ser Ala Glu Leu Asp Glu
 565 570 575
 Tyr Asn Met Phe Lys Thr Pro Val Cys Trp Ala Arg Tyr Lys Gly Glu
 580 585 590
 Ala Phe Glu Ala Asp Thr Ser Thr Val Thr His Met Asp Val Ser Pro
 595 600 605
 Lys Gln Leu Val Ser Val Val Thr Gly Leu Ile Pro Phe Leu Glu His
 610 615 620
 Asp Asp Ala Asn Arg Ala Leu Met Gly Ser Asn Met Gln Arg Gln Ala
 625 630 635 640
 Val Pro Leu Leu Lys Thr Glu Ala Ala Ile Val Gly Thr Gly Leu Glu
 645 650 655
 Gly Arg Ala Ala Lys Asp Ser Gly Ala Ile Ile Val Ala Gln Glu Asp
 660 665 670
 Gly Val Val Glu Tyr Val Asp Ser Tyr Glu Ile Val Val Ala Lys Lys
 675 680 685
 Asn Asn Pro Thr Leu Lys Asp Arg Tyr Gln Leu Lys Lys Phe Leu Arg
 690 695 700
 Ser Asn Ser Gly Thr Cys Ile Asn Gln Thr Pro Leu Cys Ser Val Gly
 705 710 715 720
 Asp Val Val Thr His Gly Asp Val Leu Ala Asp Gly Pro Ala Thr Asp
 725 730 735
 Lys Gly Glu Leu Ala Leu Gly Lys Asn Val Leu Val Ala Phe Met Pro
 740 745 750
 Trp Tyr Gly Tyr Asn Phe Glu Asp Ala Ile Ile Ile Ser Glu Arg Leu
 755 760 765
 Ile Lys Gln Asp Ala Tyr Thr Ser Ile Tyr Ile Glu Glu Phe Glu Leu
 770 775 780
 Thr Ala Arg Asp Thr Lys Leu Gly Lys Glu Glu Ile Thr Arg Asp Ile
 785 790 795 800
 Pro Asn Val Ser Glu Glu Val Leu Ala Asn Leu Gly Glu Asp Gly Ile
 805 810 815
 Val Arg Ile Gly Ala Glu Val Lys Pro Gly Asp Ile Leu Val Gly Lys
 820 825 830
 Ile Thr Pro Lys Ser Glu Thr Glu Leu Ala Pro Glu Glu Arg Leu Leu
 835 840 845
 Arg Ala Ile Phe Gly Glu Lys Ala Ala Asp Val Lys Asp Ala Ser Leu
 850 855 860
 Thr Val Pro Pro Gly Thr Glu Gly Val Val Met Asp Val Lys Val Phe
 865 870 875 880
 Ser Arg Lys Asp Arg Leu Ser Lys Ser Asp Asp Glu Leu Val Glu Glu
 885 890 895
 Ala Val His Leu Lys Asp Leu Gln Lys Glu Tyr Lys Ser Gln Leu Ala
 900 905 910
 Gln Leu Lys Val Glu His Arg Glu Lys Leu Gly Ala Leu Leu Leu Asn
 915 920 925
 Glu Lys Ala Pro Ala Ala Ile Val His Arg Arg Ser Ala Asp Ile Leu
 930 935 940
 Val Gln Glu Gly Ala Ile Phe Asp Gln Glu Thr Ile Glu Leu Leu Glu
 945 950 955 960
 Arg Glu Ser Leu Val Asp Leu Leu Ile Ala Pro Cys Asp Met Tyr Asp
 965 970 975
 Val Leu Lys Asp Ile Leu Ser Ser Tyr Glu Thr Ala Val Gln Arg Leu
 980 985 990

Glu Val Asn Tyr Lys Thr Glu Ala Glu His Ile Lys Glu Gly Asp Ala
 995 1000 1005
 Asp Leu Asp His Gly Val Ile Arg Gln Val Lys Val Tyr Val Ala Ser
 1010 1015 1020
 Lys Arg Lys Leu Gln Val Gly Asp Lys Met Ala Gly Arg His Gly Asn
 1025 1030 1035 1040
 Lys Gly Val Val Ser Lys Ile Val Pro Glu Ala Asp Met Pro Phe Leu
 1045 1050 1055
 Ala Asn Gly Glu Thr Val Gln Met Ile Leu Asn Pro Leu Gly Val Pro
 1060 1065 1070
 Ser Arg Met Asn Leu Gly Gln Val Leu Glu Thr His Leu Gly Tyr Ala
 1075 1080 1085
 Ala Lys Thr Ala Gly Ile Tyr Val Lys Thr Pro Val Phe Glu Gly Phe
 1090 1095 1100
 Pro Glu Ser Arg Ile Trp Asp Met Met Ile Glu Gln Gly Leu Pro Glu
 1105 1110 1115 1120
 Asp Gly Lys Ser Tyr Leu Phe Asp Gly Lys Thr Gly Glu Arg Phe Asp
 1125 1130 1135
 Ser Lys Val Val Val Gly Tyr Ile Tyr Met Leu Lys Leu Ser His Leu
 1140 1145 1150
 Ile Ala Asp Lys Ile His Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val
 1155 1160 1165
 Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Met Gly Gly Gln Arg Phe
 1170 1175 1180
 Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Val Ala His Met
 1185 1190 1195 1200
 Leu Gln Glu Ile Leu Thr Val Lys Ser Asp Asp Val Ser Gly Arg Thr
 1205 1210 1215
 Arg Ile Tyr Glu Ser Ile Val Lys Gly Glu Asn Leu Leu Arg Ser Gly
 1220 1225 1230
 Thr Pro Glu Ser Phe Asn Val Leu Ile Lys Glu Met Gln Gly Leu Gly
 1235 1240 1245
 Leu Asp Val Arg Pro Met Val Val Asp Ala
 1250 1255

(2) INFORMATIONS POUR LA SEQ ID NO: 119:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 1396 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 119823..124010

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 119:

Met Phe Arg Glu Gly Ser Arg Asp Asp Ala Ala Leu Val Lys Glu Gly
 1 5 10 15
 Leu Phe Asp Lys Leu Glu Ile Gly Ile Ala Ser Asp Val Thr Ile Arg
 20 25 30
 Asp Lys Trp Ser Cys Gly Glu Ile Lys Lys Pro Glu Thr Ile Asn Tyr
 35 40 45
 Arg Thr Phe Lys Pro Glu Lys Gly Gly Leu Phe Cys Glu Lys Ile Phe
 50 55 60
 Gly Pro Thr Lys Asp Trp Glu Cys Tyr Cys Gly Lys Tyr Lys Lys Ile

65
 Lys His Lys Gly Ile Val Cys Asp Arg Cys Gly Val Glu Val Thr Leu
 85 90 95
 Ser Lys Val Arg Arg Glu Arg Met Ala His Ile Glu Leu Ala Val Pro
 100 105 110
 Ile Val His Ile Trp Phe Phe Lys Thr Thr Pro Ser Arg Ile Gly Asn
 115 120 125
 Val Leu Gly Met Thr Ala Ser Asp Leu Glu Arg Val Ile Tyr Tyr Glu
 130 135 140
 Glu Tyr Val Val Ile Asp Pro Gly Asn Thr Asp Leu Val Lys Lys Gln
 145 150 155 160
 Leu Leu Asn Asp Ala Lys Tyr Arg Glu Val Val Glu Lys Trp Gly Lys
 165 170 175
 Asp Ala Phe Val Ala Lys Met Gly Gly Glu Ala Val Tyr Asp Leu Leu
 180 185 190
 Lys Ser Glu Asp Leu Glu Ser Leu Leu Gly Glu Leu Lys Asp Arg Leu
 195 200 205
 Arg Lys Thr Lys Ser Gln Gln Ala Arg Met Lys Leu Ala Lys Arg Leu
 210 215 220
 Lys Ile Val Glu Gly Phe Val Ser Ser Ser Asn Arg Pro Glu Trp Met
 225 230 235 240
 Val Leu Lys Asn Ile Pro Val Val Pro Pro Asp Leu Arg Pro Leu Val
 245 250 255
 Pro Leu Asp Gly Gly Arg Phe Ala Thr Ser Asp Leu Asn Asp Leu Tyr
 260 265 270
 Arg Arg Val Ile Asn Arg Asn Asn Arg Leu Lys Ala Ile Leu Arg Leu
 275 280 285
 Lys Thr Pro Glu Val Ile Val Arg Asn Glu Lys Arg Met Leu Gln Glu
 290 295 300
 Ala Val Asp Ala Leu Phe Asp Asn Gly Arg His Gly His Pro Val Met
 305 310 315 320
 Gly Ala Gly Asn Arg Pro Leu Lys Ser Leu Ser Glu Met Leu Lys Gly
 325 330 335
 Lys Asn Gly Arg Phe Arg Gln Asn Leu Leu Gly Lys Arg Val Asp Tyr
 340 345 350
 Ser Gly Arg Ser Val Ile Ile Val Gly Pro Glu Leu Lys Phe Asn Gln
 355 360 365
 Cys Gly Leu Pro Lys Glu Met Ala Leu Glu Leu Phe Glu Pro Phe Ile
 370 375 380
 Ile Lys Arg Leu Lys Asp Gln Gly Ser Val Tyr Thr Ile Arg Ser Ala
 385 390 395 400
 Lys Lys Met Ile Gln Arg Gly Ala Pro Glu Val Trp Asp Val Leu Glu
 405 410 415
 Glu Ile Ile Lys Gly His Pro Val Leu Leu Asn Arg Ala Pro Thr Leu
 420 425 430
 His Arg Leu Gly Ile Gln Ala Phe Glu Pro Val Leu Ile Glu Gly Lys
 435 440 445
 Ala Ile Arg Val His Pro Leu Val Cys Ala Ala Phe Asn Ala Asp Phe
 450 455 460
 Asp Gly Asp Gln Met Ala Val His Val Pro Leu Ser Ile Glu Ala Gln
 465 470 475 480
 Leu Glu Ala Lys Val Leu Met Met Ala Pro Asp Asn Ile Phe Leu Pro
 485 490 495
 Ser Ser Gly Lys Pro Val Ala Thr Pro Ser Lys Asp Met Thr Leu Gly
 500 505 510
 Ile Tyr Tyr Leu Met Ala Asp Pro Thr Tyr Phe Pro Glu Glu His Gly
 515 520 525
 Gly Lys Thr Lys Ala Phe Lys Asp Glu Val Glu Val Leu Arg Ala Leu
 530 535 540

Asn Ala Gly Gly Phe Ile Leu Lys Asp Glu Ile Cys Gly Ser Arg Arg
 545 550 555 560
 Asp Glu Thr Gly Arg Gly Ile His Ile His Glu Lys Ile Lys Val Arg
 565 570 575
 Ile Asp Gly Gln Ile Ile Glu Thr Thr Pro Gly Arg Val Phe Phe Asn
 580 585 590
 Thr Ile Val Pro Lys Glu Leu Gly Phe Gln Asn Tyr Ser Met Pro Ser
 595 600 605
 Lys Arg Ile Ser Glu Leu Ile Leu Gln Cys Tyr Lys Lys Val Gly Leu
 610 615 620
 Glu Ala Thr Val Arg Phe Leu Asp Asp Leu Lys Glu Leu Gly Phe Val
 625 630 635 640
 Gln Ser Thr Lys Ala Ala Ile Ser Met Gly Leu Lys Asp Val Lys Ile
 645 650 655
 Pro Glu Ile Lys Lys Glu Ile Leu Lys Asp Ala Tyr Asp Lys Val Ala
 660 665 670
 Ile Val Lys Lys Gln Tyr Glu Asp Gly Ile Ile Thr Asp Gly Glu Arg
 675 680 685
 His Ser Lys Thr Ile Ser Ile Trp Thr Glu Val Ser Asp Leu Leu Ser
 690 695 700
 Asn Ala Leu Tyr Ser Glu Ile Lys Lys Gln Thr Asn Ser Lys His Asn
 705 710 715 720
 Pro Leu Phe Leu Met Val Xaa Ser Gly Ala Arg Gly Asn Lys Ser Gln
 725 730 735
 Leu Lys Gln Leu Gly Ala Leu Arg Gly Leu Met Ala Lys Pro Asn Gly
 740 745 750
 Ala Ile Ile Glu Ser Pro Ile Thr Ser Asn Phe Arg Glu Gly Leu Thr
 755 760 765
 Val Leu Glu Tyr Ser Ile Ser Ser His Gly Ala Arg Lys Gly Leu Ala
 770 775 780
 Asp Thr Ala His Lys Thr Ala Asp Ser Gly Tyr Leu Thr Arg Arg Leu
 785 790 795 800
 Val Asp Val Ala Gln Asp Val Ile Ile Thr Glu Arg Asp Cys Gly Thr
 805 810 815
 Leu Asn His Ile Glu Val Ser Thr Ile Arg Gln Gly Ser Glu Glu Leu
 820 825 830
 Leu Pro Leu Lys Asp Arg Val Tyr Gly Arg Thr Val Ser Glu Asn Ile
 835 840 845
 Tyr Gln Pro Gly Asp Lys Ser Asn Val Leu Ala Tyr Ala Gly Asp Val
 850 855 860
 Leu Thr Ser Ala Gln Ala Glu Ala Ile Asp Asp Ala Gly Ile Glu Ser
 865 870 875 880
 Val Lys Ile Arg Ser Thr Leu Thr Cys Glu Ser Arg Arg Gly Val Cys
 885 890 895
 Ala Lys Cys Tyr Gly Leu Asn Leu Ala Asn Gly His Leu Ile Gly Leu
 900 905 910
 Gly Glu Ala Val Gly Ile Ile Ala Ala Gln Ser Ile Gly Glu Pro Gly
 915 920 925
 Thr Gln Leu Thr Met Arg Thr Phe His Leu Gly Gly Val Ala Ala Thr
 930 935 940
 Ser Ser Thr Pro Glu Ile Val Ala Glu Cys Asp Gly Ile Leu Val Tyr
 945 950 955 960
 Leu Asp Leu Arg Val Val Val Asp Gln Glu Gly Asn Asn Leu Val Leu
 965 970 975
 Asn Lys Met Gly Ala Leu His Leu Val Gln Asp Glu Gly Arg Ser Leu
 980 985 990
 Ser Glu Tyr Lys Lys Leu Leu Ser Thr Lys Ser Ile Glu Ser Leu Ala
 995 1000 1005
 Thr Phe Pro Val Glu Leu Gly Ala Lys Ile Leu Val Asn Asp Gly Ala

1010 1015 1020
 Ala Val Thr Ala Gly Gln Arg Ile Ala Glu Val Glu Leu His Asn Ile
 1025 1030 1035 1040
 Pro Ile Ile Cys Asp Lys Pro Gly Phe Val His Tyr Glu Asp Leu Val
 1045 1050 1055
 Glu Gly Val Ser Thr Glu Lys Val Ala Asn Lys Asn Thr Gly Leu Val
 1060 1065 1070
 Glu Leu Ile Val Lys Gln His Arg Gly Glu Leu His Pro Gln Ile Ala
 1075 1080 1085
 Ile Tyr Ala Asp Ala Asn Met Lys Glu Leu Val Gly Thr Tyr Ala Ile
 1090 1095 1100
 Pro Ser Gly Ala Ile Ile Ser Val Glu Glu Gly Gln Arg Ile Ala Pro
 1105 1110 1115 1120
 Gly Met Leu Leu Ala Arg Leu Pro Arg Gly Ala Ile Lys Thr Lys Asp
 1125 1130 1135
 Ile Thr Gly Gly Leu Pro Arg Val Ala Glu Leu Val Glu Ala Arg Lys
 1140 1145 1150
 Pro Glu Asp Ala Ala Asp Ile Ala Lys Ile Asp Gly Val Val Asp Phe
 1155 1160 1165
 Lys Gly Ile Gln Lys Asn Lys Arg Ile Leu Val Val Arg Asp Glu Ile
 1170 1175 1180
 Thr Gly Met Glu Glu Glu His Leu Ile Ser Leu Thr Lys His Leu Ile
 1185 1190 1195 1200
 Val Gln Arg Gly Asp Ser Val Ile Lys Gly Gln Gln Leu Thr Asp Gly
 1205 1210 1215
 Leu Val Val Pro His Glu Ile Leu Ala Ile Cys Gly Val Arg Glu Leu
 1220 1225 1230
 Gln Lys Tyr Leu Val Asn Glu Val Gln Glu Val Tyr Arg Leu Gln Gly
 1235 1240 1245
 Val Asp Ile Asn Asp Lys His Ile Glu Ile Ile Val Arg Gln Met Leu
 1250 1255 1260
 Gln Lys Val Arg Ile Thr Asp Pro Gly Asp Thr Thr Leu Leu Phe Gly
 1265 1270 1275 1280
 Glu Asp Val Asp Lys Lys Glu Phe Tyr Glu Glu Asn Arg Arg Thr Glu
 1285 1290 1295
 Glu Asp Gly Gly Lys Pro Ala Gln Ala Val Pro Val Leu Leu Gly Ile
 1300 1305 1310
 Thr Lys Ala Ser Leu Gly Thr Glu Ser Phe Ile Ser Ala Ala Ser Phe
 1315 1320 1325
 Gln Asp Thr Thr Arg Val Leu Thr Asp Ala Ala Cys Ser Ser Lys Thr
 1330 1335 1340
 Asp Tyr Leu Leu Gly Phe Lys Glu Asn Val Ile Met Gly His Met Ile
 1345 1350 1355 1360
 Pro Gly Gly Thr Gly Phe Asp Thr His Lys Arg Ile Lys Gln His Leu
 1365 1370 1375
 Glu Lys Glu Gln Glu Asp Leu Val Phe Asp Phe Asp Ser Glu Phe Glu
 1380 1385 1390
 Ser Val Ala Gly
 1395

(2) INFORMATIONS POUR LA SEQ ID NO: 120:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 124095..124988

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 120:

His	Leu	Glu	Ser	Lys	Ile	Asp	Lys	Val	Phe	Met	Ser	Ser	Gln	Phe	Asp	1	5	10	15
Gln	Phe	Lys	Leu	Trp	Ser	Val	Leu	Val	Gly	Asp	Thr	Gly	Asp	Pro	Ala	20	25	30	
Leu	Ile	Lys	Thr	Leu	Gly	Val	Gln	Asp	Ala	Thr	Thr	Asn	Pro	Ser	Leu	35	40	45	
Ile	Leu	Lys	Val	Ala	Gln	Glu	Pro	Lys	Tyr	Gln	Ser	Met	Leu	Thr	Glu	50	55	60	
Ala	Ile	Ser	Trp	Gly	Ile	Arg	Gln	Asn	Gly	Asp	Asp	Val	Gln	Thr	Leu	65	70	75	80
Thr	Phe	Val	Leu	Asp	Lys	Ile	Gln	Val	Asn	Leu	Gly	Leu	Glu	Ile	Leu	85	90	95	
Lys	His	Val	Pro	Gly	Arg	Val	Ser	Leu	Glu	Ile	Asp	Ala	Arg	Leu	Ser	100	105	110	
Phe	Asn	Thr	Glu	Ala	Met	Val	Gln	Arg	Ala	Ile	Phe	Leu	Ser	Gln	Leu	115	120	125	
Phe	Glu	Lys	Met	Gly	Gly	Asp	Lys	Lys	Arg	Leu	Leu	Val	Lys	Ile	Pro	130	135	140	
Gly	Thr	Trp	Glu	Gly	Ile	Cys	Ala	Ala	Glu	Val	Leu	Glu	Ser	Gln	Gly	145	150	155	160
Ile	Ala	Cys	Asn	Val	Thr	Leu	Ile	Phe	Asn	Leu	Val	Gln	Ala	Ile	Ala	165	170	175	
Ala	Ala	Lys	Ala	Lys	Val	Thr	Leu	Val	Ser	Pro	Phe	Val	Gly	Arg	Ile	180	185	190	
Tyr	Asp	Trp	Trp	Ile	Ala	Ala	Tyr	Gly	Ala	Glu	Gly	Tyr	Ser	Ile	Glu	195	200	205	
Ala	Asp	Pro	Gly	Val	Ala	Ser	Val	Ala	Asn	Ile	Tyr	Ser	Tyr	Tyr	Lys	210	215	220	
Lys	Phe	Asp	Ile	Pro	Thr	Gln	Ile	Met	Ala	Ala	Ser	Phe	Arg	Thr	Lys	225	230	235	240
Glu	Gln	Val	Leu	Ala	Leu	Ala	Gly	Cys	Asp	Phe	Leu	Thr	Val	Ser	Pro	245	250	255	
Lys	Leu	Leu	Glu	Glu	Leu	Lys	Lys	Asp	Gln	Gln	Pro	Val	Glu	Arg	Lys	260	265	270	
Leu	Ser	Val	Glu	Glu	Ala	Lys	Lys	Ile	Arg	Tyr	Ser	Thr	Cys	Gly	Val	275	280	285	
Val	Arg	Glu	Cys	Ile	Ser	Val	Leu	Asn	Glu							290	295		

(2) INFORMATIONS POUR LA SEQ ID NO: 121:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 78 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 124873..125106

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 121:

```

Lys Asn Ser Arg Lys Ile Ser Ser Leu Leu Lys Glu Ser Leu Ala Trp
1      5      10      15
Lys Lys Arg Lys Lys Leu Asp Ile Gln Pro Val Glu Leu Ser Glu Ser
20      25      30
Val Phe Arg Phe Leu Met Asn Glu Asp Ala Met Ala Thr Glu Lys Leu
35      40      45
Ala Glu Gly Ile Arg Ile Phe Ser Gly Asp Thr Gln Ile Leu Glu Ser
50      55      60
Ala Val Thr Glu Phe Ile Arg Gln Ile Ala Ala Gln Glu Ala
65      70      75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 122:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 242 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(125536..126261)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 122:

```

Asn Gln Thr Leu Asn Leu Met Lys Arg Val Ile Leu Cys Ser Leu Leu
1      5      10      15
Phe Ala Ser Phe Pro Ile Val Ser Lys Ala Ala Ala Glu Gly Lys Pro
20      25      30
Leu Ser Arg Ala Ala Gln Leu Arg Glu Lys Arg Lys Asp Leu His Val
35      40      45
Ser Arg Lys Pro Ser Pro Arg Tyr Ala Leu Lys Lys Arg Ala Leu Glu
50      55      60
Ala Lys Lys Asn Arg Pro Ser Ile Ser Trp Ile Thr Tyr Ser Asn Ala
65      70      75      80
Thr Tyr Ser Phe Leu Ile Pro Asn Thr Trp Gln Cys Ile Asp Asp Lys
85      90      95
Thr Gln Leu Pro Glu Lys Leu Asp Val Leu Phe Ile Gly Lys Gly Ala
100      105      110
Gly Gly Leu Thr Pro Thr Ile Asn Ser Ala His Glu Ile Ile His Lys
115      120      125
Thr Glu Asp Ala Tyr Ile Glu Glu Ile Leu Asp Tyr His Arg Ala Asn
130      135      140
Glu Asn Thr Leu Glu Ser Ser Ile Phe Ala His Ile Gln Ala Pro Ser
145      150      155      160
Gly Lys Phe Thr Ile Ile Lys Thr Glu Lys Asn Thr Ser Trp Gly Arg
165      170      175
Val Phe Cys Leu Gln Gly Val Thr Val Ile Asp His Thr Ala Tyr Ile
180      185      190
Phe Thr Ser Thr Ser Thr Ile Asp Asp Tyr Pro Asn Val Ser Leu Ala
195      200      205
Leu Leu Lys Ala Ala Ser Ser Phe Lys Leu Ser Glu Lys Glu Glu Ala
210      215      220
Ala Arg Gly Asp Ala Ile Leu Glu Lys Ala Leu Lys Asp Leu Gln Asn
225      230      235      240
Gly Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 123:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 201 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 126328..126930

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 123:

```

Thr Leu Phe Phe Leu Val Ser Asp Met Ala Asp Leu Ser Ala Gln Asp
1          5          10          15
Lys Leu Lys Gln Ile Cys Asp Ala Leu Arg Glu Glu Thr Leu Lys Pro
20          25          30
Ala Glu Glu Glu Ala Gly Ser Ile Val His Asn Ala Arg Glu Gln Ala
35          40          45
Lys Arg Ile Val Glu Glu Ala Lys Glu Glu Ala Gln Arg Ile Ile Arg
50          55          60
Ser Ala Glu Glu Thr Ala Asp Gln Thr Leu Lys Lys Gly Glu Ala Ala
65          70          75          80
Leu Val Gln Ala Gly Lys Arg Ser Leu Glu Asn Leu Lys Gln Ala Val
85          90          95
Glu Thr Lys Ile Phe Arg Glu Ser Leu Gly Glu Trp Leu Asp His Val
100         105         110
Ala Thr Asp Pro Glu Val Ser Ala Lys Leu Val Gln Ala Leu Val Gln
115         120         125
Ala Val Asp Ala Gln Gly Ile Ser Gly Asn Leu Ser Ala Tyr Ile Gly
130         135         140
Lys His Val Ser Ala Arg Ala Val Asn Glu Ala Leu Gly Lys Glu Ile
145         150         155         160
Thr Ser Lys Leu Lys Glu Lys Gly Val Ser Val Gly Lys Phe Ser Gly
165         170         175
Gly Ala Gln Leu Lys Val Glu Glu Arg Asn Trp Val Leu Asp Met Ser
180         185         190
Ser Glu Val Leu Leu Asp Phe Ile Asp
195         200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 124:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 216 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 127138..127785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 124:

Glu Arg Val Met Asn Gln Tyr Tyr Phe Leu Ser Ser Phe Leu Ser Pro

```

1          5          10          15
Gln Gln Pro Glu Ser Ser Pro Leu Tyr Ser Phe Gln Glu Ile Asn Asp
20          25          30
Leu Leu Ala Leu Asn Phe Thr Asp Lys Asp Trp Arg Ser Tyr Val Ile
35          40          45
Leu Arg Arg Phe Phe Asp Leu Glu Asn Phe Ala Phe Phe Trp Ala Gly
50          55          60
Lys Ser Ile Pro Phe Ser Phe Gly Thr Val Thr Asn Ser Asn Val Glu
65          70          75          80
Ser Leu Leu Arg Leu Gln Met Trp Ser Asp Glu Trp Glu Phe Glu Asp
85          90          95
Phe Phe Lys Asp Phe Leu Leu Arg Tyr Lys Thr Pro Arg Glu Arg Leu
100          105          110
Thr His Phe Ser Glu Leu Val Arg Asp Phe Leu Asp His Tyr Gln Asp
115          120          125
Tyr Pro Ser Glu Phe Leu Arg Thr Tyr Phe Arg Phe Lys Gln Asp Leu
130          135          140
Arg Ile Ile Leu Ala Gly Phe Arg Ala Arg Val Met Gln Lys Asp Val
145          150          155          160
Ser Phe Val Leu Arg Asp Glu Asp Ser Ser Asn Pro Ile Val Leu His
165          170          175
Val Leu Met Gln Lys Asp Ser Pro Asn Tyr Glu Leu Pro Asp Glu Phe
180          185          190
Phe Glu Leu Arg Asp Val Leu Gly Arg Leu Arg Ala Ser Ser Thr His
195          200          205
Val Glu Ser Asp Ser Leu Phe Leu
210          215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 125:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 597 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 127924..129714

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 125:

```

Asp Gly Glu Arg Asn Gln Met Val Ala Thr Ser Lys Gln Thr Thr Gln
1          5          10          15
Gly Tyr Val Val Glu Ala Tyr Gly Asn Leu Leu Arg Val His Val Asp
20          25          30
Gly His Val Arg Gln Gly Glu Val Ala Tyr Val Ser Val Asp Asn Thr
35          40          45
Trp Leu Lys Ala Glu Ile Ile Glu Val Val Gly Met Lys Leu Arg Phe
50          55          60
Gln Val Phe Glu Glu Thr Gln Gly Ile Ser Arg Gly Ala Leu Val Thr
65          70          75          80
Phe Ser Gly His Leu Leu Glu Ala Glu Leu Gly Pro Gly Leu Leu Gln
85          90          95
Gly Ile Phe Asp Gly Leu Gln Asn Arg Leu Glu Ile Leu Ala Asp Thr
100          105          110
Ser Leu Phe Leu Arg Arg Gly Glu Tyr Val Asn Ala Ile Cys Arg Glu
115          120          125

```


Thr	Val	Trp	Ala	Tyr	Thr	Gln	Lys	Ala	Ser	Val	Gly	Ser	Val	Leu	Ser
130						135					140				
Arg	Gly	Asp	Val	Leu	Gly	Thr	Val	Lys	Glu	Gly	Arg	Phe	Asp	His	Lys
145					150					155					160
Ile	Met	Val	Pro	Phe	Ser	Cys	Phe	Glu	Glu	Val	Thr	Ile	Thr	Trp	Val
				165					170						175
Ile	Ser	Ser	Gly	Asn	Tyr	Thr	Val	Asp	Thr	Val	Val	Ala	Lys	Gly	Arg
			180					185					190		
Thr	Ser	Thr	Gly	Glu	Glu	Leu	Glu	Phe	Thr	Met	Val	Gln	Lys	Trp	Pro
			195				200					205			
Ile	Lys	Gln	Ala	Phe	Leu	Glu	Gly	Glu	Lys	Val	Pro	Ser	His	Glu	Ile
	210					215				220					
Met	Asp	Val	Gly	Leu	Arg	Val	Leu	Asp	Thr	Gln	Ile	Pro	Val	Leu	Lys
225					230					235					240
Gly	Gly	Thr	Phe	Cys	Thr	Pro	Gly	Pro	Phe	Gly	Ala	Gly	Lys	Thr	Val
				245					250						255
Leu	Gln	His	His	Leu	Ser	Lys	Tyr	Ala	Ala	Val	Asp	Ile	Val	Val	Leu
			260					265					270		
Cys	Ala	Cys	Gly	Glu	Arg	Ala	Gly	Glu	Val	Val	Glu	Ile	Leu	Gln	Glu
		275					280					285			
Phe	Pro	His	Leu	Lys	Asp	Pro	His	Thr	Gly	Gln	Ser	Leu	Met	His	Arg
	290					295					300				
Thr	Cys	Ile	Ile	Cys	Asn	Thr	Ser	Ser	Met	Pro	Val	Ala	Ala	Arg	Glu
305					310					315					320
Ser	Ser	Ile	Tyr	Leu	Gly	Ile	Thr	Ile	Ala	Glu	Tyr	Tyr	Arg	Gln	Met
				325					330						335
Gly	Leu	His	Ile	Leu	Leu	Leu	Ala	Asp	Ser	Thr	Ser	Arg	Trp	Ala	Gln
			340					345					350		
Ala	Leu	Arg	Glu	Ile	Ser	Gly	Arg	Leu	Glu	Glu	Ile	Pro	Gly	Glu	Glu
		355					360					365			
Ala	Phe	Pro	Ala	Tyr	Leu	Ala	Ser	Arg	Ile	Ala	Ala	Phe	Tyr	Glu	Arg
	370					375					380				
Gly	Gly	Ala	Val	Lys	Met	Lys	Asp	Gly	Ser	Glu	Gly	Ser	Leu	Thr	Ile
385					390					395					400
Cys	Gly	Ala	Val	Ser	Pro	Ala	Gly	Gly	Asn	Phe	Glu	Glu	Pro	Val	Thr
				405					410						415
Gln	Ala	Thr	Leu	Ser	Val	Val	Gly	Ala	Phe	Cys	Gly	Leu	Ser	Lys	Ala
			420				425					430			
Arg	Ala	Asp	Ala	Arg	Arg	Tyr	Pro	Ser	Ile	Asp	Pro	Met	Ile	Ser	Trp
		435				440						445			
Ser	Lys	Tyr	Leu	Asp	Ser	Val	Ala	Glu	Ile	Leu	Glu	Lys	Lys	Val	Pro
	450					455					460				
Gly	Trp	Gly	Glu	Ser	Val	Lys	Gln	Ala	Ser	Arg	Phe	Leu	Glu	Glu	Gly
465					470					475					480
Ala	Glu	Ile	Gly	Lys	Arg										

595

(2) INFORMATIONS POUR LA SEQ ID NO: 126:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 129720..131033

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 126:

Met Gln Thr Ile Tyr Thr Lys Ile Thr Asp Ile Lys Gly Asn Leu Ile
 1 5 10 15
 Thr Val Glu Ala Glu Gly Ala Ser Leu Gly Glu Leu Val Gln Ile Glu
 20 25 30
 Arg Ala Asp Gly Arg Ser Ser Tyr Ala Ser Val Leu Arg Phe Asp Ala
 35 40 45
 Arg Lys Val Thr Leu Gln Val Phe Gly Gly Thr Ser Gly Leu Ser Thr
 50 55 60
 Gly Asp Lys Val Ile Phe Leu Gly Arg Pro Met Glu Val Ile Tyr Gly
 65 70 75 80
 Asp Ser Leu Leu Gly Arg Arg Phe Asn Gly Thr Gly Lys Pro Ile Asp
 85 90 95
 His Glu Asp Glu Cys Phe Gly Glu Pro Ile Pro Ile Thr Thr Pro Ser
 100 105 110
 Phe Asn Pro Val Cys Arg Ile Val Pro Arg Glu Met Val Arg Thr Asn
 115 120 125
 Ile Pro Met Ile Asp Met Phe Asn Cys Leu Val Lys Ser Gln Lys Ile
 130 135 140
 Pro Ile Phe Ser Ser Ser Gly Glu Asn His Asn Ala Leu Leu Met Arg
 145 150 155 160
 Ile Ala Ala Gln Thr Asp Ala Asp Ile Val Ile Ile Gly Gly Met Gly
 165 170 175
 Leu Thr Phe Val Asp Tyr Asn Phe Phe Val Glu Glu Ser Gln Arg Leu
 180 185 190
 Gly Phe Ala Asp Lys Cys Val Lys Phe Ile His Lys Ala Val Asp Ala
 195 200 205
 Pro Val Glu Cys Val Leu Ile Pro Asp Met Ala Leu Ala Cys Ala Glu
 210 215 220
 Arg Phe Ala Leu Glu Gln Gln Lys Asn Val Leu Val Leu Leu Thr Asp
 225 230 235 240
 Met Thr Ala Phe Ala Asp Ala Leu Lys Glu Ile Ala Ile Thr Met Asp
 245 250 255
 Gln Ile Pro Ala Asn Arg Gly Tyr Pro Gly Ser Leu Tyr Ser Asp Leu
 260 265 270
 Ala Val Arg Tyr Glu Lys Ala Val Asp Ile Ala Gln Gly Gly Ser Ile
 275 280 285
 Thr Leu Ile Ser Val Thr Thr Met Pro Gly Asp Asp Ile Thr His Pro
 290 295 300
 Val Pro Asp Asn Thr Gly Phe Ile Thr Glu Gly Gln Phe Tyr Leu Lys
 305 310 315 320
 Asp Asn Arg Ile Asp Pro Phe Gly Ser Leu Ser Arg Leu Lys Gln Leu
 325 330 335

```

Val Ile Gly Lys Lys Thr Arg Glu Asp His Gly Asp Leu Ala Asn Ala
      340      345      350
Leu Ile Arg Leu Tyr Ala Asp Ser Arg Lys Ser Ala Glu Arg Met Ser
      355      360      365
Met Gly Phe Lys Leu Ser Asn Trp Asp Lys Lys Leu Leu Ala Phe Ser
      370      375      380
Glu Leu Phe Glu Ala Arg Leu Met Ser Leu Glu Val Asn Ile Pro Leu
      385      390      395      400
Glu Glu Ala Leu Asp Ile Gly Trp Lys Ile Leu Ser Gln Ser Phe His
      405      410      415
Ser Glu Glu Val Gly Ile Lys Glu Gln Leu Ile Gln Lys Tyr Trp Pro
      420      425      430
Lys Ala Cys Leu His Lys
      435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 127:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 131018..131629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 127:

```

Ser Met Ser Ser Gln Ile Lys Leu Thr Lys Asn Ser Tyr Arg Ala Glu
1      5      10      15
Lys Gln Lys Leu Asn Met Leu Gly Met Tyr Leu Pro Thr Leu Lys Leu
      20      25      30
Lys Lys Ala Leu Leu Gln Ala Glu Val Gln Ser Ala Ile Arg Leu Ala
      35      40      45
Ala Glu Ser Thr Ala Thr Asn Glu Gln Ala Arg Asp Arg Met Tyr Ala
      50      55      60
Phe Ala Glu Leu Phe Ser Ile Pro Leu Tyr Thr Asp Ala Val Glu Gln
      65      70      75      80
Cys Phe Ser Val Asp Ile Leu Glu Lys Asp Val Glu Asn Ile Ala Gly
      85      90      95
Val Glu Val Pro Leu Leu Lys Arg Val Val Leu Thr Ser Pro Glu Tyr
      100      105      110
Ser Leu Leu Asp Thr Pro Ile Trp Leu Asp Ser Leu Leu Ala Ser Val
      115      120      125
Lys Glu Tyr Val Val Ser Lys Ile Tyr Ala Glu Asn Ala Gln Glu Arg
      130      135      140
Leu Leu Leu Leu Glu Glu Glu Leu Arg Arg Val Ser Ile Arg Val Asn
      145      150      155      160
Leu Phe Glu Lys Lys Leu Ile Pro Thr Thr Ser Gln Thr Leu Lys Lys
      165      170      175
Ile Ala Ile Phe Leu Ser Asp Arg Ser Ile Thr Asp Val Gly Gln Met
      180      185      190
Lys Met Ala Lys Lys Lys Ile Gln His Lys Glu
      195      200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 128:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 441 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 131834..133156

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 128:

```

Ser Thr Lys Ser Gly Tyr Leu Val Thr Glu Gln Leu Leu Gln Glu Ile
1      5      10      15
Phe Asp Leu Asn Gln Glu Ile Thr Thr Leu Thr Glu Ser Leu Lys Ala
20      25      30
Leu Gly Lys Xaa Ile Val Arg Val Lys Pro Leu Gly Asp Phe Ser Ser
35      40      45
Glu Glu Ile Arg Glu Leu Thr Leu Lys Thr Gly Leu Ala Val Arg Phe
50      55      60
Phe Tyr Lys Arg His Ile Glu Gly Ala Pro Leu Glu Val Glu Glu Glu
65      70      75      80
Asn Val Phe Tyr Leu Ala Thr Ala Tyr Asn Tyr Asp Tyr Tyr Ala Val
85      90      95
Ile Gly Ile Val Ser Leu Ser Lys Asp Ile Phe Thr Glu Ile Glu Ala
100     105     110
Pro Arg Ser Val Asn Glu Leu Arg Glu Glu Ala Gly His Leu Gln Ala
115     120     125
Leu Leu Arg Lys Lys Lys Ala Arg Val Cys Glu Leu Tyr Ala Tyr Arg
130     135     140
Glu Asp Leu Leu Glu Ala Leu Cys Glu Gln Cys Asn Glu Gln Ser Leu
145     150     155     160
Gln His Ala Glu Ala Ser Ala Glu Asp Leu Phe Asp Asp Lys Val Phe
165     170     175
Ser Ala Leu Gly Trp Val Ile Val Asp Arg Leu Asp Glu Val Lys Lys
180     185     190
Leu Cys Asp Ser Leu Gly Ile Tyr Leu Glu Arg Val Gln Pro Asp Pro
195     200     205
Asp Glu Val Ile Pro Thr Tyr Leu Glu Asn His Gly Leu Gly Ala Leu
210     215     220
Gly Glu Ser Leu Val Asn Ile Tyr Asp Thr Pro Ala Ser Thr Asp Lys
225     230     235     240
Asp Pro Ser Leu Trp Val Phe Phe Ser Phe Phe Val Phe Phe Ser Met
245     250     255
Ile Ile Asn Asp Ala Gly Tyr Gly Leu Val Phe Leu Ala Thr Ser Leu
260     265     270
Phe Leu Ser Phe Lys Ala Arg Lys Gln Ile Lys Arg Ser Ile Ala Leu
275     280     285
Lys Arg Phe Leu Gln Met Phe Met Ile Leu Gly Leu Gly Cys Val Cys
290     295     300
Trp Gly Gly Ala Thr Thr Ser Phe Phe Gly Val Ser Val Ser Tyr Thr
305     310     315     320
Ser Pro Phe Arg Glu Tyr Ser Leu Thr His Phe Leu Ala Leu Lys Lys
325     330     335
Ala Glu Tyr Tyr Leu Lys Glu Arg Pro Lys Gly Tyr Lys Glu Leu Val
340     345     350
His Asp Tyr Pro Ile Leu Lys Glu Lys Lys Thr Pro Lys Glu Phe Leu
355     360     365

```

```

Leu Ala Gln Ser Thr Ser Ser Gly Asp Ser Val Tyr Lys Ala Val Val
  370          375          380
Tyr Asp Lys Phe Ile Asp Asn Ile Leu Met Glu Ile Ala Leu Leu Val
385          390          395          400
Gly Val Val His Leu Ser Leu Gly Met Leu Arg Tyr Cys Arg Gln Arg
          405          410          415
Tyr Ser Ser Ile Gly Trp Val Ile Phe Met Cys Gly Asp Ile Cys Ile
          420          425          430
Cys Leu Ser Ile Cys Lys Pro Tyr Leu
          435          440

```

(2) INFORMATIONS POUR LA SEQ ID NO: 129:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 170 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 133075..133584

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 129:

```

Thr Ala Val Phe Phe Tyr Arg Met Gly Asn Leu Tyr Val Arg Arg Tyr
1          5          10          15
Met Tyr Leu Pro Ile Tyr Leu Gln Ala Val Ser Leu Ile His Tyr Ala
          20          25          30
Leu His Ile Pro Tyr Glu Leu Gly Gly Leu Val Gly Tyr Tyr Val Thr
          35          40          45
Phe Ile Gly Leu Gly Val Ala Ile Leu Gly Gly Val Ile Gln Arg Gly
          50          55          60
Leu Arg Gly Leu Asp Glu Ile Thr Ala Val Ile Gln Val Phe Ser Asp
          65          70          75          80
Val Leu Ser Tyr Leu Arg Leu Tyr Ala Leu Ser Leu Ala Gly Glu Met
          85          90          95
Val Gly Asn Thr Val Met Val Met Ser Glu Arg Phe Ser Pro Ala Val
          100          105          110
Gly Ile Leu Ile Ile Ile Phe Gly His Thr Val Asn Ile Ala Leu Ser
          115          120          125
Ile Met Gly Gly Val Ile His Gly Leu Arg Leu Asn Phe Ile Glu Trp
          130          135          140
Tyr His Tyr Ser Phe Asp Gly Gly Gly Lys Phe Leu His Pro Leu Lys
          145          150          155          160
Lys Val Ile Tyr Gln Lys Ser Gln Asn Leu
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 130:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 125 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 133625..133999

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 130:

```

Glu Met Ser Ser Glu Arg Lys Tyr Met Ile Asp Val Ser Val Val Gly
1      5      10
Pro Val Leu Ala Met Ala Leu Ala Met Ile Gly Ser Ala Val Gly Cys
      20      25      30
Gly Met Ala Gly Val Ala Ser His Ala Val Met Ser Arg Ile Asp Glu
      35      40      45
Gly His Gly Lys Ile Ile Gly Leu Ser Ala Met Pro Ser Ser Gln Ser
      50      55      60
Ile Tyr Gly Leu Ile Phe Met Leu Leu Leu Asn Asp Ala Ile Lys Asp
65      70      75      80
Gly Lys Val Ser Ala Val Ser Gly Ile Val Met Gly Ile Ala Val Gly
      85      90      95
Ser Ala Leu Leu Leu Ser Ala Phe Met Gln Gly Lys Cys Cys Val Ser
      100      105      110
Ala Ile Gln Ala Tyr Ala Arg Ser Ser Ala Asn Ile Trp
      115      120      125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 131:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 133861..134508

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 131:

```

Gly Trp Lys Ser Leu Cys Ser Gln Trp Tyr Arg Asn Gly Tyr Ser Cys
1      5      10
Arg Ile Cys Val Ile Ala Phe Cys Phe Tyr Ala Arg Glu Val Leu Cys
      20      25      30
Glu Cys Tyr Ser Ser Leu Cys Ala Phe Leu Cys Lys Tyr Met Val Asn
      35      40      45
His Leu Leu Arg Leu Gly Leu Leu Ser Leu Leu Arg Tyr Leu Leu Ser
      50      55      60
Phe Leu Arg Tyr Cys Tyr Ser Lys Trp Xaa Ala Ala Ala Phe Ser Ala
65      70      75      80
Leu Cys Leu Gly Gly Cys Ser Gln Pro Ala Leu Ser Ser Phe Leu Glu
      85      90      95
Phe Ile Asp Asn Asp Tyr Thr Ala Ala Ala His Leu Gly Ile Asp Arg
      100      105      110
Gly Cys Val Thr Glu Ser Val Gly Gln Gln Leu Val Val Thr Trp Gly
      115      120      125
Leu Pro Ser Arg Phe Arg Asp Ser Leu Pro Met Val Leu His Val Trp
      130      135      140
Val Tyr Tyr Gly Asn Gly Glu Ala Ala Lys Phe Ser Tyr Asp Val Gln
145      150      155      160
His Leu Ser Gly Tyr Gln Val Tyr Thr Leu Lys Glu Asn Asp Tyr Gln
      165      170      175

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Asp Arg Gln Gly Ile Xaa Ser Tyr Lys Val Ser Leu Thr Lys Asp Gly
      180                      185                      190
Lys Glu Ile Leu Ser Arg Ser His His Leu Trp Met Glu Val Ile Ser
      195                      200                      205
Leu Lys Ala Phe Ser Gln Leu Ser
      210                      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 132:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 939 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 134638..137454

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 132:

```

Met Asn Glu Asp Gln Phe Pro Lys Ala Tyr Asp Pro Lys Ser Ser Glu
1      5      10      15
Thr Gly Val Tyr Ser Phe Trp Glu Arg Ser Gly Met Phe Val Ala Asn
      20      25      30
Ala Ser Ser Glu Lys Pro Ala Tyr Ser Ile Val Met Pro Pro Pro Asn
      35      40      45
Val Thr Gly Ile Leu His Met Gly His Ala Leu Val Asn Thr Leu Gln
      50      55      60
Asp Thr Leu Ile Arg Tyr Lys Arg Met Gln Gly Phe Glu Val Cys Trp
      65      70      75      80
Val Pro Gly Thr Asp His Ala Gly Ile Ala Thr Gln Thr Val Val Glu
      85      90      95
Arg His Leu Lys Ala Ser Leu Gly Lys Arg Arg Thr Asp Phe Ser Arg
      100      105      110
Glu Glu Phe Leu Lys His Val Trp Asp Trp Lys Glu Lys Ser Gln Asn
      115      120      125
Val Ile Leu Ser Gln Leu Arg Gln Leu Gly Cys Ser Cys Asp Trp Ser
      130      135      140
Arg Gln Arg Phe Thr Met Asp Pro Gly Ala Asn Arg Ala Val Lys Lys
      145      150      155      160
Ala Phe Lys Ile Leu Phe Asp Lys Gly Val Ile Tyr Arg Gly Tyr Tyr
      165      170      175
Leu Val Asn Trp Asp Pro Ile Leu Gln Thr Ala Leu Ala Asp Asp Glu
      180      185      190
Val Glu Tyr Glu Glu Arg Asp Gly Trp Leu Tyr Tyr Ile Arg Tyr Gln
      195      200      205
Val Val Asn Ser Glu Glu Phe Ile Thr Val Ala Thr Thr Arg Pro Glu
      210      215      220
Thr Leu Leu Gly Asp Thr Ala Ile Ala Val Ser Pro Glu Asp Gln Arg
      225      230      235      240
Tyr Ser His Leu Ile Gly Ala Lys Val Val Val Pro Phe Val Asn Arg
      245      250      255
Glu Ile Pro Ile Ile Gly Asp Phe Ser Val Asp Ala Ser Phe Gly Thr
      260      265      270
Gly Ala Val Lys Ile Thr Pro Ala His Asp Lys Asp Asp Tyr Lys Thr
      275      280      285
Gly Met Asn His Gln Leu Pro Met Ile Asn Ile Leu Thr Ser Thr Gly

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290 295 300
 Glu Ile Asn Glu Asn Gly Gly Ile Phe Thr Gly Leu Ser Arg Glu Val
 305 310 315 320
 Ala Arg Glu Asn Ile Ile Thr Ser Leu Glu Ala Leu Gly Leu Phe Val
 325 330 335
 Lys Lys Glu Ala Tyr Ser Ser Arg Val Gly Val Ser Tyr Arg Ser Gly
 340 345 350
 Ala Ile Ile Glu Pro Tyr Leu Ser Lys Gln Trp Phe Val Ser Val Asp
 355 360 365
 Ser Phe Arg Asp Ser Leu Arg Glu Phe Val Asn Ser Glu Glu Ile Arg
 370 375 380
 Ile Phe Pro Pro Glu Phe Val Arg Asn Tyr Leu Thr Trp Val Asn Asn
 385 390 395 400
 Leu Lys Asp Trp Cys Ile Ser Arg Gln Leu Trp Trp Gly His Arg Ile
 405 410 415
 Pro Val Trp His Asn Lys His Asp Glu Asn Val Ile Cys Phe Asp Gly
 420 425 430
 Glu Gly Gly Pro Glu Glu Val Met Arg Asp Pro Glu Ser Trp Tyr Gln
 435 440 445
 Asp Pro Asp Val Leu Asp Thr Trp Phe Ser Ser Gly Leu Trp Pro Leu
 450 455 460
 Thr Cys Phe Gly Trp Pro Asp Glu Asp Ser Leu Asp Leu Lys Lys Phe
 465 470 475 480
 Tyr Pro Thr Ala Val Leu Val Thr Gly His Asp Ile Leu Phe Phe Trp
 485 490 495
 Val Thr Arg Met Val Leu Met Cys Ser Ala Met Val Asp Thr Glu Pro
 500 505 510
 Phe Ser Asp Val Phe Leu His Gly Leu Ile Phe Gly Lys Ser Tyr Arg
 515 520 525
 Glu Tyr Asp Glu Lys Gly Glu Trp Phe Tyr Val Ser Gly Glu Arg Lys
 530 535 540
 Arg Asp Tyr Asp Lys Gly Lys Ala Leu Pro Lys Asn Val Val Ala Lys
 545 550 555 560
 Trp Glu Lys Leu Ser Lys Ser Lys Gly Asn Val Ile Asp Pro Ile Glu
 565 570 575
 Met Ile Glu Ala Tyr Gly Ala Asp Ala Val Arg Leu Thr Leu Cys Ser
 580 585 590
 Cys Ala Asn Arg Gly Glu Gln Ile Asp Leu Asp Tyr Arg Leu Phe Glu
 595 600 605
 Glu Tyr Lys Asn Phe Ile Asn Lys Leu Trp Asn Gly Ala Arg Phe Ile
 610 615 620
 Phe Gly His Ile Ser Glu Leu Thr Ser Arg Asp Leu Glu Glu Gly Val
 625 630 635 640
 Asn Gln Asp Leu Leu Gly Leu Glu Asp Phe Tyr Ile Leu Asp Arg Phe
 645 650 655
 Asn Glu Leu Leu Asp Leu Ile Asp Gly His Tyr Asn Cys Tyr Ser Phe
 660 665 670
 Asp Lys Ile Ala Ser Leu Ala Tyr Asp Phe Phe Lys Asn Asp Leu Cys
 675 680 685
 Ser Thr Tyr Leu Glu Ile Ile Lys Pro Thr Leu Phe Gly Lys Gln Gly
 690 695 700
 Ser Asp Gln Gln Arg Ala Thr Lys Arg Lys Leu Ala Thr Leu Leu
 705 710 715 720
 Ile Asn Ile Leu Gly Val Leu His Pro Ile Val Pro Tyr Ile Thr Glu
 725 730 735
 Thr Leu Phe Gln Lys Leu Lys Ala Thr Leu Gly Thr Val Glu Asn Gly
 740 745 750
 Lys Gly Asp Ser Val Thr Gly His Ala Val Ser Met Leu Arg Ser Glu
 755 760 765

Ala Cys Met Val Ala Glu Tyr Pro Lys Pro Ile His Val Ala Phe Pro
 770 775 780
 Gln Gly Leu Arg Glu Ser Phe Gly Ile Ala Glu Arg Leu Val Tyr Thr
 785 790 795 800
 Ile Arg Asn Ile Arg Gly Glu Met Gln Leu Asp Pro Arg Glu Pro Leu
 805 810 815
 Gln Ala Phe Val Ile Ser Ser Glu Lys Lys Glu Leu Val Asp Val Cys
 820 825 830
 Ile Pro Ile Met Cys Ala Leu Gly Gly Val Lys Thr Val Glu Gln Leu
 835 840 845
 Ala Glu Ala Pro Lys Asp Ser Ile Phe Ser Leu Gly Val Val Glu Gly
 850 855 860
 Ile Gln Val Gly Val Ile Leu Pro Pro Glu His Leu Ala Lys Glu Arg
 865 870 875 880
 Val Arg Leu Glu Lys Glu Lys Thr Arg Leu Glu Lys Ser Ile Asp Ser
 885 890 895
 Val Ser Lys Leu Leu Ala Ser Glu Asp Phe Arg Thr Arg Ala Asn Pro
 900 905 910
 Ser Leu Val Gln Ala Lys Lys Asp Ser Leu Arg Asn Ser Gln Arg Glu
 915 920 925
 Leu Gln Ser Ile Leu Asp Lys Leu Ala Ser Leu
 930 935

(2) INFORMATIONS POUR LA SEQ ID NO: 133:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 945 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 137442..140276

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 133:

Thr Arg Ile Ala Leu Lys Glu Ala Val Leu Leu Gln Arg Tyr Glu Leu
 1 5 10 15
 Ile Arg Leu Ile Gly Lys Gly Gly Met Gly Glu Val Tyr Leu Ala His
 20 25 30
 Asp Lys Ala Cys Ser Arg Arg Val Ala Leu Lys Arg Ile Arg Glu Asp
 35 40 45
 Leu Ser Gly Asn Ala Leu Leu Arg Lys Arg Phe Leu Arg Glu Ala Lys
 50 55 60
 Ile Ala Ala Asp Leu Ile His Pro Gly Ile Val Pro Val Tyr Ser Ile
 65 70 75 80
 Cys Ser Asp Gly Glu Ala Val Tyr Tyr Thr Met Pro Tyr Ile Glu Gly
 85 90 95
 Phe Ser Leu Lys Ser Leu Leu Lys Ser Val Trp Gln Lys Glu Val Leu
 100 105 110
 Ser Lys Glu Leu Glu Glu Lys Thr Ser Val Lys Ser Phe Leu Pro Ile
 115 120 125
 Phe Asp Lys Ile Cys Ala Thr Val Glu Tyr Ile His Ser Lys Gly Val
 130 135 140
 Leu His Arg Asp Leu Lys Pro Asp Asn Ile Leu Leu Gly Leu Phe Gly
 145 150 155 160
 Glu Val Val Ile Val Asp Trp Gly Ala Ala Ile Phe Lys His Ala Lys

Glu Leu Lys 165
 180
 Arg Asn Ile Cys Tyr Ser Ser Met 170
 185
 Thr Pro Asp Tyr Met Ala Pro Glu Ser Leu Leu Gly Val Ser Phe Asp Glu
 190
 195
 200
 210
 215
 Glu Lys Thr Asp Ile Tyr Ala Leu Gly Leu Ile Leu Tyr Gln Met Leu
 225
 230
 235
 Thr Leu Ala Phe Pro Tyr Arg Arg Lys Lys Gly Arg Lys Leu Ser Tyr
 245
 250
 Arg Asp Val Val Leu Pro Pro Ile Glu Met Ser Pro Tyr Arg Glu Ile
 260
 265
 Pro Pro Ser Leu Ser Gln Ile Ala Met Lys Ala Ile Ala Ile Asn Pro
 275
 280
 285
 Ala Asp Arg Phe Ser Ser Ile Gln Glu Leu Arg Gln Ala Leu Gln Pro
 290
 295
 300
 Tyr Leu Gln Gly Asp Pro Glu Trp Thr Val Lys Ala Thr Leu Met Ala
 305
 310
 315
 Lys Glu Lys Ser Cys Trp Lys Tyr Tyr Asp Pro Ile Leu Leu Ser Arg
 325
 330
 335
 Tyr Phe Pro Val Leu Ala Ser Ser Pro Ala Gln Trp Tyr Asn Phe Met
 340
 345
 350
 Leu Ser Glu Val Glu Ile Ser Ala Ser Thr Arg Val Glu Tyr Thr Val
 355
 360
 365
 Thr Lys Ser Ala Val His Glu Gly Met Gly Ile Leu Phe Leu Pro Ser
 370
 375
 380
 Lys Glu Ala Glu Arg Gly Glu Phe Tyr Cys Gly Tyr Gly Leu Trp Phe
 385
 390
 395
 Ser Val Gln Asn His Glu Leu Thr Val Ser Leu Ile Lys Asn Gly Ile
 405
 410
 415
 Glu Ile Gln Lys Lys Ser Gln Glu Met Ile Ser Gln Gln Tyr Arg Phe
 420
 425
 430
 Ala Ile Leu Ile Glu Lys Ser Asp Asn Arg Ile Ala Val Phe Val Glu
 435
 440
 445
 Gln Ala Leu Phe Ile Leu His Ile Asp Tyr Leu Pro Ser Leu Gly Asn
 450
 455
 460
 Arg Leu Gly Val Ile Ile Gln Asp Leu Gln Gly Met Ser Asn Ile Ala
 465
 470
 475
 Ile Ser Glu Ser Ile Gly Ala Leu Arg Val Ser Cys Leu Ala Val Pro
 485
 490
 495
 Asp Ala Phe Leu Ser Glu Lys Leu Tyr Asp Gln Ala Ala Ile Phe Tyr
 500
 505
 510
 Arg Lys Ile Arg Asp Ser Phe Pro Gly Arg Lys Glu Ser Tyr Glu Ala
 515
 520
 525
 Gln Phe Arg Leu Gly Val Thr Leu Leu Thr Gln Ile Glu Glu Gln Gly
 530
 535
 540
 Gly Asp Leu Thr Gln Ala Leu Ser Ser Phe Asp Tyr Leu His Gly Gly
 545
 550
 555
 Ala Gly Ala Pro Leu Glu Tyr Leu Gly Lys Ala Leu Val Tyr Gln Arg
 565
 570
 575
 Asn Gly Ser Phe Val Glu Glu Ile Arg Cys Leu Leu Phe Ala Leu Lys
 580
 585
 590
 Arg Tyr Ser Gln His Pro Glu Ile Pro Arg Leu Glu Asp His Leu Cys
 595
 600
 605
 Phe Arg Leu Tyr Asp Ser Leu His Lys His Arg Ser Glu Ala Leu Val
 610
 615
 620
 Phe Met Leu Leu Ile Leu Trp Ile Ala Pro Glu Lys Ile Ser Val Arg
 625
 630
 635
 640

Glu Glu Lys Arg Phe Leu Arg Ile Ile Tyr His Lys Gln Gln Ala Thr
 645 650 655
 Leu Phe Cys Gln Val Asp Lys Ala Pro Leu Gln Phe Arg Ser Ser Lys
 660 665 670
 Met Glu Leu Phe Leu Ser Phe Trp Thr Ala Phe Ser Leu Phe Leu Pro
 675 680 685
 Glu Leu Phe Arg Arg Ala Gly Glu Leu Arg Asp Tyr Gln Ala Leu Ala
 690 695 700
 Asp Ile Phe Tyr Val Ala Gly Val Ser Gly Asn Arg Glu Ala Phe Met
 705 710 715 720
 Gln Phe Ser Thr Ala Leu Ala Asn Val Ser Asp Glu Ile Thr Phe Pro
 725 730 735
 Glu Ser Leu His Asn Gln Lys Val Ala Glu Leu Met Phe Phe Val Lys
 740 745 750
 Gly Val Glu Ala Leu Arg Asn Lys Asp Tyr Gln Lys Ala Lys Lys Ala
 755 760 765
 Phe Met Gly Lys Thr Pro Phe Thr Leu Gln Leu Tyr Ala Leu Asp Ile
 770 775 780
 Phe His Ile Gln Ala Phe Leu Asp Glu Glu Ile Glu Ser Phe Ile Asp
 785 790 795 800
 Leu Leu Gln Ala Ile Tyr Asp Pro Ala Ser Glu Glu Glu Arg Asp His
 805 810 815
 Ile Leu Val Tyr Ile Ile Gln Thr His Leu Trp Asn Arg Asp Leu Glu
 820 825 830
 Arg Ala Tyr Lys Leu Leu Asn Asp Arg Phe Pro Leu Asp Glu Glu Leu
 835 840 845
 Ala Glu Tyr Ser Glu Ala Phe Ile Leu Trp Gly Cys Tyr Leu Ala Leu
 850 855 860
 Thr Gly Asp Arg Val Ala Val Lys Ala His Phe Ser Arg Cys Arg Tyr
 865 870 875 880
 Lys Tyr Gly Lys Ser Ala Leu Ile Gly Lys Cys Val Asp Gly Asp Ile
 885 890 895
 Phe Asp Tyr Leu Asp Asn Leu Val Trp Trp Glu Lys Lys Met Thr Leu
 900 905 910
 Phe Gln Ser Tyr Phe Leu Leu Arg Cys Leu Asn Glu Ser Pro Arg Arg
 915 920 925
 Tyr Glu Lys Tyr Arg Gln Ala Tyr Leu Ser Met Glu Asn Asn Phe Phe
 930 935 940
 Asp
 945

(2) INFORMATIONS POUR LA SEQ ID NO: 134:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(140335..140733)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 134:

Pro Pro Leu Gly Asn Gln Ser Val Ile Cys Thr Gly Pro Ile Phe Leu
 1 5 10 15
 Glu Ile Cys Val Met Ser Ser Ile Ser Ser Pro Gly Asn Ile Gln His

Phe Ser
225

(2) INFORMATION POUR LA SEQ ID NO: 136:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 454 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(141780..143141)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 136:

Met 1	Thr	Thr	Lys	Ile 5	Lys	Thr	Gln	Trp	Thr 10	Cys	Thr	Glu	Cys	Gly 15	Thr
His	Ser	Pro	Lys 20	Trp	Leu	Gly	Gln	Cys 25	Ser	Gly	Cys	Leu	Gln 30	Trp	Asn
Thr	Leu	Val 35	Glu	Glu	Arg	Thr	Ala 40	Pro	Lys	Leu	Asn	Thr 45	Ser	Ser	Tyr
Ser	Ser 50	Ser	Ser	Ser	Ile	Pro 55	Ile	Pro	Leu	Asn	Asn 60	Val	Glu	Phe	Gln
Glu 65	Glu	Ile	Arg	Ile	His 70	Thr	Gln	Ala	Gln	Gly 75	Trp	Asn	Arg	Leu	Leu 80
Gly	Gly	Gly	Thr 85	Val	Arg	Gly	Ser	Leu	Ala 90	Leu	Leu	Gly	Gly 95	Glu	Pro
Gly	Ile	Gly	Lys 100	Ser	Thr	Leu	Leu 105	Leu	Gln	Ile	Ser	Ser 110	Gln	Phe	Ala
Ala	Ala	Gly 115	His	Lys	Val	Leu	Tyr 120	Val	Cys	Gly	Glu	Glu 125	Ser	Val	Ser
Gln	Thr 130	Ser	Leu	Arg	Ala	Gln 135	Arg	Leu	Gln	Ile	Ser 140	Ser	Asn	Asn	Ile
Phe 145	Leu	Phe	Pro	Glu	Thr 150	Asn	Leu	Glu	Asp	Ile 155	Lys	Gln	Gln	Ile	Asp 160
Asn	Ile	Ala	Pro 165	Asp	Ile	Leu	Val	Ile	Asp 170	Ser	Ile	Gln	Ile 175	Ile	Phe
Ser	Pro	Ser 180	Leu	Ser	Ser	Ala	Pro 185	Gly	Ser	Val	Ala	Gln 190	Val	Arg	Glu
Thr	Thr 195	Ala	Glu	Leu	Met	His 200	Ile	Ala	Lys	Gln	Lys 205	Gln	Ile	Thr	Thr
Phe 210	Ile	Ile	Gly	His	Val 215	Thr	Lys	Ser	Gly	Glu	Ile 220	Ala	Gly	Pro	Arg
Ile 225	Leu	Glu	His	Leu	Val 230	Asp	Thr	Val	Leu	Tyr 235	Phe	Glu	Gly	Asn	Val 240
His	Ala	Asn	Tyr 245	Arg	Met	Ile	Arg	Ser	Val 250	Lys	Asn	Arg	Phe	Gly 255	Pro
Thr	Asn	Glu 260	Leu	Leu	Ile	Leu	Ser 265	Met	His	Thr	Asp 270	Gly	Leu	Arg	Glu
Val	Glu 275	Asn	Pro	Ser	Gly	Leu	Phe 280	Leu	Gln	Glu	Lys 285	Ile	Val	Glu	Thr
Thr 290	Gly	Ser	Thr	Ile	Ile	Pro 295	Ile	Val	Glu	Gly	Ser 300	Glu	Thr	Leu	Leu
Val 305	Glu	Val	Gln	Ala	Leu 310	Val	Ser	Ser	Ser	Pro 315	Phe	Ser	Asn	Pro	Val 320
Arg	Lys	Thr	Ser	Gly	Phe	Asp	Pro	Asn	Arg	Phe	Ser	Leu	Leu	Leu	Ala

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          325          330          335
Val Leu Glu Lys Arg Ala Asn Ile Lys Leu Tyr Thr Ser Asp Val Phe
          340          345          350
Leu Ser Ile Ala Gly Gly Leu Lys Ile Thr Gln Pro Ser Ala Asp Leu
          355          360          365
Gly Ala Val Leu Ser Val Val Ser Ser Leu Tyr Asn Arg Tyr Leu Pro
          370          375          380
Lys Asn Tyr Thr Tyr Thr Gly Glu Ile Gly Leu Gly Gly Glu Ile Arg
385          390          395          400
His Val Ser His Met Glu His Arg Ile Lys Glu Ser Ile Ile Met Gly
          405          410          415
Phe Lys Gly Ile Val Met Pro Phe Gly Gln Ile Lys Gly Leu Pro Lys
          420          425          430
Glu Phe Leu Asp Gln Ile Asp Ile Ile Gly Val Lys Thr Ile Lys Asp
          435          440          445
Ala Val Arg Leu Leu Gln
          450

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(2) INFORMATIONS POUR LA SEQ ID NO: 137:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(143128..143829)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 137:

```

Lys Ile Val Met Gln His Thr Val Asp Ile Gln Ala Ile Glu Ser Lys
1          5          10          15
Leu Asn Phe Thr Phe Ser His Pro Arg Leu Leu Ile Thr Ala Leu Thr
          20          25          30
His Pro Ser Tyr Arg Asn Glu Phe Pro Ser Ala Glu Glu Asp Ser Glu
          35          40          45
Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu Val Val Thr Glu
          50          55          60
His Leu Phe Leu Leu Phe Pro Ala Leu Asn Glu Gly Leu Leu Ser Thr
65          70          75          80
Thr Arg Ala Ala Leu Val Asn Ala Glu Ala Cys Phe Glu Tyr Thr Gln
          85          90          95
Lys Leu Ser Leu Gly Glu His Leu Leu Ile Gly Arg Gly Glu Lys Met
          100          105          110
Gln Ser His Arg Gly Lys Ile Ser Ala Tyr Ala Asn Leu Phe Glu Ala
          115          120          125
Ile Leu Gly Ala Val Tyr Leu Asp Gly Gly Leu Ser Pro Ala Arg Gln
          130          135          140
Ile Ile Val Pro Leu Leu Pro Asp Lys Glu Ser Ile Leu Pro Leu Met
145          150          155          160
Leu Val Asn Pro Lys Asn Arg Leu Gln Gln Phe Thr Gln Gln Thr Leu
          165          170          175
Lys Val Leu Pro Ser Tyr Lys Ala Leu Pro Trp Lys Ser Glu Asp Gly
          180          185          190
Ser Pro Gly Tyr His Val Gln Val Phe Val Asn Gly Asp Leu Trp Gly
          195          200          205

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Glu Gly Phe Ala Gly Ser Lys Lys Glu Ala Glu Lys Leu Ala Ala Lys
 210 215 220
 Gln Ala Leu Ser Thr His Asp Asn Lys Asn
 225 230

(2) INFORMATIONS POUR LA SEQ ID NO: 138:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 143923..144393

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 138:

Val Ser Met Arg Ala Val Leu His Leu Glu His Lys Arg Tyr Phe Gln
 1 5 10 15
 Asn His Gly His Ile Leu Phe Glu Gly Leu Ala Pro Val Ser Asp Cys
 20 25 30
 Lys Gln Leu Glu Ala Glu Leu Lys Leu Phe Leu Lys Glu Val Ala Val
 35 40 45
 Val Lys Asp Arg His Leu Gln Arg Trp Arg Glu Asn Val His Arg Thr
 50 55 60
 Leu Pro Gly Val Gln Met Ile Val Lys Arg Val Arg Leu Asp His Leu
 65 70 75 80
 Ala Ala Glu Leu Thr His Arg Ser Arg Val Ala Leu Val Arg Asp Leu
 85 90 95
 Trp Val Gln Lys Gln Glu Glu Ile Leu Phe Asp Asp Cys Asp Cys Ser
 100 105 110
 Val Leu Leu Cys Leu Ser Gly Glu Lys Ala Gly Trp Gly Leu Phe Phe
 115 120 125
 Ser Gly Glu Tyr Pro Gln Asp Val Phe Asp Trp Gly Ala Gly Asp Thr
 130 135 140
 Ala Ile Ile Leu Arg Phe Ser Ser Ala Gly Phe Pro Asn
 145 150 155

(2) INFORMATIONS POUR LA SEQ ID NO: 139:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 583 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 144578..146326

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 139:

Met Phe Asp Pro Gln Thr Ala Lys Asn Ile Leu Ser Trp Leu Glu Asp
 1 5 10 15
 Val Val Cys Asp His Thr Ser Val Leu Thr Leu Leu Asp Asn Asp Pro

20 25 30
 Glu Arg Leu Arg Glu Leu Phe Ser Glu Thr Leu Thr Phe Gly Thr Ala
 35 40 45
 Gly Leu Arg Gly Leu Met Gly Ile Gly Thr Asn Arg Leu Asn Val Phe
 50 55 60
 Thr Ile Arg Arg Ala Thr Gln Gly Leu Ala Arg Val Leu Lys Arg Arg
 65 70 75 80
 Tyr Pro Asp Glu Lys Ile Ser Val Val Ile Gly Tyr Asp Thr Arg His
 85 90 95
 Asp Ser Phe Glu Phe Gly Gln Glu Thr Ala Lys Val Leu Ala Gly Asn
 100 105 110
 Gly Ile Leu Ala Tyr Leu Phe Gln Ile Pro Glu Pro Leu Ala Leu Val
 115 120 125
 Ser Tyr Ser Val Arg Glu Leu Gln Ala Lys Ala Gly Val Met Ile Thr
 130 135 140
 Ala Ser His Asn Pro Pro Ala Tyr Asn Gly Tyr Lys Val Tyr Met Ser
 145 150 155 160
 Thr Gly Gly Gln Val Leu Pro Pro Met Asp Gln Glu Ile Met Glu Glu
 165 170 175
 Phe Gln Lys Val Glu Met Val Ser Ala Val Glu Ser Leu Asp His Pro
 180 185 190
 Tyr Ile Arg Met Ile Gln Glu Asp Met Glu Asn Tyr Tyr Glu Glu Thr
 195 200 205
 Leu His Lys Leu Gln Leu Cys Glu Glu Asp Asn Arg Arg His Gly Ser
 210 215 220
 Leu Leu Arg Ile Ser Tyr Ser Pro Leu His Gly Thr Gly Val Thr Met
 225 230 235 240
 Ile Pro Arg Ile Leu Lys Asp Trp Gly Phe Ser Ser Val Ser Leu Val
 245 250 255
 Glu Lys Gln Met Val Pro Asp Gly Asp Phe Pro Thr Val Val Leu Pro
 260 265 270
 Asn Pro Glu Asp Pro Glu Ala Leu Val Leu Gly Ile Gln Gln Met Val
 275 280 285
 Glu Gln Lys Asp Asp Leu Phe Ile Ala Thr Asp Pro Asp Ser Asp Arg
 290 295 300
 Ile Gly Val Val Ser Leu Glu Lys Glu Gly Pro Tyr Arg Phe Asn Gly
 305 310 315 320
 Asn Gln Ile Ala Cys Leu Leu Ala Ala His Ile Leu Ser Lys Glu Ser
 325 330 335
 Gln Lys Ala Pro Leu Gly Ala Glu Asp Lys Val Val Lys Ser Leu Val
 340 345 350
 Thr Thr Glu Leu Leu Thr Ala Ile Ser Glu Ser Tyr Gly Ala Asn Ile
 355 360 365
 Val Asn Val Gly Ala Gly Phe Lys Tyr Ile Gly Glu Lys Ile Glu Leu
 370 375 380
 Trp Arg Ser Gly Met Glu Arg Phe Ile Phe Gly Ala Glu Glu Ser Tyr
 385 390 395 400
 Gly Tyr Leu Tyr Gly Ser Tyr Val Glu Asp Lys Asp Ala Met Ile Ala
 405 410 415
 Ala Val Leu Ile Ser Glu Ala Ala Leu Gln Gln Lys Ile Arg Gly Cys
 420 425 430
 Thr Leu Arg Asp Ala Leu Leu Glu Leu Tyr Glu Val Tyr Gly Tyr Tyr
 435 440 445
 Ala Asn Arg Thr Glu Ser Ile Asp Leu Pro Ile Asp Gln Pro Gln Arg
 450 455 460
 Lys Gln Glu Leu Leu Asp Arg Trp Glu Thr Gln Asp Pro Leu Arg Met
 465 470 475 480
 Ser Leu Ser Ser Arg Lys Leu Ile Ala Phe Glu Asn Tyr Asn Thr Gly
 485 490 495

Glu Gly Arg Asp Leu Val Thr Asp Ile Thr Tyr Lys Leu Ser Leu Pro
 500 505 510
 Lys Met Ser Met Leu Cys Phe Tyr Tyr Glu Gly Asp Cys Arg Val Ile
 515 520 525
 Val Arg Pro Ser Gly Thr Glu Pro Lys Met Lys Leu Tyr Phe Glu Ile
 530 535 540
 Lys Gln Ser Phe Ser Glu Phe Ser Lys Glu Arg Thr Val Arg Glu Ala
 545 550 555 560
 Arg Glu Lys Glu Ser Phe Glu Ala Leu Gln Gln Phe Ile Lys Glu Thr
 565 570 575
 Lys Ser His Leu Phe Tyr Ser
 580

(2) INFORMATIONS POUR LA SEQ ID NO: 140:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 146413..147078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 140:

Lys Ile Glu Lys Val Ala Arg Ile Val Thr Leu Phe Phe Arg Met Ala
 1 5 10 15
 Met Val Phe Ser Ser Tyr Met Leu Pro Ala Leu Pro Tyr Asp Tyr Asp
 20 25 30
 Ala Leu Glu Pro Val Ile Ser Ala Glu Ile Met Gln Leu His His Gln
 35 40 45
 Lys His His Gln Gly Tyr Ile Asn Asn Leu Asn Glu Ala Leu Lys Ser
 50 55 60
 Leu Asp Val Ala Asn Ala Thr Gln Asp Leu Thr Arg Leu Ile Ala Ile
 65 70 75 80
 Asn Pro Ala Leu Arg Phe Asn Gly Gly Gly His Ile Asn His Ser Leu
 85 90 95
 Phe Trp Glu Met Leu Ala Pro Gln Gly Lys Gly Gly Gly Val Pro Pro
 100 105 110
 Arg His Glu Leu Leu Lys Leu Ile Glu Lys Phe Trp Gly Ser Phe Asp
 115 120 125
 Ser Phe Leu Lys Asn Phe Ile Ala Ser Ser Ala Ala Val Gln Gly Ser
 130 135 140
 Gly Trp Gly Trp Leu Ala Phe Cys Pro Lys Lys Gln Glu Phe Val Val
 145 150 155 160
 Gln Thr Thr Ala Asn Gln Asp Pro Leu Glu Ala Thr Thr Gly Met Ile
 165 170 175
 Pro Leu Pro Gly Val Asp Val Trp Glu His Ala Tyr Tyr Leu Gln Tyr
 180 185 190
 Lys Asn Val Arg Ile Asp Tyr Leu Lys Ser Phe Pro Ser Ile Ile Asn
 195 200 205
 Trp Asp Tyr Ile Glu Asn Arg Phe Val Glu Met Ser Lys Gln
 210 215 220

(2) INFORMATIONS POUR LA SEQ ID NO: 141:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 312 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 147140..148075

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 141:

Glu Asp Gly Phe Val Arg Leu Phe Ser Tyr Asp Lys Pro Lys Ile Lys
 1 5 10 15
 Val Gln Lys Ile Lys Ala Asp Gly Phe Ser Gly Trp Leu Lys Cys Thr
 20 25 30
 His Cys Ser Glu Met Ile His Ala Asn Glu Leu Gly Gln Asn Phe Asn
 35 40 45
 Cys Cys Pro Lys Cys Ser Tyr His Tyr Arg Ile Ser Val Ser Glu Arg
 50 55 60
 Ile Ala Leu Leu Ala Asp Lys Asp Ser Trp Asn Pro Leu Phe Ser Asp
 65 70 75 80
 Leu Arg Ser Gln Asp Pro Leu Asn Phe Val Asp Thr Asp Thr Tyr Pro
 85 90 95
 Asn Arg Leu Glu Lys Ala Arg Lys Asp Asn Pro Asp Ser Glu Gly Val
 100 105 110
 Leu Val Gly Ala Cys Thr Ile Gly Ser Tyr Pro Val Ala Leu Ala Val
 115 120 125
 Met Asp Phe Ser Phe Met Ala Gly Ser Met Gly Ala Val Val Gly Glu
 130 135 140
 Lys Leu Thr Arg Leu Ile Glu Lys Ala Ile Asp Ser Arg Leu Pro Val
 145 150 155 160
 Ile Ile Val Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ser Val Phe
 165 170 175
 Ser Leu Met Gln Met Ala Lys Thr Ser Ala Ala Leu Ala Lys Leu His
 180 185 190
 Glu Ala Lys Leu Pro Tyr Ile Ser Val Leu Thr Asn Pro Thr Ser Gly
 195 200 205
 Gly Val Thr Ala Ser Phe Ala Ser Leu Gly Asp Val Ile Ile Ala Glu
 210 215 220
 Pro Lys Ala Leu Ile Cys Phe Ala Gly Pro Arg Val Val Ser Gln Val
 225 230 235 240
 Ile Gly Glu Asp Leu Pro Glu Gly Ala Gln Lys Ser Glu Phe Leu Leu
 245 250 255
 Glu His Gly Met Ile Asp Lys Val Val Glu Arg Lys Gln Leu Lys Thr
 260 265 270
 Thr Leu Glu Ser Leu Leu Ser Phe Phe Ser Cys Gln Ala Tyr Ser Gly
 275 280 285
 Gly Lys Gly Asn Cys Pro Arg Asp Ile Ser Lys Thr Ile Lys Glu Ile
 290 295 300
 Phe Leu Leu Thr Asp Asp Asn Lys
 305 310

(2) INFORMATIONS POUR LA SEQ ID NO: 142:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 148115..148549

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 142:

```

Met Lys Phe Phe Cys Lys Leu Glu Ser Gly Ser Ser Leu Pro Glu Tyr
1      5      10      15
Ala Thr Ser Gly Ala Ser Gly Ala Asp Val Arg Ala Asn Ile Asn Glu
      20      25      30
Pro Ile Ala Ile Leu Pro Gly Gln Arg Ala Leu Ile Pro Thr Gly Ile
      35      40      45
Ser Val Glu Ile Pro His Gly Tyr Glu Ile Gln Val Arg Ser Arg Ser
      50      55      60
Gly Leu Ala Ser Lys Tyr Gly Val Ile Val Leu Gln Ser Pro Gly Thr
65      70      75      80
Val Asp Ala Asp Tyr Arg Gly Glu Ile Arg Val Ile Leu Ala Asn Leu
      85      90      95
Gly Glu Xaa Thr Phe Ile Val Glu Pro Gly Met Arg Ile Ala Gln Leu
      100      105      110
Val Val Ala Lys Val Glu Gln Val Ser Phe Val Glu Thr Gln Glu Glu
      115      120      125
Leu Thr Ala Thr Ala Arg Gly Thr Gly Gly Phe Gly His Thr Gly Glu
      130      135      140
Cys
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 143:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 158 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 148554..149027

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 143:

```

Met Thr Cys Val Ala Asp His Lys Gln Ala Val Thr Leu Ser Ser Leu
1      5      10      15
Leu Ser Ser Asp Leu Ile Thr Phe Leu His Ser Asp Thr Arg Glu Asp
      20      25      30
Ile Leu Phe Glu Leu Ser Glu Leu Ala Ala Arg Ala Gly Leu Leu Glu
      35      40      45
Asp Arg Glu Ala Phe Phe Arg Ala Leu Leu Ala Arg Glu Asn Ile Met
      50      55      60
Ser Thr Gly Ile Gly Met Gly Val Ala Ile Pro His Gly Lys Ile Asp
65      70      75      80
Gly Ser Ala Asp Phe Phe Ile Ala Leu Gly Ile His Ser Glu Gly Ile
      85      90      95
Leu Trp Asp Ala Ile Asp Gly Leu Ser Val Arg Leu Val Phe Leu Ile

```

```

          100          105          110
Gly Gly Pro Ser Asp Ala Pro Ser Lys Tyr Leu Lys Leu Leu Ser Ala
          115          120          125
Leu Thr Gln Ser Leu Arg Asp Glu Ala Arg Arg Ser Gln Leu Leu Gln
          130          135          140
Val Gln Thr Val Glu Glu Val Met Ser Val Phe Ser Gly Val
145          150          155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 144:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 102 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149000..149305

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 144:

```

Arg Ser Tyr Glu Cys Phe Phe Arg Ser Leu Val Met Asp Leu Arg Leu
1          5          10          15
Asp Gln Leu Ala Val Leu Leu Asp Val Ala Glu Asp Ser Ile Arg Gln
          20          25          30
Trp Val Ser Cys Gly Gly Ile Pro Ser Tyr Thr Ile Asn Asp Glu Leu
          35          40          45
Arg Phe Asn Arg Glu Glu Val Glu Asp Trp Leu Ile His Asn His Gly
          50          55          60
Val Ile Pro Asp Glu Lys Arg Glu Glu Lys Gly Glu Ser Lys Asp Leu
          65          70          75          80
Ser Leu Arg Tyr Ser Leu Tyr Arg Ala Xaa Tyr Xaa Gly Arg Gly Ser
          85          90          95
Lys Lys Cys Ser Cys Arg
          100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 145:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 160 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149229..149708

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 145:

```

Pro Arg Ile Cys His Leu Asp Ile Ala Tyr Ile Glu Xaa Phe Ile Xaa
1          5          10          15
Gly Gly Val Leu Lys Asn Val Leu Val Asp Ser Lys Glu Gly Ala Leu
          20          25          30
Arg Tyr Ala Ala His Tyr Ile Ala Asn Lys Phe Glu Leu Asp Pro Val
          35          40          45

```

```

Val Leu Phe Glu Met Leu Met His Arg Glu Ser Leu Met Ser Thr Gly
  50                      55                      60
Ile Gly Glu Gly Ile Ala Leu Pro His Ala Lys Asp Phe Leu Ile Asn
  65                      70                      75                      80
Val Gly Tyr Asp Ile Ile Val Pro Val Phe Leu Ser Gln Ser Ile Glu
                      85                      90                      95
Tyr Gly Ala Leu Asp Gly Lys Pro Val Asp Thr Leu Phe Phe Leu Phe
                      100                      105                      110
Ala Asn Gln Asp Arg Asn His Leu Asn Leu Val Asn Lys Ile Val His
                      115                      120                      125
Leu Gly Met Ser Ile Gln Ala Arg Leu Phe Leu Lys Glu His Pro Asp
                      130                      135                      140
Gln Pro Gln Leu Leu Ala Phe Val Lys Asn Trp Glu Ala Gln Ile His
  145                      150                      155                      160

```

(2) INFORMATIONS POUR LA SEQ ID NO: 146:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 149712..150911

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 146:

```

Val Ile Asn Lys Lys Arg Ile Val Arg Pro Ser Cys Glu Lys Ser Phe
  1                      5                      10                      15
Asn Val Ala Met Val Ile Pro Lys Val Asp Leu Gly Glu Ser Ala Val
                      20                      25                      30
Met Leu Gly Tyr Lys Leu Thr Ser Gln Leu Ala Met Leu Ser Ile Leu
                      35                      40                      45
Leu Thr Phe Thr His Thr Met Gly His Ala Ser Gln Met Ser Gln Thr
                      50                      55                      60
Leu Pro Thr Ile Met Glu Ala Gln Ala Glu Glu Ala Leu Gln Ala Asp
  65                      70                      75                      80
Arg Gly Val Ser Gly Gln Ala Leu Lys Lys Leu Arg Lys Lys Arg Cys
                      85                      90                      95
Ala Ser Arg Lys Ser Ala Trp Lys Ala Ser Phe Glu Lys Lys Asp Phe
                      100                      105                      110
Phe Ser Cys Ile Thr Asn Gly Leu Phe Ser Arg Asn His Glu Gln Arg
                      115                      120                      125
Leu Thr Ala Lys Lys Glu Asn Lys Ala Arg Gly Lys Glu Pro Arg Val
                      130                      135                      140
Val Val Gln Thr Thr Lys Lys Arg Gln Thr Thr Gln Ser Glu Lys Glu
  145                      150                      155                      160
Phe Phe Asp Trp Leu Cys Asn Ser Lys Arg Asp Asp Lys Arg Lys Leu
                      165                      170                      175
Leu Lys Lys Lys Pro Val Asn Thr Ser Leu Ala Lys Ser Glu Glu Leu
                      180                      185                      190
Ser Pro Lys Glu Ala Ala Ile Ala Ala Arg Ala Ser Leu Ser Pro
                      195                      200                      205
Glu Glu Lys Arg Gln Leu Ile Arg Glu Trp Leu Ala Glu Glu Lys Thr
                      210                      215                      220
Ala Arg Lys Ser Gly Arg Ala Ala Cys Ala Val Ser Glu Asn Leu Lys

```

-

Leu	Phe	Pro	Ile	Pro	Asn	Asn	Asp	Glu	Asn	Ala	Lys	Thr	Lys	Glu	Ser
			180					185					190		
Gln	Leu	Leu	Asp	Ser	Glu	Asn	Asp	Ser	Asn	Ser	Glu	Phe	Gln	Glu	Ile
		195					200					205			
Ile	Asn	Lys	Gly	Leu	Glu	Ala	Ala	Asn	Lys	Arg	Arg	Ala	Asp	Ala	Lys
	210					215					220				
Ser	Lys	Phe	Tyr	Thr	Glu	Asp	Glu	Thr	Ser	Asp	Lys	Lys	Phe	Ser	Ile
225					230					235				240	
Trp	Lys	Pro	Thr	Lys	Asn	Leu	Ala	Leu	Glu	Asp	Leu	Trp	Arg	Val	His
			245					250					255		
Asp	Glu	Ala	Cys	Asn	Glu	Glu	Gln	Gln	Ala	Leu	Leu	Leu	Glu	Asp	Tyr
			260					265					270		
Met	Ser	Tyr	Lys	Thr	Ser	Glu	Cys	Gln	Ala	Ala	Leu	Gln	Lys	Val	Ser
		275					280					285			
Gln	Glu	Leu	Lys	Ala	Ala	Gln	Lys	Ser	Phe	Pro	Val	Leu	Glu	Lys	His
	290					295					300				
Ala	Leu	Asp	Arg	Ser	Tyr	Glu	Ser	Ser	Leu	Thr	Met	Met	Asp	Leu	Ala
305					310					315				320	
Arg	Ala	Asn	Gln	Glu	Thr	His	Arg	Leu	Leu	Asn	Ile	Leu	Ser	Glu	Leu
			325					330						335	
Gln	Gln	Leu	Ala	Gln	Tyr	Leu	Leu	Asp	Asn	His					
			340					345							

(2) INFORMATIONS POUR LA SEQ ID NO: 148:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(151999..152664)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 148:

His	Thr	Pro	Lys	Thr	Phe	Pro	Leu	Lys	Val	His	His	Ser	Phe	Ser	Asp
1				5					10					15	
Lys	His	Pro	Gln	Ile	Ala	Lys	Ala	Met	Trp	Ile	Thr	Gly	Ile	Ala	Leu
			20					25					30		
Ala	Ala	Leu	Ser	Leu	Leu	Ala	Val	Val	Ala	Cys	Val	Ile	Ala	Val	Ser
		35					40					45			
Ala	Gly	Gly	Ala	Ala	Ile	Pro	Leu	Thr	Val	Val	Gly	Gly	Ile	Ala	Ala
	50					55					60				
Met	Ser	Gly	Leu	Leu	Ser	Ala	Ala	Thr	Ile	Ile	Cys	Ser	Ala	Lys	Lys
65					70					75				80	
Ala	Leu	Ala	Gln	Arg	Lys	Gln	Lys	Gln	Leu	Glu	Ala	Ser	Leu	Pro	Leu
			85					90						95	
Asp	Asn	Ala	Thr	Glu	His	Val	Asn	Tyr	Leu	Thr	Ser	Asp	Thr	Pro	Tyr
			100					105					110		
Phe	Asn	Gln	Trp	Glu	Ser	Leu	Asp	Ala	Leu	Asn	Lys	Gln	Leu	Ser	Gln
		115					120					125			
Ile	Asp	Leu	Thr	Ile	Gln	Ala	Pro	Glu	Lys	Lys	Leu	Leu	Lys	Glu	Val
	130					135					140				
Leu	Gly	Ser	Arg	Tyr	Asp	Ser	Ile	Asn	His	Ser	Ile	Glu	Glu	Ile	Ser
145				150						155				160	
Asp	Arg	Phe	Thr	Lys	Met	Leu	Ser	Leu	Leu	Arg	Leu	Arg	Glu	His	Phe

				165				170					175				
Tyr	Arg	Gly	Glu	Glu	Arg	Tyr	Thr	Pro	Tyr	Leu	Thr	Pro	Pro	Leu	Leu		
			180					185					190				
Lys	Lys	Asn	Arg	Leu	Leu	Ile	Gln	Ile	Thr	Ser	Asn	Met	Ile	Arg	Met		
		195					200					205					
Leu	Pro	Lys	Phe	Gly	Gly	Val	Phe	Ser	Leu	Lys	Ala	Ile	His				
	210					215					220						

(2) INFORMATIONS POUR LA SEQ ID NO: 149:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 151 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 152900..153352

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 149:

Thr	Lys	Ala	Phe	Ser	Gly	Phe	Ile	Val	Arg	Lys	Thr	Val	Ile	Val	Ala		
1				5					10					15			
Met	Ser	Gly	Gly	Val	Asp	Ser	Ser	Val	Val	Ala	Tyr	Leu	Leu	Lys	Lys		
			20					25					30				
Gln	Gly	Glu	Tyr	Asn	Val	Val	Gly	Leu	Phe	Met	Lys	Asn	Trp	Gly	Glu		
		35					40					45					
Gln	Asp	Glu	Asn	Gly	Glu	Cys	Thr	Ala	Thr	Lys	Asp	Phe	Arg	Asp	Val		
	50					55					60						
Glu	Arg	Ile	Ala	Glu	Gln	Leu	Ser	Ile	Pro	Tyr	Tyr	Thr	Val	Ser	Phe		
65					70					75					80		
Ser	Lys	Glu	Tyr	Lys	Glu	Arg	Val	Phe	Ser	Arg	Phe	Leu	Arg	Glu	Tyr		
				85					90					95			
Ala	Asn	Gly	Tyr	Thr	Pro	Asn	Pro	Asp	Val	Leu	Cys	Asn	Arg	Glu	Ile		
		100						105					110				
Lys	Phe	Asp	Leu	Leu	Gln	Lys	Lys	Val	Leu	Glu	Leu	Lys	Gly	Asp	Phe		
		115					120					125					
Leu	Ala	Thr	Gly	His	Tyr	Cys	Arg	Gly	Gly	Ala	Asp	Gly	Thr	Gly	Phe		
	130					135					140						
Val	Gln	Arg	Lys	Arg	Pro	Gln											
145					150												

(2) INFORMATIONS POUR LA SEQ ID NO: 150:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 203 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 153389..153997

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 150:


```

Asp Ala Leu Ser Asn Val Leu Phe Pro Leu Gly Gly Met Tyr Lys Thr
1      5      10      15
Glu Val Arg Arg Ile Ala Gln Glu Ala Gly Leu Ala Thr Ala Thr Lys
20      25      30
Lys Asp Ser Thr Gly Ile Cys Phe Ile Gly Lys Arg Pro Phe Lys Ser
35      40      45
Phe Leu Glu Gln Phe Val Ala Asp Ser Pro Gly Asp Ile Ile Asp Phe
50      55      60
Asp Thr Gln Gln Val Val Gly Arg His Glu Gly Ala His Tyr Tyr Thr
65      70      75      80
Ile Gly Gln Arg Arg Gly Leu Asn Ile Gly Gly Met Glu Lys Pro Cys
85      90      95
Tyr Val Leu Ser Lys Asn Met Glu Lys Asn Ile Val Tyr Ile Val Arg
100     105     110
Gly Glu Asp His Pro Leu Leu Tyr Arg Gln Glu Leu Leu Ala Lys Glu
115     120     125
Leu Asn Trp Phe Val Pro Leu Gln Glu Pro Met Ile Cys Ser Ala Lys
130     135     140
Val Arg Tyr Arg Ser Pro Asp Glu Lys Cys Ser Val Tyr Pro Leu Glu
145     150     155     160
Asp Gly Thr Val Lys Val Ile Phe Asp Val Pro Val Lys Ala Val Thr
165     170     175
Pro Gly Gln Thr Val Ala Phe Tyr Gln Gly Asp Ile Cys Leu Gly Gly
180     185     190
Gly Val Ile Glu Val Pro Met Ile His Gln Leu
195     200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 151:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 431 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(153984..155276)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 151:

```

Ser Trp Ser Ser Cys Thr Ser Gln Tyr Asp Gly Thr Thr Ser Asp Leu
1      5      10      15
Met Arg Leu Glu Ala Glu Ile Glu Lys Thr Lys Gln Ala Lys Glu Gln
20      25      30
Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala Ser Leu Arg Asp Glu
35      40      45
Glu Lys Lys Leu Arg Glu Lys Leu Gly Asn Met Lys Gln Gln Trp Glu
50      55      60
Ser Asn Lys Glu Glu His Gln Val Pro Val Asp Glu Glu Ala Val Ala
65      70      75      80
Gln Val Val Ser Val Gln Thr Gly Ile Pro Ala Ala Arg Leu Thr Glu
85      90      95
Ala Glu Ser Glu Lys Leu Leu Thr Leu Glu Thr Thr Leu Gln Lys Lys
100     105     110
Val Ile Gly Gln Ser Gln Ala Val Ala Ser Ile Cys Arg Ala Ile Arg
115     120     125
Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg Pro Met Gly Ser Phe

```

130 135 140
 Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Leu Leu Ala Gln Gln
 145 150 155 160
 Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ser Leu Ile Gln Val Asp
 165 170 175
 Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr Lys Met Met Gly Ser
 180 185 190
 Pro Pro Gly Tyr Val Gly His Glu Gly Gly His Leu Thr Glu Gln
 195 200 205
 Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe Asp Glu Ile Glu Lys
 210 215 220
 Ala His Pro Asp Ile Met Asp Leu Met Leu Gln Ile Leu Glu Gln Gly
 225 230 235 240
 Arg Leu Thr Asp Ser Phe Gly Arg Lys Ile Asp Phe Arg Asn Thr Ile
 245 250 255
 Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu Ile Arg Lys Ser Gly
 260 265 270
 Glu Ile Gly Phe Gly Leu Arg Ser His Met Asp Tyr Ala Val Ile Lys
 275 280 285
 Glu Lys Ile Asp Ala Ala Val Lys Lys His Leu Lys Pro Glu Phe Ile
 290 295 300
 Asn Arg Leu Asp Glu Ser Val Ile Phe Lys Pro Leu Glu Lys Glu Ala
 305 310 315 320
 Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys Leu Gly Ser Arg Leu
 325 330 335
 Gln Asn Tyr Gln Met Asp Leu Asn Ile Pro Asp Ser Val Ile Ser Phe
 340 345 350
 Leu Val Thr Lys Gly His Ser Pro Glu Met Gly Ala Arg Pro Leu Arg
 355 360 365
 Arg Val Val Glu Gln Tyr Leu Glu Asp Pro Leu Ala Glu Met Leu Leu
 370 375 380
 Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu Arg Ala Arg Leu Thr
 385 390 395 400
 Glu Glu Arg Val Val Phe Glu Arg Glu Glu Glu Ala Val Ser Ala Leu
 405 410 415
 Ala Ile Glu Gly Asp Gly Ser Glu Pro Ile Thr Ala Asp Glu Ser
 420 425 430

(2) INFORMATIONS POUR LA SEQ ID NO: 152:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(155231..156544)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 152:

Met Phe Glu Lys Phe Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala
 1 5 10 15
 Lys Lys Glu Ala Gln Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His
 20 25 30
 Ile Leu Leu Gly Leu Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val
 35 40 45

```

Leu Arg Thr Leu Gly Val Asp Phe Asp Thr Ala Lys His Glu Val Glu
50          55          60
Arg Leu Ile Gly Tyr Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala
65          70          75          80
Leu Thr Gly Arg Val Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala
85          90          95
Ala Leu Leu Glu His Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly
100         105         110
Ile Leu Asn Gln Ser Asp Gly Val Ala Leu Gln Val Leu Glu Asn Leu
115         120         125
His Val Asp Pro Lys Glu Ile Arg Lys Glu Ile Leu Lys Glu Leu Glu
130         135         140
Thr Phe Asn Leu Gln Leu Pro Pro Ser Ser Ser Ile Thr Pro Arg Asn
145         150         155         160
Thr Asn Ser Ser Ser Ser Ser Lys Ser Ser Ser Pro Leu Gly Gly His
165         170         175
Thr Leu Gly Gly Asp Lys Pro Glu Lys Leu Ser Ala Leu Lys Ala Tyr
180         185         190
Gly Tyr Asp Leu Thr Glu Met Phe Lys Glu Ser Arg Leu Asp Pro Val
195         200         205
Ile Gly Arg Ser Ala Glu Val Glu Arg Leu Ile Leu Ile Leu Cys Arg
210         215         220
Arg Arg Lys Asn Asn Pro Val Leu Val Gly Glu Ala Gly Val Gly Lys
225         230         235         240
Thr Ala Ile Val Glu Gly Leu Ala Gln Lys Ile Val Ser Gly Glu Val
245         250         255
Pro Glu Ala Leu Arg Lys Lys Arg Leu Ile Thr Leu Asp Leu Ala Leu
260         265         270
Met Ile Ala Gly Thr Lys Tyr Arg Gly Gln Phe Glu Glu Arg Ile Lys
275         280         285
Ala Val Met Asp Glu Val Arg Lys His Gly Asn Ile Leu Leu Phe Ile
290         295         300
Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ala Glu Gly Ala Ile
305         310         315         320
Asp Ala Ser His Ile Leu Lys Pro Ala Leu Ala Arg Gly Glu Ile Gln
325         330         335
Cys Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys
340         345         350
Asp Ala Ala Leu Glu Arg Arg Phe Gln Lys Ile Val Val Gln Pro Pro
355         360         365
Ser Val Asp Glu Thr Val Glu Ile Leu Arg Gly Leu Lys Lys Lys Tyr
370         375         380
Glu Glu His His Asn Val Phe Ile Thr Asp Glu Ala Leu Val Ala Ala
385         390         395         400
Ala Lys Leu Ser Asp Gln Tyr Val His Gly Arg Phe Leu Pro Asp Lys
405         410         415
Ala Ile Asp Leu Leu Asp Glu Ala Gly Ala Arg Val Arg Val Asn Thr
420         425         430
Met Gly Gln Leu Arg Thr
435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 153:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 240 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 156806..157525

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 153:

```

Ile Met Arg Thr Arg Val Ile Asp Ser Ile Arg Gly Thr Pro Lys Asp
1      5      10      15
Leu Met Gln Lys Asp Arg Leu Leu Leu Asp Ser Leu Arg Lys Gly Glu
20      25      30
Val Ile Leu His Leu Tyr Glu Trp Glu Gly Ile Phe Pro Leu Thr Tyr
35      40      45
Gly Cys Phe Ile Lys Pro Glu Arg Phe Leu Lys Ala Asn Trp Glu Ser
50      55      60
Leu Gly Val Ser Ala Ala Ser Arg Pro Thr Gly Gly Gly Val Thr Phe
65      70      75      80
His Asn Ser Asp Tyr Ala Phe Ser Leu Leu Val Ser Ser Glu His Pro
85      90      95
Leu Tyr Gln Asp Ser Ile Leu Ala Asn Tyr His Thr Val Asn Arg Phe
100     105     110
Val Leu Lys Thr Ile Asn Lys Leu Phe Gly Leu Glu Gly Ser Leu Ser
115     120     125
Pro Ile Glu Val Ser Thr Asp Arg Ala Glu Ser Ser Asn Phe Cys Val
130     135     140
Ala Lys Thr Ser Lys Tyr Asp Val Leu Ile Gly Asn Arg Lys Val Gly
145     150     155     160
Gly Ala Ala Gln Arg Ser Val Lys Gln Gly Phe Leu His Gln Gly Ser
165     170     175
Ile Phe Leu Ser Gly Asn Ser Leu Asp Phe Tyr Arg Asn Ile Leu Leu
180     185     190
Pro Asp Leu Val Asp Lys Ile Gly Pro Glu Val Glu Lys Ser Ala Phe
195     200     205
Phe Pro Leu Gly Met Glu Ala Ser Ser Thr Val Leu Lys Glu Val Arg
210     215     220
Lys Glu Val Lys Asp Ser Leu Met Arg Ile Phe Met Gln Glu Gly Ile
225     230     235     240

```

(2) INFORMATIONS POUR LA SEQ ID NO: 154:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 489 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 157489..158955

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 154:

```

Arg Leu Phe Asp Ala Asp Leu Tyr Ala Gly Gly Asp Leu Ile Arg Met
1      5      10      15
Lys Met Ala Phe Leu Arg Lys Ile Phe Val Phe Val Ala Cys Val Val
20      25      30
Ser Leu Asn Gly Phe Ala His Thr Ile Ala Ile Pro Asp Gly Asp Lys
35      40      45

```

Lys Ala Lys Val Leu Ile His Asp Asn Gly Tyr Glu Met Tyr Glu His
 50 55 60
 Leu Leu Ala Ala Ile Ser Ser Ala Lys Tyr Thr Val Glu Leu Cys Pro
 65 70 75 80
 Cys Leu Ala Gly Gly Glu Ile Leu Ser Thr Val Leu Gln Arg Leu Glu
 85 90 95
 Gln Arg Met Glu Glu Val Pro Ala Leu Val Ser Tyr Ile Leu Val Gln
 100 105 110
 Pro Thr Cys Ile Asp Asp Asn Asp Arg Lys Asn Leu Lys Thr Leu Gln
 115 120 125
 Glu Asn Tyr Pro Asp Arg Phe Phe Tyr Leu Phe Ser Asp Trp Pro Pro
 130 135 140
 Tyr Cys Asn Val Phe Phe Pro Asn Val Thr Glu Ser His Thr Lys Leu
 145 150 155 160
 Ser Ile Val Asp Gly Lys Tyr Ile Phe Ile Gly Gly Ser Asn Leu Glu
 165 170 175
 Asp Leu Gln Cys Ser Lys Gly Asp Val Asp Leu Glu Val Ser Asp Ser
 180 185 190
 Pro Arg Ala Val Ile Gly Gly Val Leu Arg Pro Ser Ala Met Arg Asp
 195 200 205
 Gln Asp Val Thr Ile Val Ser Glu Glu Tyr Gly Ala Leu Leu Arg Lys
 210 215 220
 Glu Phe Cys Ala His Tyr Ala Leu Trp Lys Asp Phe Thr Gln Lys Leu
 225 230 235 240
 Trp Leu Asn Lys Lys Leu Asp Asp Phe Arg Gly Ile Asp Pro Ile Asn
 245 250 255
 Leu Ser Ile Glu Lys Ala Arg Ser Ser Phe Cys Ala Met Ile Glu Thr
 260 265 270
 Ser Leu Cys Ala Val Ser Val Pro Leu Asp Lys Met His Phe Ile Phe
 275 280 285
 Ser Gly Pro Asp Glu Ser Asn Asn Thr Ile Ala Glu Glu Tyr Val Arg
 290 295 300
 Leu Ile Asn Gln Ala Gln His Ser Ile Arg Ile Ala Gln Met Phe Phe
 305 310 315 320
 Ile Pro Val Ala Lys Ile Tyr Asp Ser Leu Met Ala Ala Cys Trp Asp
 325 330 335
 Arg Gly Val Glu Ile Tyr Leu Val Thr Asn Gly Arg Thr Asp Arg Ser
 340 345 350
 Pro Glu Ile Thr Arg Ser Tyr Ala Trp Gly Asn Arg Ile Asn Tyr Phe
 355 360 365
 Pro Leu Thr Phe Gly Ser Arg Pro Leu Leu Trp Glu Arg Phe Leu Tyr
 370 375 380
 Ser Pro Ser Arg Ala Ser Met Lys Phe Tyr Val Ser Glu Phe Tyr Val
 385 390 395 400
 Ala Asn Thr Gln Leu His Lys Lys Cys Met Leu Val Asp Asp His Ile
 405 410 415
 Leu Val Ile Gly Ser Tyr Asn Phe Gly Lys Lys Ser Asn Asp Cys Asp
 420 425 430
 Tyr Glu Cys Ile Val Val Ile Asp Ser Lys Glu Ala Val Ser Lys Ala
 435 440 445
 Gln Val Val Phe Glu Lys Asp Leu Arg Leu Ser Lys Ser Val Thr His
 450 455 460
 Asp Asp Ile Ile Asn Trp Tyr Phe Asp Pro Val His Tyr Cys Leu Gly
 465 470 475 480
 Tyr Leu Glu Gln Arg Tyr Met Pro Ser
 485

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 286 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 159104..159961

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 155:

Phe	Ser	Phe	Phe	Phe	Leu	Lys	Gly	Leu	Phe	Ser	Lys	Lys	Lys	Gly	Leu
1				5				10						15	
Leu	Leu	Ala	Phe	Phe	Asn	Lys	His	Gln	Lys	Lys	Phe	Ile	Gly	Leu	Val
			20					25					30		
Ile	Ala	Gly	Val	Cys	Leu	Ser	Gly	Val	Gly	Val	Ser	Val	Gly	Gln	Thr
		35					40					45			
Val	Lys	Lys	Thr	Asn	Lys	Leu	Gly	Ser	Gly	Lys	Thr	Val	Tyr	Arg	Thr
	50					55					60				
Pro	Ser	Gly	Arg	Lys	Tyr	Ser	Glu	Lys	Glu	Phe	Leu	Leu	Leu	Lys	His
65					70					75				80	
Phe	Leu	Ser	Asn	Glu	Ala	Tyr	Pro	Phe	Thr	Gly	Asn	Pro	Arg	Glu	Trp
				85					90					95	
Asn	Phe	Leu	Asn	Glu	Gly	Leu	Leu	Thr	Glu	Arg	Phe	Leu	Thr	Asn	Lys
			100					105					110		
Leu	Gly	Glu	Lys	Leu	Phe	Leu	Ser	Ile	Tyr	Lys	Ser	Gly	Phe	Pro	Ala
	115						120					125			
Phe	Asp	Lys	Glu	Arg	Ser	Tyr	Glu	Gly	Tyr	Arg	Arg	Phe	Asp	Ala	Pro
	130					135					140				
Phe	Ile	Ser	Ser	Glu	Glu	Val	Trp	Lys	Ser	Ser	Ala	Pro	Gln	Leu	Arg
145					150					155				160	
Glu	Ala	Phe	His	Ile	Phe	Gln	Gln	Leu	Thr	Asp	Pro	Val	Ser	Pro	Glu
			165						170					175	
Gly	Phe	Ala	Val	Arg	Val	Arg	Leu	Phe	Leu	Glu	Glu	Lys	Lys	Phe	Pro
			180					185					190		
His	Tyr	Val	Leu	Arg	Gln	Met	Leu	Glu	Tyr	Arg	Arg	Gln	Met	Phe	Asn
		195				200						205			
Leu	Pro	Val	Asp	Asn	Ser	Leu	Val	Gln	Gly	Arg	Asp	Leu	Arg	Leu	Phe
	210					215					220				
Gly	Tyr	Lys	Asn	Val	Lys	Asp	Trp	Phe	Gly	Asp	Lys	Tyr	Ile	Ser	Ser
225					230					235				240	
Val	Thr	Glu	Ala	Met	Leu	Cys	Phe	Ile	Asp	Glu	Gln	Lys	Lys	Lys	Val
			245						250					255	
Gly	Met	Pro	Ser	Leu	Lys	Glu	Ala	Arg	Gln	Asp	Phe	Tyr	Asp	Lys	Ala
			260					265					270		
Gln	Met	His	Leu	Pro	Asp	Leu	Val	Asn	Met	Leu	Ser	Leu	Ile		
			275				280						285		

(2) INFORMATIONS POUR LA SEQ ID NO: 156:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 435 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 159916..161220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 156:

Ser	Ala	Asp	Ala	Phe	Ala	Arg	Leu	Ser	Lys	His	Ala	Glu	Phe	Asn	Leu	1	5	10	15
Thr	Phe	Glu	Gln	Leu	Val	Ala	Ser	Phe	Tyr	Ala	Phe	Met	Gly	Val	Glu	20	25	30	
Glu	Ser	Asp	Phe	Leu	Gly	Met	Tyr	Arg	Glu	Ile	Leu	Leu	Tyr	Lys	Lys	35	40	45	
Ala	Leu	Leu	Ser	Leu	Glu	Gly	Ala	Val	Ser	Phe	Asp	Tyr	Tyr	Pro	Leu	50	55	60	
Gln	Lys	Phe	Phe	Ser	Met	Gly	Lys	Asp	Ser	Val	Ser	Val	Glu	Leu	Phe	65	70	75	80
His	Leu	Pro	Asp	Ser	Leu	Val	Phe	Lys	Asp	Lys	Glu	Asp	Leu	Glu	Ala	85	90	95	
Phe	Glu	Thr	Tyr	Leu	His	Leu	Thr	Ala	Phe	Pro	Ser	Val	His	Val	Leu	100	105	110	
Asp	Val	Pro	Thr	Lys	Ala	Phe	Pro	Ile	Glu	Arg	Val	Arg	Ser	Lys	Ala	115	120	125	
Glu	Cys	Leu	Val	Gly	Lys	Arg	Phe	Ala	Val	Ser	Tyr	Gln	Ser	Val	Lys	130	135	140	
Leu	Ala	Asp	Leu	Glu	Lys	Tyr	Val	Pro	Met	Ala	Gln	Val	Tyr	Gln	Trp	145	150	155	160
Tyr	Gln	Asn	Pro	Glu	Asn	Phe	Glu	Glu	Ile	Leu	Leu	Glu	Phe	Pro	Glu	165	170	175	
Leu	Glu	Thr	Ser	Ser	Ser	Leu	Arg	Asp	Ile	Leu	Asn	Leu	Lys	Pro	Thr	180	185	190	
Ile	Val	Glu	Lys	Ala	His	Ser	Tyr	Val	Arg	Lys	Ala	Ile	Leu	Arg	Ala	195	200	205	
Asp	Pro	Glu	Arg	Ile	Gln	Ser	Glu	Leu	Ala	Lys	Lys	Glu	Arg	Gln	Glu	210	215	220	
Glu	Glu	Leu	Phe	Leu	Ser	Ile	Gly	Lys	Asp	His	Val	Leu	Pro	Gly	Ile	225	230	235	240
Gln	Asn	Gly	Val	Arg	Leu	Ala	Asn	Val	Leu	Met	Gln	Gln	Asp	Ser	Val	245	250	255	
Asp	Ser	Tyr	Thr	Gln	Asp	Asn	Glu	His	Phe	Tyr	Ser	Ile	Ser	Val	Ile	260	265	270	
Ser	Arg	Ala	Asp	Lys	Asp	Glu	Val	Leu	Pro	Tyr	Lys	Glu	Val	Leu	Arg	275	280	285	
Lys	Gly	Leu	Lys	Lys	Val	Leu	Leu	Glu	Lys	Tyr	Lys	Ala	Glu	Glu	Arg	290	295	300	
Ile	Ser	Arg	Val	Leu	Thr	His	Leu	Gln	Glu	Ser	Phe	Pro	Asn	Ser	Gln	305	310	315	320
Gly	Gln	Asp	Leu	Tyr	Gln	Arg	Arg	Leu	Val	Arg	Phe	Val	Lys	Ala	Phe	325	330	335	
Gln	Thr	Gly	Lys	Leu	Ala	Gln	Gly	Asp	Leu	Phe	Gly	Gly	Leu	Glu	Lys	340	345	350	
Thr	Met	Lys	Thr	Phe	Ser	Arg	Gly	Asp	Gln	Gly	Ala	Pro	Gln	Glu	Phe	355	360	365	
Glu	Asp	Met	Phe	Ala	Leu	Lys	Glu	Gly	Gln	Val	Ser	Asp	Val	Leu	Phe	370	375	380	
Asp	Leu	Asp	Lys	Gly	Pro	Phe	Tyr	Tyr	Thr	Ala	Ile	Ser	Lys	Ser	Cys	385	390	395	400
Cys	Asp	Tyr	Pro	Val	Ser	Leu	Asp	Lys	Leu	Leu	Phe	Ala	Lys	Ser	His	405	410	415	
Leu	Asn	Glu	Glu	Phe	Leu	Arg	Pro	Tyr	Leu	Glu	Glu	Val	Phe	Phe	His				

Asn Pro Ser 420 425 430
435

(2) INFORMATIONS POUR LA SEQ ID NO: 157:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 137 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 161183..161593

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 157:

Asp	Pro	Ile	Trp	Lys	Lys	Phe	Phe	Phe	Thr	Thr	Leu	Val	Lys	Gly	Leu
1				5					10					15	
Ser	Arg	Thr	Asn	Met	Lys	Gly	Gln	Lys	Tyr	Tyr	Ser	Asp	Tyr	His	Val
			20					25					30		
Trp	Ile	Glu	Pro	Ile	His	Ser	Arg	Ile	Val	Lys	Leu	Gly	Leu	Ser	Ser
		35					40					45			
Gln	Met	Ala	Gly	Xaa	Leu	Gly	Asn	Ile	Leu	His	Ile	Asp	Leu	Pro	Ser
	50					55					60				
Val	Gly	Ser	Phe	Ile	Lys	Glu	Gly	Glu	Glu	Leu	Cys	Ile	Leu	Glu	Ser
65					70				75					80	
Ser	Lys	Ser	Ala	Ile	Glu	Val	Leu	Ser	Pro	Val	Ser	Gly	Glu	Val	Leu
				85					90				95		
Glu	Val	Asn	Thr	Ala	Leu	Glu	Asp	Asp	Ile	Leu	Pro	Val	Asn	Asn	Ala
		100					105						110		
Thr	Glu	Ser	Glu	Gly	Trp	Phe	Val	Val	Leu	Gln	Leu	Thr	Glu	Asp	Phe
		115					120					125			
Arg	Ser	Glu	Ser	Phe	Ser	Leu	Glu	Pro							
		130				135									

(2) INFORMATIONS POUR LA SEQ ID NO: 158:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 237 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(161623..162333)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 158:

Leu	Leu	Asn	Leu	Leu	Gly	Ile	Phe	Leu	Gln	Ala	Thr	Phe	Ile	Gln	Asn
1				5					10					15	
Ile	Leu	Leu	Ser	Thr	Phe	Leu	Gly	Met	Cys	Ser	Tyr	Leu	Ala	Cys	Ser
			20					25					30		
Ser	Arg	Leu	Ser	Thr	Ala	Asn	Gly	Leu	Gly	Met	Ser	Val	Ala	Leu	Val
		35					40					45			


```

Leu Thr Ile Thr Gly Ser Ile Asn Trp Leu Val His Tyr Phe Ile Thr
 50          55          60
Lys Pro Gly Ala Leu Ala Trp Leu Ser Pro Ala Leu Ala Asn Ile Asp
65          70          75          80
Leu Ser Phe Leu Glu Leu Ile Met Phe Ile Val Val Ile Ala Ala Phe
          85          90          95
Thr Gln Ile Leu Glu Leu Leu Leu Glu Arg Phe Ser Arg Asn Leu Tyr
          100          105          110
Leu Ala Leu Gly Ile Phe Leu Pro Leu Ile Ala Val Asn Cys Ala Ile
          115          120          125
Leu Gly Gly Val Leu Phe Gly Ile Thr Arg Asn Tyr Pro Phe Leu Pro
130          135          140
Met Val Val Phe Ser Leu Gly Ser Gly Cys Gly Trp Trp Leu Ala Ile
145          150          155          160
Val Leu Phe Ala Thr Ile Arg Glu Lys Leu Ala Tyr Ser Asp Val Pro
          165          170          175
Gln His Leu Arg Gly Thr Gly Ile Ser Phe Ile Thr Thr Gly Leu Met
          180          185          190
Ala Met Ala Phe Met Gly Leu Thr Gly Ile Asp Ile Ser Lys Pro Thr
          195          200          205
Thr Ser Lys Pro Ala Xaa Xaa Met Asn Ile Ala Thr Asp Ser Pro Gln
210          215          220
Pro Asn Thr His Ser Ser Ser Glu Glu Pro Lys Ala Ser
225          230          235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 159:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 213 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(162363..163001)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 159:

```

Met Thr Thr Asn Lys Ser Tyr Leu Thr Tyr Phe Thr Asp Ala Leu Trp
 1          5          10          15
Ile Asn Asn Gln Pro Leu Ile Ala Ile Leu Gly Ile Cys Ser Ala Leu
          20          25          30
Ala Val Thr Thr Thr Val Thr Thr Ala Leu Thr Met Gly Phe Ala Val
          35          40          45
Ser Phe Val Thr Gly Cys Ser Ser Phe Val Val Ser Leu Leu Arg Lys
50          55          60
Ile Thr Pro Glu Ser Val Arg Met Ile Ala Gln Leu Ile Ile Ile Ser
65          70          75          80
Leu Phe Val Ile Leu Ile Asp Gln Phe Leu Lys Ala Phe Phe Phe Thr
          85          90          95
Ile Ser Lys Thr Leu Ser Val Phe Val Gly Leu Ile Ile Thr Asn Cys
          100          105          110
Ile Val Met Gly Arg Ala Glu Ser Met Ala Arg His Val Ser Pro Ile
          115          120          125
Pro Ala Phe Leu Asp Gly Leu Gly Ser Gly Leu Gly Tyr Gly Trp Val
130          135          140
Leu Val Cys Ile Ser Ile Ile Arg Glu Leu Phe Gly Phe Gly Thr Ile

```

```

145          150          155          160
Leu Gly Phe Arg Val Ile Pro Glu Ile Leu Tyr Ala Ser Ala Ala His
          165          170          175
Pro Asp Gly Tyr Glu Asn Leu Gly Leu Met Val Leu Ala Pro Ser Ala
          180          185          190
Phe Phe Leu Leu Gly Ile Met Ile Trp Ile Val Asn Ile Ile Arg Ala
          195          200          205
Pro Lys Thr Lys Arg
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 160:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(162994..163785)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 160:

```

Met Leu Met Ala Ala Gln Val Ile Ser Ser Asp Asn Thr Phe Gln Val
1      5      10      15
Tyr Glu Lys Gly Asp Trp His Pro Ala Leu Tyr Asn Thr Lys Lys Gln
20     25     30
Leu Leu Glu Ile Ser Ser Thr Pro Pro Lys Val Thr Val Thr Thr Leu
35     40     45
Ser Ser Tyr Phe Gln Asn Phe Val Arg Val Leu Leu Thr Asp Thr Gln
50     55     60
Gly Asn Leu Ser Ser Phe Glu Asp His Asn Leu Asn Leu Glu Glu Phe
65     70     75     80
Leu Ser Gln Pro Thr Pro Val Ile His Gly Leu Ala Leu Tyr Val Val
85     90     95
Tyr Ala Ile Leu His Asn Asp Ala Ala Ser Ser Lys Leu Ser Ala Ser
100    105    110
Gln Val Ala Lys Asn Pro Thr Ala Ile Glu Ser Ile Val Leu Pro Ile
115    120    125
Glu Gly Phe Gly Leu Trp Gly Pro Ile Tyr Gly Phe Leu Ala Leu Glu
130    135    140
Lys Asp Gly Asn Thr Val Leu Gly Thr Ser Trp Tyr Gln His Gly Glu
145    150    155    160
Thr Pro Gly Leu Gly Ala Asn Ile Ala Asn Pro Gln Trp Gln Lys Asn
165    170    175
Phe Arg Gly Lys Lys Val Phe Leu Val Ser Ala Ser Gly Glu Thr Asp
180    185    190
Phe Ala Lys Thr Thr Leu Gly Leu Glu Val Ile Lys Gly Ser Val Ser
195    200    205
Ala Ala Leu Gly Asp Ser Pro Lys Ala Ala Ser Ser Ile Asp Gly Ile
210    215    220
Ser Gly Ala Thr Leu Thr Cys Asn Gly Val Thr Glu Ser Phe Ser His
225    230    235    240
Ser Leu Ala Pro Tyr Arg Ala Leu Leu Thr Phe Phe Ala Asn Ser Lys
245    250    255
Pro Ser Gly Glu Ser His Asp His
260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 161:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 342 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(164474..165499)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 161:

```

Arg Phe Glu Arg Val Thr Phe Ser Thr Phe Leu Ser Asp Thr Met Leu
1      5      10      15
Glu Lys Leu Val Asp Ser Leu Trp Lys Ile Cys Arg Lys Ser Lys Phe
      20      25      30
Gln His Met Thr Pro Ile Ala Asp Ala Val Asp Thr Phe Cys Phe Glu
      35      40      45
Pro Leu His Thr Pro Ser Ser Pro Pro Phe Val Arg Asp Ala Val Asp
      50      55      60
Val Lys Arg Trp Met Met Leu Val Val Ile Ala Leu Met Pro Thr Ile
65      70      75      80
Phe Ala Ala Val Trp Asn Ser Gly Leu Gln Ala Leu Val Tyr Gln Ser
      85      90      95
Ser Asn Pro Arg Ile Met Glu Ala Xaa Leu His Ile Ser Gly Phe Lys
      100      105      110
Ser Tyr Phe Ser Phe Val Ser Gln Glu Ile Gly Ile Gly Ser Val Leu
      115      120      125
Phe Ala Gly Cys Lys Ile Phe Leu Pro Leu Leu Phe Ile Ser Tyr Ala
130      135      140
Val Gly Gly Thr Cys Glu Val Leu Phe Ala Ile Ile Arg Lys His Lys
145      150      155      160
Ile Ala Glu Gly Leu Leu Val Thr Gly Met Leu Tyr Pro Leu Ile Leu
      165      170      175
Pro Pro Thr Ile Pro Tyr Trp Met Ala Ala Leu Gly Ile Ala Phe Gly
      180      185      190
Val Val Met Gly Lys Glu Leu Phe Gly Gly Thr Gly Met Asn Ile Leu
195      200      205
Asn Pro Ala Leu Thr Gly Arg Ala Phe Leu Phe Phe Thr Phe Pro Ala
210      215      220
Lys Met Ser Gly Asp Val Trp Val Gly Ser Asn Pro Ser Arg Ile Lys
225      230      235      240
Glu Ser Leu Ala Thr Met Ser Ser Leu Ala Glu Lys Ser His Phe Asp
      245      250      255
Gly Phe Ser Gln Ser Thr Cys Leu Gln Ile Leu Asn Ser Thr Pro Pro
260      265      270
Ser Val Lys Arg Val His Ile Asp Ala Ile Ala Ser Asn Ile Leu Asn
275      280      285
Leu Glu His Val Pro Thr Gln Asp Val Leu Gln Thr Gln Phe Ala Thr
290      295      300
Trp Ala Glu Ser Tyr Pro Gly Leu Thr Val Asp Gln Leu Ser Leu Glu
305      310      315      320
Xaa Thr Ser Lys Phe Cys Asn Tyr Ser Asn Asn Arg Arg Arg Phe Arg
      325      330      335
Ala Ser Ser Cys Thr Leu

```

340

(2) INFORMATIONS POUR LA SEQ ID NO: 162:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 130 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(166093..166482)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 162:

```

Asp Gln Gln Glu Gly Leu Ala Thr Gln Glu Ser Ser Phe Pro Glu Glu
1      5      10      15
Pro Glu Thr Thr Leu Gly Glu Gly Val Ser Phe Lys Gly Glu Leu Thr
      20      25      30
Phe Glu Arg Leu Leu Arg Ile Asp Gly Thr Phe Glu Gly Ile Leu Val
      35      40      45
Ser Lys Gly Lys Ile Ile Val Gly Pro Gln Gly Tyr Val Lys Ala Asn
      50      55      60
Ile Glu Leu Glu Glu Ala Val Ile Ala Gly Val Val Glu Gly Asn Ile
65      70      75      80
Thr Val Thr Gly Arg Val Ser Leu Gln Gly Arg Ala Met Val Thr Gly
      85      90      95
Asp Ile Gln Ala Gly Ser Leu Cys Val Asp Glu Gly Val Arg Leu Cys
      100      105      110
Gly Tyr Val Ser Ile Gln Gly Ala Pro Ser Asn Glu Gln Glu Glu Ile
      115      120      125
Asp Ser
      130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 163:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 455 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(166729..168093)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 163:

```

Met Leu Thr Cys Asn Asp Cys Ser Thr Trp Glu Gln Phe Val Asn Tyr
1      5      10      15
Ile Lys Thr Arg Cys Ser Lys Thr Ala Phe Glu Asn Trp Ile Ala Pro
      20      25      30
Ile Gln Val Leu Glu Glu Ser Ser Glu Lys Ile Arg Leu Glu Ile Pro
      35      40      45
Asn Ile Phe Val Gln Ser Tyr Leu Leu Asp Asn Tyr Lys Lys Asp Leu
      50      55      60

```

Cys	Ser	Phe	Val	Pro	Leu	Asp	Ala	Glu	Gly	Asn	Pro	Ala	Leu	Glu	Phe
65					70					75					80
Val	Val	Ala	Glu	Ile	Lys	Arg	Ser	Ser	Pro	Leu	Val	Thr	Pro	Ser	Ile
				85					90					95	
Ala	Lys	Pro	Ala	Thr	Glu	Val	Ser	Glu	Glu	Asn	Lys	Asp	Phe	Gln	Leu
			100					105					110		
Lys	Leu	Asn	Gly	Ala	Tyr	Arg	Phe	Asp	Asn	Phe	Ile	Glu	Gly	Pro	Ser
		115					120					125			
Asn	Gln	Phe	Val	Lys	Ser	Ala	Ala	Leu	Gly	Ile	Ala	Ala	Arg	Pro	Gly
	130					135					140				
Arg	Ser	Tyr	Asn	Pro	Leu	Phe	Ile	His	Gly	Gly	Val	Gly	Leu	Gly	Lys
145					150					155					160
Thr	His	Leu	Leu	His	Ala	Val	Gly	His	Tyr	Val	Arg	Glu	His	His	Lys
				165					170					175	
Asn	Leu	Arg	Ile	His	Cys	Ile	Thr	Thr	Glu	Ala	Phe	Ile	Asn	Asp	Leu
			180					185					190		
Val	His	His	Leu	Arg	Val	Lys	Ser	Ile	Asp	Lys	Met	Lys	Asn	Phe	Tyr
		195					200					205			
Arg	Ser	Leu	Asp	Leu	Leu	Leu	Val	Asp	Asp	Ile	Gln	Phe	Leu	Gln	Asn
	210					215					220				
Arg	Gln	Asn	Phe	Glu	Glu	Glu	Phe	Cys	Asn	Thr	Phe	Glu	Thr	Leu	Ile
225				230						235					240
His	Leu	Ser	Lys	Gln	Ile	Val	Val	Thr	Ser	Asp	Lys	Pro	Pro	Gly	Gln
				245					250					255	
Leu	Lys	Leu	Ser	Glu	Arg	Ile	Ile	Ala	Arg	Met	Glu	Trp	Gly	Leu	Val
			260					265					270		
Ala	His	Val	Gly	Val	Pro	Asp	Leu	Glu	Thr	Arg	Val	Ala	Ile	Leu	Gln
		275					280					285			
His	Lys	Ala	Glu	Gln	Lys	Gly	Leu	Asn	Ile	Pro	Asn	Glu	Met	Ala	Phe
	290					295					300				
Tyr	Ile	Ala	Asp	His	Val	Tyr	Gly	Asn	Val	Arg	Gln	Leu	Glu	Gly	Ala
305					310					315					320
Ile	Asn	Lys	Leu	Thr	Ala	Tyr	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Leu	Thr
				325					330					335	
Glu	Thr	Thr	Val	Arg	Asp	Thr	Leu	Lys	Glu	Leu	Phe	Arg	Ala	Pro	Ser
			340					345					350		
Lys	Gln	Lys	Val	Ser	Val	Glu	Ser	Ile	Leu	Lys	Ser	Val	Ala	Thr	Val
		355					360					365			
Phe	Gln	Val	Lys	Ile	Gln	Asp	Leu	Lys	Gly	Ser	Ser	Arg	Ala	Lys	Asn
	370					375					380				
Val	Pro	Leu	Ala	Arg	Gln	Val	Ala	Met	Tyr	Leu	Ala	Lys	Thr	Leu	Ile
385					390					395					400
Thr	Asp	Ser	Leu	Val	Ala	Ile	Gly	Ala	Ala	Phe	Gly	Lys	Thr	His	Ser
				405					410					415	
Thr	Val	Leu	Tyr	Ala	Cys	Lys	Thr	Ile	Glu	Gln	Lys	Ile	Glu	Lys	Asp
			420					425					430		
Ala	Leu	Leu	Lys	Asn	Gln	Ile	Ser	Leu	Cys	Lys	Asn	Asn	Ile	Ala	Ile
		435					440					445			
Asp	Ser	Pro	Gln	His	Phe	Val									
	450					455									

(2) INFORMATIONS POUR LA SEQ ID NO: 164:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 134 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(168848..169249)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 164:

```

Arg Asn Pro Asn Gly Arg Arg Arg Ile Arg Asp Ile Ala Lys His Ala
1      5      10      15
Gln Ile Leu Asp Met Thr Pro Lys Pro Ser Ala Leu Ser Thr Leu Met
20      25      30
Gln Thr Asn Lys Lys Thr Cys Trp Ala Ser Phe Ser Pro Thr Asn
35      40      45
Phe His Lys Gln Arg Phe Ser Thr Pro Tyr Leu Val Pro Ser Leu Gly
50      55      60
Ser Pro Asp Lys Gln Asp Gln Asp Met Glu Lys Ile Ser Ser Tyr Leu
65      70      75      80
Lys Val Leu Thr Arg Gly Lys Phe Ser Tyr Arg Ser Thr Ala Asp Thr
85      90      95
Leu Ser Arg Lys Asn Lys Arg Ser Ser Asp Gln Lys Arg Asn Gly Gln
100      105      110
His Phe Glu Gln Glu Glu Leu Glu Ala Glu Glu Glu Val Phe Ser Thr
115      120      125
Arg Arg His Ser Ile Ala
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 165:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 282 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 169586..170431

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 165:

```

Leu Leu Cys Arg Arg Phe Pro Val Thr Asp Ser Ile Pro His Ile Pro
1      5      10      15
Val Leu Val Lys Glu Ser Leu Ser Leu Phe Arg Gly Arg Asn Pro Val
20      25      30
Val Phe Cys Asp Val Thr Val Gly Ala Gly Gly His Ala Glu Ala Phe
35      40      45
Leu Thr Glu Phe Pro Ser Ile Glu Arg Tyr Asp Gly Ser Asp Arg Asp
50      55      60
Leu Ser Ala Leu Ala Leu Ser Glu Asn Arg Leu Leu Pro Phe Lys Asp
65      70      75      80
Arg Val Arg Leu Arg His Ala Ser Phe Glu Glu Val Asp Thr Leu Thr
85      90      95
Ser Asp Gly Thr Tyr Asp Gly Val Leu Ala Asp Leu Gly Val Ser Ser
100      105      110
Met Gln Leu Asn Asn Leu Glu Arg Gly Phe Ser Phe Gln Gly Glu Asp
115      120      125
His Pro Leu Asp Met Arg Met Asp Thr Ser Arg Gly Met Thr Ala Ser
130      135      140

```

```

Glu Val Leu Asn Ser Leu Arg Glu Glu Glu Ile Gly Glu Ile Phe Arg
145          150          155          160
Asn Tyr Gly Glu Glu Pro Leu Trp Arg Ser Ala Ala Ala Val Val
          165          170          175
His Phe Arg Lys Lys Lys Lys Ile Leu Thr Val Lys Asp Leu Lys Asp
          180          185          190
Ala Thr Ser Gly Val Phe Pro Ser Tyr Arg Leu Arg Lys Lys Ile His
          195          200          205
Pro Leu Thr Leu Ile Phe Gln Ala Leu Arg Ile Tyr Val Asn Gln Glu
          210          215          220
Gly Ala Gln Leu Lys Val Leu Leu Asp Ser Ala Phe Arg Trp Leu Arg
225          230          235          240
Pro Gly Gly Arg Leu Ala Val Ile Ser Phe Cys Ser Leu Asp Asp Arg
          245          250          255
Pro Val Lys Trp Ala Phe Arg Glu Ala Glu Ala Arg Gly Leu Gly Lys
          260          265          270
Ile Leu Thr Lys Lys Val Ile Met Pro Ser
          275          280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 166:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 185 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 170780..171334

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 166:

```

Leu Met Asn His Arg Arg Gln Leu Thr Leu Ile Val Val Gly Val Leu
1          5          10          15
Ser Leu Tyr Ala Leu Leu Ile Val Arg Tyr Tyr Lys Ile Gln Ile Cys
          20          25          30
Asp Gly Glu Arg Trp Ala Val Glu Ala Ala Asn Gln His Glu Phe Arg
          35          40          45
Val Lys Asp Pro Phe Gln Arg Gly Thr Phe Phe Ala Asn Thr Ser Leu
          50          55          60
Arg Lys Gly Glu Lys Glu Gln Phe His Pro Leu Ala Ile Asp Ile Thr
          65          70          75          80
Lys Phe His Leu Cys Leu Asp Ala Val Val Ile Pro Glu Glu Tyr Arg
          85          90          95
Asp Glu Ile Ala Arg Met Val Val Val Met Val Gly Glu Gly Asp Tyr
          100          105          110
Gln Ser Ile Arg Ser Glu Phe Asp Arg Lys Ser Arg Tyr Arg Lys Leu
          115          120          125
Tyr Val Ser Leu Asp Val Ser Ile Arg Asp Arg Ile Leu Ser Trp Trp
          130          135          140
Lys Pro Tyr Ala Val Lys His Lys Ile Pro Ser Asn Ala Leu Phe Phe
          145          150          155          160
Ile Ser Asp Tyr Gln Arg Ser Tyr Pro Phe Gly Lys Leu Leu Gly Gln
          165          170          175
Val Leu His Thr Ser Gly Asp Lys Arg
          180          185

```

(2) INFORMATIONS POUR LA SEQ ID NO: 167:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 348 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 171333..172376

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 167:

Asp	Glu	Lys	Ser	Gly	Glu	Ala	Phe	Pro	Thr	Gly	Gly	Leu	Glu	Ala	Tyr	1	5	10	15
Phe	Asn	Arg	Leu	Leu	Glu	Gly	Glu	Asn	Gly	Glu	Arg	Lys	Leu	Leu	Arg	20	25	30	
Ser	Pro	Leu	Asn	Arg	Leu	Asp	Val	Asp	Lys	Val	Thr	Lys	Ile	Pro	Arg	35	40	45	
Asp	Gly	Ser	Asp	Ile	Tyr	Leu	Thr	Ile	Asp	Ala	Asn	Val	Gln	Thr	Ile	50	55	60	
Ala	Glu	Gln	Glu	Ile	Ala	Leu	Gly	Val	Leu	Glu	Ala	Lys	Ala	Arg	Ser	65	70	75	80
Gly	Arg	Ala	Ile	Val	Leu	Asn	Ser	His	Thr	Gly	Glu	Ile	Leu	Ala	Leu	85	90	95	
Ala	Gln	Tyr	Pro	Phe	Phe	Asn	Pro	Arg	Glu	Tyr	Arg	Glu	Tyr	Phe	Asn	100	105	110	
Cys	Asn	Asp	Arg	Ile	Glu	Asp	Thr	Lys	Val	Lys	Ala	Val	Ser	Asp	Val	115	120	125	
Phe	Glu	Pro	Gly	Ser	Ile	Met	Lys	Pro	Ile	Thr	Val	Ala	Ile	Ala	Leu	130	135	140	
Leu	Ala	Asn	Glu	Glu	Met	Gln	Lys	Arg	Ala	Gly	Glu	Asn	Leu	Phe	Asp	145	150	155	160
Pro	Tyr	Glu	Pro	Leu	Asp	Val	Ser	Arg	Arg	Val	Phe	Pro	Gly	Arg	Gln	165	170	175	
Lys	Met	Pro	Leu	Lys	Asp	Ile	Val	Ser	Asn	Arg	Tyr	Leu	Asn	Met	Tyr	180	185	190	
Met	Ala	Ile	Gln	Lys	Ser	Ser	Asn	Val	Tyr	Met	Ala	Gln	Leu	Ala	Asp	195	200	205	
Arg	Ile	Val	Gln	Lys	Leu	Gly	Ala	Asp	Trp	Tyr	Glu	Gln	Arg	Leu	Gln	210	215	220	
Asp	Phe	Gly	Phe	Gly	Lys	Arg	Thr	Gly	Ile	Glu	Leu	Pro	Ala	Glu	Ala	225	230	235	240
Val	Gly	Leu	Val	Pro	Ser	Arg	Lys	Arg	Phe	His	Lys	Asn	Gly	Ser	Pro	245	250	255	
Glu	Trp	Ser	Leu	Ser	Thr	Pro	Tyr	Ser	Leu	Ala	Met	Gly	Tyr	Asn	Leu	260	265	270	
Leu	Ala	Thr	Ser	Met	Gln	Met	Val	Gln	Ala	Tyr	Ala	Val	Phe	Gly	Asn	275	280	285	
Gly	Gly	Phe	Leu	Ile	Arg	Pro	Thr	Leu	Val	Arg	Lys	Ile	Val	Ser	Pro	290	295	300	
Ser	Gly	Glu	Glu	Lys	Ile	Leu	Ser	Ser	Asn	Pro	Lys	Lys	Ile	Arg	Val	305	310	315	320
Leu	Ser	Glu	Lys	Ile	Val	Ala	Gly	Cys	Cys	Ser	Cys	Tyr	Ala	Phe	His	325	330	335	
Asn	Met	Phe	Arg	Arg	Asp	Gly	Asp	Ser	Cys	Cys	Tyr					340	345		

(2) INFORMATIONS POUR LA SEQ ID NO: 168:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 172309..172722

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 168:

```

Leu Gln Asp Val Val Arg Ala Met Arg Phe Thr Thr Cys Leu Gly Gly
1          5          10          15
Thr Gly Ile Arg Ala Ala Thr Lys Gly Tyr Ser Ser Ala Gly Lys Thr
          20          25          30
Gly Thr Thr Glu Lys Leu Val Asp Gly Lys Tyr Asp Lys Lys Arg His
          35          40          45
Ile Ala Ser Phe Ile Gly Leu Thr Pro Ile Ala Ala Leu Ser Asp Thr
          50          55          60
Ala Val Pro Leu Val Ile Leu Val Ser Ile Asp Asp Pro Ala Tyr Gly
65          70          75          80
Val Arg Glu Asp Arg Thr Lys Asn Tyr Met Gly Gly Arg Cys Ala Ala
          85          90          95
Pro Val Phe Ser Arg Ile Ala Ser Arg Val Leu Pro Tyr Leu Gly Val
          100          105          110
Pro Leu Asp Glu Gln Leu His Thr Tyr Arg Glu Glu Val Ser Gln Leu
          115          120          125
Lys Leu Leu Tyr Glu Glu Trp Asn Arg Lys
          130          135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 169:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 483 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 173048..174496

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 169:

```

Met His Leu Asp Gln Leu Leu Arg Asn Ile Pro Ala Lys Ile Tyr Gly
1          5          10          15
Lys Val Glu Ser Ile Pro Val Arg Asn Leu Thr Arg Asp Ser Arg Cys
          20          25          30
Val Gly Val Gly Asp Ile Phe Ile Ala Arg Gln Gly Gln Phe Cys Asn
          35          40          45
Gly Asn Asp Tyr Ser Ser Gln Ala Val Ala Asn Gly Ala Ile Ala Val
          50          55          60
Leu Ser Ser Leu Tyr Asn Pro Phe Leu Ser Val Val Gln Ile Ile Ala

```

(2) INFORMATION POUR LA SEQ ID NO: 170:

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 174399..174968

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 170:

Leu	Arg	Glu	Arg	Asp	Met	Arg	Gly	Ile	Arg	Ser	Ser	Asn	Ile	Arg	Arg	1	5	10	15
Leu	Ser	Leu	Met	Ile	Glu	Arg	Leu	Cys	Val	Lys	Pro	Trp	Gln	Pro	Phe	20	25	30	
Val	Asn	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Thr	Leu	Ser	Ser	Pro	Val	35	40	45	
Ser	Cys	Phe	Ala	Asp	Ala	Ala	Gly	Ile	Pro	Lys	Val	Ser	Arg	Asn	Glu	50	55	60	
Leu	Ile	Val	Ile	Asp	Pro	Gly	His	Gly	Gly	Lys	Asp	Glu	Gly	Thr	Ala	65	70	75	80
Asp	Lys	Glu	Leu	Arg	Tyr	Lys	Glu	Lys	Thr	Leu	Ala	Leu	Ser	Ile	Ala	85	90	95	
Leu	Ser	Val	Gln	Gly	Cys	Leu	Arg	Arg	Met	Gly	Tyr	Lys	Thr	Ile	Met	100	105	110	
Thr	Arg	Ala	Thr	Asp	Val	Tyr	Val	Asp	Leu	Ser	Lys	Arg	Ala	Ala	Ile	115	120	125	
Ala	Asn	Gln	Asn	Lys	Ala	Asp	Val	Phe	Val	Ser	Ile	His	Cys	Asn	His	130	135	140	
Ser	Ser	Asn	Thr	Ser	Ala	Leu	Gly	Thr	Glu	Ile	Tyr	Phe	Tyr	Asn	Asp	145	150	155	160
Lys	Asn	Ile	Leu	Arg	Thr	Arg	Lys	Ser	Glu	Ser	Leu	Gly	Lys	Arg	Ser	165	170	175	
Trp	Leu	Leu	Cys	Lys	Lys	Met	Glu	Leu	Tyr	Ala	Asn	Val	Lys			180	185	190	

(2) INFORMATIONS POUR LA SEQ ID NO: 171:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 100 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 175411..175710

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 171:

Met	Ala	Thr	Met	Thr	Lys	Lys	Lys	Leu	Ile	Ser	Thr	Ile	Ser	Gln	Asp	1	5	10	15
His	Lys	Ile	His	Pro	Asn	His	Val	Arg	Thr	Val	Ile	Gln	Asn	Phe	Leu	20	25	30	
Asp	Lys	Met	Thr	Asp	Ala	Leu	Val	Gln	Gly	Asp	Arg	Leu	Glu	Phe	Arg	35	40	45	
Asp	Phe	Gly	Val	Leu	Gln	Val	Val	Glu	Arg	Lys	Pro	Lys	Val	Gly	Arg	50	55	60	
Asn	Pro	Lys	Asn	Ala	Ala	Val	Pro	Ile	His	Ile	Pro	Ala	Arg	Arg	Ala				


```

Ser Arg Arg Thr Gly Phe Ser Tyr Leu Gln Asp Ala Leu Phe Ser Thr
305                      310                      315                      320
Asn Ser Cys Tyr Arg Ile Asp Ile Thr Glu Gln Lys Cys His Val Ala
                      325                      330                      335
Ser Ser Leu Asp Arg Glu Asn Gln Asp Ala Phe Phe Ala Ile Phe Cys
                      340                      345                      350
Lys Gly Ser Gln Cys Gln Val Cys Asn Gly Pro Lys Leu Arg Thr Gly
                      355                      360                      365
Ser Pro Asp Ser Tyr Lys Gly Pro Ala Tyr Asp Val Leu Ile Lys Gly
                      370                      375                      380
Glu Lys Glu Thr Val Arg Ile Leu Ser Ser Ser Pro His Met Glu Ile
385                      390                      395                      400
Phe Ser Leu Gln Gly Lys Asp Arg Phe Trp Gly Ser Asn Phe Leu Ile
                      405                      410                      415
Asn Leu Pro Tyr Thr Gln Asn Ser Ile Asn Ile Leu Phe Glu Lys Ala
                      420                      425                      430

```

(2) INFORMATIONS POUR LA SEQ ID NO: 173:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 231 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 177423..178115

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 173:

```

Ser Cys Ser Cys Arg Arg Phe Ala Lys Ile Gln Xaa Gln Arg Phe Met
1                      5                      10                      15
Leu Ile Gly Gln Glu Lys Gly Cys Asp Thr Lys Ser Arg Met His Arg
                      20                      25                      30
Asn Phe Gly Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu
                      35                      40                      45
Ala Lys Met Ala Glu Lys Phe Gly Leu Pro Ile Ile Phe Leu Val Asp
50                      55                      60
Thr Pro Gly Ala Phe Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly
65                      70                      75                      80
Trp Ala Ile Ala Thr Asn Leu Phe Glu Leu Ala Arg Leu Ala Thr Pro
                      85                      90                      95
Ile Ile Val Ile Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly
100                      105                      110
Met Ala Ile Gly Asp Val Val Ala Met Leu Glu His Ser Tyr Tyr Ser
115                      120                      125
Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys
130                      135                      140
Lys Asn Ser Asp Ala Ala Ala Met Leu Lys Met His Gly Glu Asp Leu
145                      150                      155                      160
Lys Gly Phe Ala Ile Val Asp Ala Val Ile Lys Glu Pro Ile Gly Gly
                      165                      170                      175
Ala His His Asn Pro Ala Ala Thr Tyr Arg Ser Val Gln Glu Tyr Val
180                      185                      190
Leu Gln Glu Trp Val Lys Leu Lys Asp Leu Pro Val Glu Glu Leu Leu
195                      200                      205
Glu Lys Arg Tyr Gln Lys Phe Arg Thr Ile Gly Leu Tyr Glu Thr Ser

```

210
Ser Glu Ser Asp Ser Glu Ala
225 230 215

220

(2) INFORMATIONS POUR LA SEQ ID NO: 174:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 594 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 178240..180021

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 174:

Phe Gly Lys Gln Glu Gly Ala Ser Leu Val Lys Arg Lys Glu Leu Ser
1 5 10 15
Lys Asp Gln Leu Leu Glu Gln Trp Asp Asn Ile Val Gly Glu Gly Asp
20 25 30
Thr Leu Ser Leu Pro Gln Ala Asn Ala Tyr Ile Ala Lys His Ser Gly
35 40 45
Gly Ser Gln Ser Ile Thr Lys Arg Leu Ser Ala Tyr Leu Ser Gly Cys
50 55 60
Phe Asp Phe Ser Arg Leu Gln Cys Leu Ala Leu Phe Leu Val Val Val
65 70 75 80
Ala Ile Leu Lys Ser Thr Thr Leu Phe Phe Gln Arg Phe Leu Ala Gln
85 90 95
Leu Ile Ala Ile Arg Val Ser Cys Ser Leu Arg Lys Asp Tyr Phe Leu
100 105 110
Ala Leu Gln Thr Leu Pro Met Thr Phe Phe His Ala His Asp Met Gly
115 120 125
Asn Leu Ser Ser Arg Val Ile Ala Asp Ser Ser Met Ile Ala Leu Ala
130 135 140
Ile Asn Ala Leu Met Val Asn Tyr Ile Gln Ala Pro Ile Thr Met Thr
145 150 155 160
Leu Ala Leu Val Val Cys Leu Ser Ile Ser Trp Lys Phe Cys Ala Cys
165 170 175
Val Cys Leu Ala Phe Pro Ile Phe Ile Leu Pro Ile Val Ile Ile Ala
180 185 190
Lys Lys Val Lys Ala Leu Ala Lys Arg Ile Gln Lys Ser Gln Asp His
195 200 205
Ser Ala Ala Ala Leu Leu Asp Phe Leu Leu Gly Ile Leu Thr Val Lys
210 215 220
Val Phe Arg Thr Glu Gln Phe Ser Phe Ser Lys Tyr Cys Gln Lys Asn
225 230 235 240
Asp Glu Ile Ala Arg Leu Glu Glu Arg Ser Ala Val Tyr Ser Leu Ile
245 250 255
Pro Arg Pro Leu Leu His Thr Ile Ala Ser Leu Phe Phe Ala Leu Val
260 265 270
Ile Met Ile Gly Leu Tyr His Phe His Ile Pro Pro Glu Glu Leu Val
275 280 285
Val Phe Cys Gly Leu Leu Tyr Leu Ile Tyr Asp Pro Ile Lys Lys Phe
290 295 300
Ala Asp Glu Asn Ala Asn Ile Met Arg Gly Cys Ala Ala Ala Glu Arg
305 310 315 320

Phe Tyr Glu Val Leu Asp Leu Ala Lys Gln Gln Ser Asn Val Ser Glu
 325 330 335
 Lys Leu Asn Glu Phe Gln Gly Leu Gln His Ser Ile Gln Phe Cys Asn
 340 345 350
 Val Ser Phe Gly Tyr Val Glu Asp Ser Pro Val Leu Ser Asp Phe Asn
 355 360 365
 Leu Val Leu Lys Lys Gly Glu Ala Ile Gly Ile Val Gly Pro Thr Gly
 370 375 380
 Ser Gly Lys Ser Thr Ile Ala Lys Leu Leu Pro Arg Leu Tyr Glu Val
 385 390 395 400
 Ser His Gly Glu Leu Leu Ile Asp Ser Leu Pro Ile Gln Ser Tyr Cys
 405 410 415
 Lys Asn Ser Leu Arg Lys His Ile Gly Cys Val Leu Gln His Pro Phe
 420 425 430
 Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys Gly Arg Thr Phe
 435 440 445
 Leu Glu Glu Glu Val Phe His Ala Leu Lys Gln Ala His Ala Tyr Glu
 450 455 460
 Phe Val Ser Lys Met Pro Gln Gly Val His Ser Leu Leu Glu Glu Ser
 465 470 475 480
 Gly Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu Thr Ile Ala Arg
 485 490 495
 Ala Leu Leu His Asn Thr Ser Ile Leu Leu Leu Asp Glu Ala Thr Ser
 500 505 510
 Ala Leu Asp Ala Ile Ser Glu Asn Tyr Val Lys Glu Ile Val Gly Gln
 515 520 525
 Leu Lys Gly Arg Cys Thr Gln Ile Ile Ile Ala His Lys Leu Ser Thr
 530 535 540
 Leu Glu Tyr Val Asp Arg Ile Val Tyr Leu Glu Gln Gly Lys Lys Ile
 545 550 555 560
 Ala Glu Gly Thr Lys Glu Glu Leu Leu Asp Ser Cys Pro Ala Phe Gln
 565 570 575
 Arg Met Trp Val Leu Ser Gly Ala Lys Asp Trp Glu Leu Asn Ala Val
 580 585 590
 Val Lys

(2) INFORMATIONS POUR LA SEQ ID NO: 175:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 219 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(180048..180704)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 175:

Gln Lys Lys Pro Leu Thr Ser Leu Leu Ser Asp Gly Lys Leu Phe Leu
 1 5 10 15
 His Tyr Gly Arg Leu Val Val Met Phe Lys Leu Leu Leu Ile Phe Ala
 20 25 30
 Asp Pro Ala Glu Ala Ala Arg Thr Leu Ser Leu Phe Pro Phe Ser Leu
 35 40 45
 Asn Lys Glu Asn Phe Tyr Thr Tyr His Thr Glu Asn Val Leu Leu Asp

```

      50      55      60
Val Met Val Leu Lys Thr Trp Gly Tyr Arg Gly Val Val Gln Ala Leu
65      70      75      80
Ser Pro Pro Pro Ser Gly Tyr Asp Leu Trp Ile Asn Ala Gly Phe Ala
      85      90      95
Gly Ala Ala Asn Pro Asn Ile Pro Leu Leu Lys Thr Tyr Thr Ile Thr
      100      105      110
Ser Val Lys Glu Leu Thr Pro Thr Ser Val Glu Glu Glu Leu Glu
      115      120      125
Val Thr Pro Ile Pro Arg Leu Pro Leu Ala Gln Leu Thr Ser Val Arg
      130      135      140
Ser Pro Tyr Arg Asp Gly Phe His Glu His Leu Gln Leu Val Asp Met
145      150      155      160
Glu Gly Phe Phe Ile Ala Lys Gln Ala Ser Leu Val Ala Cys Pro Cys
      165      170      175
Ser Met Ile Lys Val Ser Ser Asp Tyr Thr Thr Arg Glu Gly Gln Asp
      180      185      190
Phe Leu Lys Asn Asn Lys Val Lys Leu Ser Gln Lys Leu Ala Glu Ala
      195      200      205
Ile Phe Pro Ile Tyr Ser Ser Phe Ile Asp Val
      210      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 176:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 256 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(180631..181398)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 176:

```

Met Thr Phe Ser Ala Ala Phe Ser Pro Cys Pro Asn Asp Ile Phe Leu
1      5      10      15
Phe Arg Ser Phe Leu Glu Lys His Lys Gly Phe Pro Ser Leu Arg Gln
      20      25      30
Ile Met Ile Ala Asp Ile Ser Ser Leu Asn Tyr Tyr Ala Leu Glu Thr
      35      40      45
Arg Phe Pro Leu Ile Lys Ile Ser Ala Ser Leu Tyr Pro Gln Ile Ala
      50      55      60
Asp Ser Tyr Asp Val Leu Asn Val Gly Thr Thr Leu Gly Tyr Lys Ile
65      70      75      80
Gly Pro Leu Ile Leu Ser Lys Gln Leu Asp Ser Pro Leu Lys Ser Leu
      85      90      95
Ala Thr Pro Gly Glu Thr Thr Thr Ala His Ala Leu Cys Arg Leu Phe
      100      105      110
Tyr Pro Arg Ala Glu Leu Val Pro Met Lys Tyr His Glu Ile Ile Pro
      115      120      125
Ala Ile Leu Ser Asn Arg Val Asp Gly Gly Ala Val Ile His Glu Glu
      130      135      140
Arg Phe Ser Phe Pro Lys Asp Leu Cys Ile Val Glu Asp Leu Gly Gln
145      150      155      160
Leu Trp Glu Lys Thr Trp His Leu Pro Leu Pro Leu Gly Cys Ile Val
      165      170      175

```



```

Ile Ser Lys Lys Val Ser Asp Asp Asp Ser Tyr Leu Leu Ser His Ala
      180      185      190
Leu Gln Glu Ser Leu Lys Lys Ser Leu Thr Asp Ser Ala Leu Ala Ile
      195      200      205
Gln Lys Ala Ser Glu Tyr Ser Arg Asp Lys Asn Pro Thr Thr Ile Gln
      210      215      220
His Phe Ile Asp Thr Tyr Val Thr Glu Glu Thr Phe Asn Leu Ser Ser
225      230      235      240
Ile Gly Arg Gln Ala Phe Ser Thr Leu Trp Thr Ala Cys Arg Asn Val
      245      250      255

```

(2) INFORMATIONS POUR LA SEQ ID NO: 177:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(181398..182414)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 177:

```

Phe Pro Tyr Gln Ile Gln Gln Asn Gln Arg Asp Thr Thr Ala Arg Leu
1      5      10
Leu His Leu Val Asn Arg Asp Ile Asp Ile Pro Gly Phe Gly Met Asp
      20      25      30
Glu Glu Gln Asn Ile Ile Phe Tyr Arg Leu Val Ile Pro Cys Leu Lys
      35      40      45
Gly Glu Ile Asn Glu Asp Leu Leu Arg Val Tyr Ile Asp Thr Ile Lys
      50      55      60
Leu Ile Cys Asp Ser Phe Phe His Ala Ile Gly Leu Ile Ser Thr Gly
65      70      75      80
Asn Met Asp Leu Asp Glu Leu Lys Lys Gln Ala Lys Leu Glu Asn Asn
      85      90      95
Gln Ser Asp Gln Leu Glu Xaa Leu Glu Leu Val Pro Ala Leu Ile
      100      105      110
Phe Tyr Asp Thr Glu Thr Thr Gly Thr Gln Ile Asp Lys Asp Arg Ile
      115      120      125
Val Glu Leu Ala Ala Tyr Asn Gly Thr Thr Ser Glu Ser Phe Gln Thr
      130      135      140
Leu Val Asn Pro Glu Ile Pro Ile Pro Ala Glu Ala Thr Lys Ile His
145      150      155      160
Gly Ile Thr Thr Ala Glu Val Ala Asp Ala Pro Arg Phe Pro Glu Ala
      165      170      175
Tyr Gln Lys Phe Ile Glu Phe Cys Gly Thr Asp Asn Ile Leu Val Ala
      180      185      190
His Asn Asn Asn Ala Phe Asp Tyr Pro Leu Leu Val Arg Glu Cys Arg
      195      200      205
Arg His Gly Leu Ser Glu Pro Gln Leu Arg Thr Ile Asp Ser Leu Lys
      210      215      220
Trp Ala Lys Lys Tyr Arg Thr Asp Leu Pro Gln His Ser Leu Gln Tyr
225      230      235      240
Leu Arg Gln Val Tyr Gly Phe Glu Glu Asn Gln Ala His Arg Ala Leu
      245      250      255
Asp Asp Val Ile Thr Leu Tyr Arg Val Phe Ser Ala Leu Val Gly Asp

```

260 265 270
 Leu Ser Pro Asp Gln Ile Tyr Asp Leu Leu Asn Glu Thr Cys His Pro
 275 280 285
 Arg Ile Phe Lys Met Pro Phe Gly Lys Tyr Lys Gly Lys Pro Leu Ser
 290 295 300
 Glu Val Pro Ser Ser Tyr Ile Ala Trp Leu Gln Lys Gly Asp Tyr Leu
 305 310 315 320
 Leu Gln Pro Glu Asn Lys Glu Ile Lys Ala Ala Ile Glu Ala Tyr Gln
 325 330 335
 Gln Leu Lys

(2) INFORMATIONS POUR LA SEQ ID NO: 178:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 248 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 182913..183656

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 178:

Met Ile Val Ala Asp Phe Glu Tyr Phe Gly Leu Ser Asp Val Gly Leu
 1 5 10 15
 Val Arg His Asn Asn Glu Asp Phe Trp Gln Val Asn Tyr Asp Ser Gln
 20 25 30
 Leu Ile Ala Ile Ala Asp Gly Met Gly Gly His Arg Ala Gly Ala Val
 35 40 45
 Ala Ser Tyr Glu Ala Val Gly Asn Leu Met Gln Leu Val Asp Leu His
 50 55 60
 Lys Val Asp Leu Glu Arg Phe Gly Asp Glu Gln Tyr Lys Glu Ser Ile
 65 70 75 80
 Lys Thr Ile Val Ser Glu Val Asn Leu Leu Ile Tyr Arg Gln Gly Leu
 85 90 95
 Ser Asn Glu Glu Phe Lys Gly Met Gly Thr Thr Leu Ser Cys Met Gln
 100 105 110
 Phe Arg Arg Gly Lys Ala Trp Leu Phe His Val Gly Asp Cys Arg Val
 115 120 125
 Tyr Arg Leu Arg Asn Lys Met Leu Glu Arg Leu Thr Glu Asp His Ser
 130 135 140
 Leu Ala Asn His Leu Ala Ser Arg Tyr Gly Leu Ser Lys Gln Ser Val
 145 150 155 160
 Lys Arg Tyr Pro Gly Arg Asn Val Leu Thr Asn Val Leu Gly Ser Arg
 165 170 175
 Pro His Val Ser Leu Asp Ile Arg Glu Met Ser Tyr Glu Lys Glu Asp
 180 185 190
 Leu Phe Val Phe Cys Ser Asp Gly Leu Thr Ser Ala Val Ser Asp His
 195 200 205
 Asp Met Leu Asp Ile Leu Thr Gln Thr Thr Thr Leu Glu Glu Gly Gly
 210 215 220
 Asn Ile Leu Ile Ser Leu Ala Asn Ser Arg Gly Gly Arg Asp Asn Ala
 225 230 235 240
 Thr Val Ile Leu Val Arg Met Arg
 245

(2) INFORMATIONS POUR LA SEQ ID NO: 179:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 374 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 183665..184786

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 179:

Met	Thr	Ile	Tyr	Leu	Asp	Thr	Asn	Ala	Ser	Ala	Leu	Leu	Glu	Pro	Gly	1	5	10	15
Val	Leu	Met	Cys	Leu	His	Ser	Leu	Phe	Ile	Gly	Glu	Gly	Gly	Phe	Gly	20	25	30	
Asn	Pro	Ser	Ser	Val	His	Ser	Phe	Gly	Lys	Lys	Thr	Lys	Lys	Leu	Val	35	40	45	
Lys	Glu	Thr	Ser	Thr	Leu	Ile	Glu	Lys	Ala	Leu	Gly	Phe	Ser	His	Cys	50	55	60	
Arg	Val	Ile	Tyr	Thr	Ser	Gly	Ala	Thr	Glu	Ser	Leu	Asn	Leu	Ala	Ile	65	70	75	80
Gln	Asn	Ile	Pro	Thr	Gly	Ser	His	Val	Ile	Thr	Ser	Ser	Met	Glu	His	85	90	95	
Pro	Ala	Val	Ile	Glu	Pro	Leu	Lys	Gln	Ala	Lys	Leu	Ser	Val	Thr	Tyr	100	105	110	
Leu	Asp	Pro	Ile	Pro	Gly	Glu	Cys	Val	Val	Ser	Leu	Glu	Gln	Ile	Lys	115	120	125	
Glu	Ala	Val	Gln	Ser	Asp	Thr	Ser	Ala	Ile	Val	Leu	Gly	Trp	Val	Asn	130	135	140	
Ser	Glu	Val	Gly	Val	Arg	Ile	Asp	Leu	Glu	Ala	Ile	Ala	Glu	Phe	Ala	145	150	155	160
Lys	Glu	Arg	Gln	Leu	Leu	Leu	Ile	Val	Asp	Ala	Thr	Ala	Ile	Val	Gly	165	170	175	
Lys	Glu	Val	Ile	His	Ile	Pro	Glu	Gly	Val	Ser	Met	Val	Ala	Phe	Ser	180	185	190	
Gly	His	Lys	Phe	His	Ala	Leu	Ser	Gly	Ile	Gly	Val	Leu	Leu	Thr	Ser	195	200	205	
Pro	Lys	Ile	Lys	Ile	Ser	Pro	Ile	Ile	Ser	Gly	Gly	Gly	Gln	Gln	Gly	210	215	220	
Gly	Ile	Arg	Ser	Gly	Thr	Glu	His	Ile	His	Gly	Ile	Ala	Ser	Leu	Arg	225	230	235	240
Tyr	Ile	Phe	Ser	Lys	Leu	Leu	Val	Glu	Gln	Pro	Ala	Ile	Ala	Gln	Thr	245	250	255	
Met	Arg	Ser	Tyr	Arg	Asp	Leu	Phe	Glu	Ser	Arg	Ile	Gln	Glu	Ala	Phe	260	265	270	
Pro	Glu	Cys	Ile	Val	His	Cys	Gln	Asp	Lys	Pro	Arg	Val	Ser	Asn	Leu	275	280	285	
Ser	Ala	Ile	Ala	Phe	Pro	Gly	Leu	Glu	Gly	Glu	Val	Met	Gln	Ile	Ala	290	295	300	
Leu	Asp	Leu	Glu	Gly	Val	Ala	Cys	Gly	Tyr	Gly	Ser	Ala	Cys	Ser	Ser	305	310	315	320
Gly	Ala	Thr	Thr	Val	Phe	Lys	Ser	Leu	Thr	Val	Met	Lys	Val	Pro	Gln	325	330	335	
Asp	Leu	Ala	Val	Ala	Thr	Leu	Arg	Phe	Ser	Phe	Ser	Tyr	Leu	Leu	Ser				

340 345 350
 Glu Glu Glu Ile Leu Thr Ala Ala Gln Arg Val Ile Arg Val Val Lys
 355 360 365
 His Leu Gln Gln Tyr Ala
 370

(2) INFORMATIONS POUR LA SEQ ID NO: 180:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 389 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(184796..185962)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 180:

Cys Ile Phe Val Gln Gly Phe Phe Ser Met Met Glu Met Ala Cys Val
 1 5 10 15
 Ser Phe Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Ser Asn Lys
 20 25 30
 Lys Ala Ser Tyr Ile Asn Phe Leu Ile Arg Arg Pro Tyr Arg Leu Phe
 35 40 45
 Gly Thr Val Met Leu Gly Val Asn Ile Ala Leu Gln Ile Gly Ser Glu
 50 55 60
 Ser Ser Arg Thr Cys Tyr Lys Leu Leu Gly Ile Ser Pro Glu Tyr Ala
 65 70 75 80
 Pro Ala Thr Gln Ile Ile Leu Val Val Ile Phe Ala Glu Leu Ile Pro
 85 90 95
 Leu Ala Ile Ser Arg Lys Ile Pro Glu Lys Ile Ala Leu Lys Gly Ala
 100 105 110
 Pro Ile Leu Tyr Phe Ala His Tyr Leu Phe Tyr Pro Leu Ile Gln Cys
 115 120 125
 Val Gly Gly Ile Thr Asn Met Ile Tyr Phe Ile Leu Asn Ile Lys Glu
 130 135 140
 Glu Thr Ile His Ser Thr Leu Ser Arg Asp Glu Leu Gln Lys Thr Leu
 145 150 155 160
 Glu Thr His His Glu His Asp Phe Asn Val Ile Ala Thr Asn Ile
 165 170 175
 Phe Ser Leu Ser Ala Thr Ser Val Glu Gln Val Cys Gln Tyr Leu Asp
 180 185 190
 Gln Ile Pro Ile Leu Ser Ala Thr Ala Ser Val Arg Asp Val Cys Gln
 195 200 205
 Leu Val Arg Arg His Arg Leu Asp Phe Val Pro Val Tyr His Lys Val
 210 215 220
 Lys Lys Asn Val Val Gly Ile Ala Phe Pro Lys Asn Leu Ile Asn Arg
 225 230 235 240
 Asn Pro Ser Asp Pro Val Val Pro Tyr Leu Ser Ser Pro Trp Phe Ile
 245 250 255
 Thr Ala Lys Ser Lys Leu Ile His Ala Ile Gln Glu Phe Arg Lys Asn
 260 265 270
 Ser Ser Lys Ile Ala Ile Val Leu Asn Asn Asn Gly Glu Pro Met Gly
 275 280 285
 Val Leu Gly Leu His Thr Val Phe Lys Thr Leu Phe Asn Thr Arg Asn
 290 295 300

Ile Thr Gln Leu Lys Pro Lys Pro Thr Ser Leu Ile Glu Arg Thr Phe
 305 310 315 320
 Ser Gly Asn Thr Pro Leu Ser Glu Ile Glu Asn Glu Leu Asp Ile Ile
 325 330 335
 Phe Met Asp Asn Asp Cys Thr Thr Ile Glu Gln Leu Met Leu Lys Leu
 340 345 350
 Leu Asp Thr Pro Pro Glu Val Gly Ala Ser Ile Ile Ile Asn Asp Leu
 355 360 365
 Leu Leu Glu Val Lys Glu Ile Ser Leu Tyr Gly Ile Lys Thr Val Ala
 370 375 380
 Ile Lys Asp Thr Leu
 385

(2) INFORMATIONS POUR LA SEQ ID NO: 181:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 283 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(186000..186848)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 181:

Lys Phe Arg Pro Ile Phe Asp Trp Ala Ile Ser Gly Ile Asn Phe Ile
 1 5 10 15
 Val Gln Lys Met Leu Ala Arg Gln Glu Ser Asp Phe Ile Gln Pro Gln
 20 25 30
 Glu Leu Lys Glu Val Leu Arg Ser Cys Lys Asp Phe Gly Val Val Asn
 35 40 45
 His Glu Glu Ser Arg Leu Leu Phe Gly Tyr Leu Ser Met Glu Glu Gly
 50 55 60
 Ser Ile Lys Glu Arg Met Thr Pro Lys Gln Glu Ile Ile Phe Tyr Asp
 65 70 75 80
 Val Leu Thr Pro Ile Glu Asn Leu Tyr Lys Leu Phe Ser Gly Pro Lys
 85 90 95
 Gln Ser Tyr Ser Lys Val Leu Val Cys Lys Gly Gly Leu Gln Asn Leu
 100 105 110
 Leu Gly Val Cys Ser Ala Lys Leu Leu Leu Tyr Lys Glu Lys Leu
 115 120 125
 Gln Ser Ala Glu Glu Leu Leu Pro Leu Leu Arg Lys Pro His Tyr Ile
 130 135 140
 Pro Glu Thr Val Ser Ala Lys Thr Ala Leu Tyr His Leu Ala Gly Glu
 145 150 155 160
 Asp Cys Gly Leu Gly Ile Ile Ile Asp Glu Tyr Gly Ser Ile Glu Gly
 165 170 175
 Leu Ile Thr Gln Asn Asp Leu Phe Lys Ile Val Ser Asp Glu Val Ala
 180 185 190
 His Asn Arg Pro Ser Phe Lys Gln Phe Ala His Ser Asp Lys Asn Val
 195 200 205
 Val Ile Ala Ala Gly Thr Tyr Glu Leu Ser Asp Phe Tyr Asp Leu Phe
 210 215 220
 Gly Val Asp Leu Pro Thr Ala Asn Cys Val Thr Ile Gly Gly Trp
 225 230 235 240
 Leu Thr Glu Gln Leu Gly Glu Ile Pro Glu Thr Gly Thr Lys Phe Ala

				245					250					255	
Trp	Gly	Gln	Phe	Val	Phe	Gln	Ile	Leu	Asp	Ala	Ala	Pro	Asn	Cys	Val
				260				265						270	
Lys	Arg	Val	Tyr	Ile	Arg	Lys	Thr	His	Gly	Asn					
		275					280								

(2) INFORMATIONS POUR LA SEQ ID NO: 182:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 174 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(186749..187270)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 182:

Ser	Gly	Ser	Ala	His	Asn	Asn	Pro	Asn	Arg	Met	Phe	Ser	Ser	Ala	Ile
1				5					10					15	
Val	Ile	Leu	Thr	Ala	Ile	Phe	Val	Leu	Cys	Ser	Gly	Phe	Val	Ser	Leu
			20					25					30		
Ser	His	Ile	Ala	Leu	Phe	Ser	Leu	Pro	Ser	Ser	Leu	Ile	Ala	His	Tyr
		35					40					45			
Ser	His	Ser	Lys	Asn	Arg	Gln	Leu	Arg	Gln	Ile	Ala	Asn	Leu	Met	Ala
		50				55					60				
Tyr	Pro	Asn	His	Leu	Leu	Ile	Thr	Leu	Val	Phe	Phe	Asp	Ile	Gly	Ile
65				70						75				80	
Asn	Ile	Gly	Val	Gln	Asn	Cys	Ile	Ala	Thr	Leu	Val	Gly	Asp	Ser	Ala
			85						90				95		
Ser	Leu	Leu	Leu	Thr	Val	Gly	Val	Pro	Leu	Ala	Leu	Thr	Leu	Val	Leu
			100					105					110		
Gly	Glu	Ile	Val	Pro	Lys	Val	Ile	Ala	Ile	Pro	Tyr	Asn	Ala	Arg	Ile
		115					120					125			
Ala	Lys	Ile	Val	Thr	Pro	Ile	Ile	Phe	Ala	Ser	Thr	Lys	Ser	Ser	Ala
		130				135					140				
Leu	Tyr	Leu	Ile	Gly	Leu	Ser	Arg	Val	Ser	Ile	Leu	Ser	Phe	Arg	Lys
145					150					155					160
Cys	Trp	Pro	Val	Lys	Lys	Val	Ile	Leu	Phe	Asn	Pro	Lys	Asn		
			165						170						

(2) INFORMATIONS POUR LA SEQ ID NO: 183:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 128 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 187426..187809

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 183:

```

Ile Met Glu Glu Lys Gly Ile Leu Gln Leu Val Glu Ile Ser Arg Ala
1           5           10           15
Met Ala Leu Gln Gly Val Cys Pro Trp Thr Asn Leu Gln Ser Val Glu
20           25           30
Ser Met Leu Gln Tyr Ile Ala Gly Glu Cys Gln Glu Leu Ala Asp Ala
35           40           45
Val Gln Glu Asn Lys Ala Ser Leu Glu Ile Ala Ser Glu Ala Gly Asp
50           55           60
Val Leu Thr Leu Val Leu Thr Leu Cys Phe Leu Leu Glu Arg Glu Gly
65           70           75           80
Lys Leu Lys Ala Glu Val Phe Val Glu Ala Leu Ala Lys Leu Arg
85           90           95
Arg Arg Ser Pro His Val Phe Asp Pro His Asn Gln Ile Ser Leu Glu
100          105          110
Gln Ala Glu Tyr Trp Ala Arg Ile Lys Gln Gln Glu Lys Ile Ser
115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 184:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 228 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(188798..189481)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 184:

```

Gly His Lys Ile Glu Ser Ile Phe Ser Leu Ser Cys Val Met Arg Lys
1           5           10           15
Phe Trp Leu Leu Ala Ser Phe Gly Leu Leu Ser Leu Thr Thr Thr Thr
20           25           30
Leu Ser Ser Cys Ala Val Ser Asn Ser Gly Ser Tyr Asn Ala Arg Leu
35           40           45
Tyr Thr Lys Gly Ser Lys Ala Lys Gly Val Val Ala Met Leu Pro Val
50           55           60
Phe Tyr Arg Thr Glu Lys Ser Ala Glu Leu Leu Pro Trp Asn Leu Gln
65           70           75           80
Ala Glu Phe Ser Glu Glu Ile Ser Arg Arg Leu His Ser Ser Asp Lys
85           90           95
Leu Leu Leu Ile Xaa Xaa His Ala Ser Ala Gly Val Ala Ala Gln Phe
100          105          110
Phe Ser Pro Thr Pro Asn Ile Ser Pro Glu Leu Ala Thr Gln Leu Leu
115          120          125
Pro Ala Glu Phe Val Val Ala Ala Glu Ile Leu Glu Gln Lys Thr Thr
130          135          140
Glu Asp Val Leu Asn Pro Ser Ile Ser Ala Ser Val Arg Val Arg Val
145          150          155          160
Phe Asp Ile Arg His Asn Lys Val Ser Met Ile Tyr Gln Glu Ile Leu
165          170          175
Asp Ala Ser Gln Ser Leu Ala Ser Gly Ser Asn Asp Tyr His Arg Tyr
180          185          190
Gly Trp Arg Ser Lys Asn Phe Asp Ser Thr Pro Met Gly Leu Met His
195          200          205
Gln Arg Leu Phe Arg Glu Ile Val Ala Arg Val Glu Gly Tyr Val Cys

```

210
Ala Asn Tyr Ser
225

215

220

(2) INFORMATIONS POUR LA SEQ ID NO: 185:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 220 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 189693..190352

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 185:

Val	Ile	His	Trp	Asp	Gln	Ser	Arg	Thr	Leu	Leu	Ser	Phe	Pro	Arg	Val
1				5					10					15	
Gly	Leu	His	Leu	Ser	Trp	Tyr	Gly	Ile	Leu	Phe	Ser	Leu	Gly	Ile	Phe
			20					25					30		
Leu	Ser	Ser	Phe	Ser	Gly	Ile	Lys	Leu	Ala	Thr	Ala	Leu	Cys	Lys	Asp
			35				40					45			
Arg	Glu	Glu	Lys	Lys	Glu	Leu	Arg	Thr	Ser	Leu	Glu	Asn	Phe	Ala	Leu
			50			55					60				
Gly	Ala	Leu	Leu	Ala	Ile	Ile	Ile	Gly	Ala	Arg	Leu	Ala	Tyr	Val	Leu
					70				75					80	
65															
Phe	Tyr	Gly	Gly	Ser	Phe	Tyr	Phe	Glu	Asn	Pro	Ser	Glu	Ile	Ile	Lys
				85					90					95	
Ile	Trp	Lys	Gly	Gly	Leu	Ser	Ser	His	Gly	Ala	Val	Ile	Ser	Val	Val
					100			105						110	
Ile	Trp	Ala	Ala	Val	Phe	Ser	Arg	Leu	His	Ile	Arg	Lys	Leu	Pro	Met
							120						125		
Leu	Ser	Val	Thr	Tyr	Ile	Cys	Asp	Leu	Cys	Gly	Ala	Val	Phe	Gly	Cys
											140				
Ala	Ala	Leu	Leu	Ile	Arg	Val	Gly	Asn	Phe	Met	Asn	Gln	Glu	Ile	Leu
											155			160	
145															
Gly	Thr	Pro	Thr	Ser	Met	Pro	Trp	Gly	Val	Ile	Phe	Ser	Asn	Gly	Gly
														175	
Gly	Gln	Ile	Pro	Arg	His	Pro	Val	Gln	Leu	Tyr	Glu	Gly	Leu	Gly	Tyr
														190	
Leu	Val	Leu	Ser	Cys	Ile	Leu	Cys	Arg	Leu	Trp	Leu	Ser	Trp	Cys	Tyr
														205	
Ile	Val	Trp	Val	Leu	Ala	Ile	Val	Gln	Gln	Ala	Leu				
210							215								

(2) INFORMATIONS POUR LA SEQ ID NO: 186:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 190235..190510

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 186:

Thr	Ser	Cys	Ser	Ala	Leu	Arg	Arg	Pro	Trp	Leu	Phe	Ser	Ala	Phe	Leu
1				5					10					15	
Tyr	Ser	Val	Gln	Ala	Leu	Ala	Ile	Val	Val	Leu	Tyr	Arg	Leu	Gly	Ser
			20					25					30		
Gly	Tyr	Ser	Ala	Ala	Gly	Ala	Leu	Ile	Gly	Val	Ala	Val	Ile	Arg	Phe
			35				40					45			
Cys	Ala	Glu	Phe	Phe	Lys	Thr	His	Gln	Gly	Ala	Trp	Leu	Gly	Glu	Glu
			50			55					60				
Asn	Ile	Leu	Thr	Ile	Gly	Gln	Trp	Leu	Ser	Ile	Pro	Met	Val	Phe	Leu
65					70					75					80
Gly	Val	Gly	Ile	Ile	Trp	Ile	Ala	Ser	Lys	Lys	Lys				
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 187:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 334 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 190785..191786

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 187:

Glu	Arg	Gly	Phe	Pro	Pro	His	Arg	Glu	Asn	Pro	Pro	Arg	Met	Arg	Met
1				5					10					15	
Asn	Lys	Arg	Thr	Leu	Leu	Phe	Val	Ser	Leu	Val	Ser	Ala	Ala	Phe	Leu
			20					25					30		
Gly	Cys	Gln	Ile	Phe	Phe	Gly	Tyr	Arg	Asp	Leu	Lys	Ser	Cys	Gln	Asp
		35				40						45			
Leu	Ala	Glu	Lys	Gln	Arg	Ala	Ile	Ser	Glu	Gln	Ile	Leu	Ala	Ser	Thr
		50				55					60				
Glu	Gln	Leu	Ser	Val	Val	Pro	Trp	Thr	Ala	Ser	Leu	Glu	Glu	Ser	Glu
65					70					75					80
Ser	Val	Asn	Gln	Tyr	Ala	Ile	Arg	Leu	Gly	Asn	Arg	Leu	Leu	Leu	Leu
			85						90					95	
Thr	Lys	Gly	Gly	Ser	His	Pro	Glu	Val	Tyr	Ser	Arg	Gly	Thr	Ser	Trp
			100					105					110		
Ser	Leu	Ile	Glu	Gln	Thr	Ser	Thr	Phe	Gly	Gly	Ile	Leu	Val	Ser	Leu
		115					120					125			
Tyr	Gly	Glu	Thr	Gly	Gln	Glu	Val	Leu	Ser	Lys	Gly	Ser	Ser	Val	Tyr
		130				135					140				
Leu	Pro	Asn	Gln	Arg	Asp	Ala	Phe	Pro	Val	Leu	Val	Ala	Glu	Phe	Arg
145					150					155					160
Ser	Asn	Gln	Glu	Pro	Leu	Val	Phe	Leu	Gly	Glu	Tyr	Lys	Asp	Gly	Lys
			165						170					175	
Ile	Ala	Asn	Lys	Ala	Gly	Ala	Ile	Tyr	Gly	Thr	Ser	Leu	Val	Phe	Leu
		180					185					190			
Asn	Thr	Gly	Asn	Glu	Phe	Val	Pro	Leu	Gly	Ile	Tyr	Asn	Ser	Lys	Glu
		195					200					205			
Glu	Cys	Val	Glu	Ser	Leu	Asp	Leu	Pro	Met	Ala	Arg	Ala	Val	Val	Phe

210 215 220
 Ala Asp Lys Glu Asn Pro Thr Ala Ser Gly Ser Tyr Tyr Met Leu Ser
 225 230 235 240
 Asn Glu Tyr Met Gln Ile Val Val Ser Gln Glu Ser Gly Ala Ile Glu
 245 250 255
 Gly Ile Asn Leu Pro Phe Ala Ser Asp Gln Glu Glu Asn Lys Ser Ile
 260 265 270
 Val Asn Glu Ile Gly Phe Asp Arg Glu Leu Ala Ile Asn Ser Pro Ser
 275 280 285
 Glu Ala Ser Phe Pro Gly Val Glu Thr Ile Asp Ser Gln Arg Gln Asn
 290 295 300
 Ile Ala Asn Val Val Gly Gly Tyr Tyr Pro Leu Leu Arg Arg Gly Thr
 305 310 315 320
 Leu Ser Asp Val Lys Lys Arg Val Pro Ala Gln Tyr Gln Ala
 325 330

(2) INFORMATIONS POUR LA SEQ ID NO: 188:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 225 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 191790..192464

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 188:

Asn Ile Val Ser Gly Arg Glu Leu Ala Ser Pro Val Ala Thr Gly Phe
 1 5 10 15
 Arg Val Val Ser Phe Asp Asn Lys Thr Leu Ile Leu Glu Ser Gly Asp
 20 25 30
 Gly Gly Ile Arg Lys Thr Tyr Ser Leu Gly Glu Gln Pro Tyr Ala Phe
 35 40 45
 Glu Leu Glu Ile Gln Thr Thr Gln Gly Arg Glu Asp Leu Trp Ile Thr
 50 55 60
 Ser Gly Val Pro Glu Val Glu Ile Met Ser Asn Ala Phe Val Pro Ala
 65 70 75 80
 Val Lys Tyr His Ala Val Lys Lys Asn Lys Ser Asp Leu Phe Asn Val
 85 90 95
 Lys Leu Pro Lys Ala Lys Asp Ser Leu Leu Val Arg Asn Asn Ala Thr
 100 105 110
 Pro Gln Trp Ile Leu Asn Ser Asn Gly Tyr Phe Gly Val Ile Leu Thr
 115 120 125
 Pro Arg Thr Pro Ile Pro Ala Gly Tyr Ala Ser Ser Phe Ile Pro Gly
 130 135 140
 Asn Val Val Pro Thr Arg Leu Ser Gln Leu Pro Pro Lys Asp Gln Ala
 145 150 155 160
 Tyr Pro Ala Ser Lys Tyr Pro Gly Tyr Thr Ala Met Leu Pro Leu Pro
 165 170 175
 Lys Glu Ala Gly Arg Tyr Gln Phe Met Val Tyr Ala Gly Pro Leu Ala
 180 185 190
 Asp Pro Thr Leu Lys Thr Leu Asp Arg Leu Thr Arg Ile Leu Lys Glu
 195 200 205
 Lys Leu Leu Ser Ile Leu Met Arg Leu Leu Ser Glu Gly Ser Leu Val
 210 215 220

Leu
225

(2) INFORMATION POUR LA SEQ ID NO: 189:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 192392..193183

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 189:

Thr 1	Asn	Ala	Asn	Ser 5	Lys	Gly	Glu	Thr	Pro 10	Glu	Tyr	Ile	Asp	Ala 15	Ile
Ala	Phe	Arg	Gly 20	Phe	Phe	Ser	Phe	Ile	Thr 25	Glu	Pro	Phe	Ala 30	Ala	Leu
Leu	Phe	Val	Ile	Met	Lys	Phe	Phe 40	Lys	Phe	Leu	Thr	Gly 45	Ser	Trp	Gly
Ile	Ser 50	Ile	Ile	Leu	Leu	Thr 55	Ile	Val	Leu	Lys	Leu 60	Leu	Leu	Tyr	Pro
Leu 65	Asn	Ala	Trp	Ser	Ile 70	Arg	Ser	Met	Arg	Arg	Met	Gln	Lys	Leu	Ser 80
Pro	Tyr	Ile	Gln	Glu 85	Ile	Gln	Gln	Lys	Tyr 90	Lys	Arg	Glu	Pro	Lys 95	Arg
Ala	Gln	Met	Glu 100	Ile	Met	Ala	Leu	Tyr 105	Lys	Met	Asn	Lys	Val 110	Asn	Pro
Ile	Thr	Gly 115	Cys	Leu	Pro	Leu	Leu 120	Ile	Gln	Ile	Pro	Phe	Leu 125	Ile	Ala
Met	Phe 130	Asp	Leu	Leu	Lys	Ser 135	Ser	Phe	Leu	Leu	Arg 140	Gly	Ala	Ser	Phe
Ile 145	Pro	Gly	Trp	Ile	Asp 150	Asn	Leu	Thr	Ala	Pro	Asp 155	Val	Leu	Phe	Ser 160
Trp	Glu	Thr	Pro	Ile 165	Trp	Phe	Ile	Gly	Lys 170	Glu	Phe	His	Leu	Leu 175	Pro
Ile	Leu	Leu	Gly 180	Val	Val	Met	Phe	Ala 185	Gln	Gln	Lys	Ile	Ser 190	Ala	Val
Lys	Arg	Ser 195	Gly	Pro	Ala	Ser	Asp 200	Gln	Gln	Arg	Gln	Gln 205	Glu	Ala	Met
Gly	Thr 210	Met	Met	Ala	Leu	Leu	Phe 215	Thr	Phe	Met	Phe 220	Tyr	Asn	Phe	Pro
Ser 225	Gly	Leu	Asn	Ile	Tyr 230	Trp	Phe	Ser	Ser	Met 235	Leu	Leu	Gly	Val	Ile 240
Gln	Gln	Trp	Val	Thr 245	Asn	Lys	Ile	Leu	Asp 250	Glu	Gln	His	Leu	Gln 255	His
Glu	Val	Ile	Ile 260	Asn	Lys	Lys	Arg								

(2) INFORMATION POUR LA SEQ ID NO: 190:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 459 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 193254..194630

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 190:

```

Asp Ser Phe Met Arg Ala Trp Glu Glu Phe Leu Leu Leu Gln Glu Lys
1      5      10      15
Glu Ile Gly Val Asp Thr Val Asn Lys Trp Leu Arg Ser Leu Lys Val
20      25      30
Leu Cys Phe Asp Ala Cys Asn Leu Tyr Leu Glu Ala Lys Asp Ser Phe
35      40      45
Gln Val Thr Trp Phe Glu Glu His Ile Arg His Lys Val Lys Ala Ser
50      55      60
Leu Ile Asn Asn Asn Gly Lys Pro Ile Arg Val Arg Val Thr Ser Leu
65      70      75      80
Asp Lys Ser Thr Pro Phe Lys Asp Thr Gln Ile Gln Gln Glu Lys Thr
85      90      95
Ala Tyr Phe Thr Met Lys Tyr Gly Asp Ile Asp Pro Asn Met Ser Phe
100      105      110
Ala Asn Phe Leu Val Thr Pro Glu Asn Asp Leu Pro Val Arg Ile Leu
115      120      125
Gln Glu Phe Ala Lys Val Ser Glu Gln Gly Lys Gly Phe Pro Phe Asn
130      135      140
Pro Ile Tyr Leu Phe Gly Pro Glu Ser Ser Gly Lys Thr His Leu Met
145      150      155      160
Gln Ala Ala Val Gly Gly Leu Arg Glu Ala Gly Val Lys Thr Leu Tyr
165      170      175
Val Thr Ser Glu Leu Phe Thr Glu His Leu Val Ser Ala Ile Arg Ser
180      185      190
Gly Glu Met Gln Arg Phe Arg Ala Phe Tyr Arg Asn Val Glu Ala Leu
195      200      205
Phe Ile Glu Asp Ile Glu Val Leu Ser Gly Lys Gly Ala Thr Gln Glu
210      215      220
Glu Phe Phe His Thr Phe Xaa Ser Leu His Thr Glu Gly Lys Leu Ile
225      230      235      240
Val Ile Ser Ser Thr Phe Ala Pro Gly Asp Leu Lys Ala Met Glu Glu
245      250      255
Arg Leu Ile Ser Arg Phe Glu Trp Gly Ile Ser Ile Pro Val Ser Pro
260      265      270
Leu Thr Arg Glu Gly Leu Lys Ser Phe Leu Glu Arg Arg Ile Glu Lys
275      280      285
Leu Asn Ile Arg Ile Glu Glu Thr Ala Leu Asp Phe Leu Ile Gln Ala
290      295      300
Leu Ser Ser His Val Lys Ser Leu Leu His Ala Leu Thr Thr Leu Ala
305      310      315      320
Lys Arg Val Ala Tyr Lys Lys Leu Ser His Gln Met Leu Tyr Gln Gly
325      330      335
Asp Ile Glu Ala Leu Leu His Asp Val Leu Gln Ala Ala Glu Ser Ile
340      345      350
Arg Leu Thr Pro Ser Gly Ile Val Arg Ala Thr Ala Gln Tyr Tyr Gly
355      360      365
Val Ser Pro Glu Ser Val Leu Gly Arg Ser Gln Ser Arg Glu Tyr Val
370      375      380
Leu Pro Arg Gln Val Ala Met Phe Leu Cys Arg Gln Lys Leu Ser Leu
385      390      395      400

```

Ser Tyr Val Lys Ile Gly Glu Val Phe Ser Arg Asp His Ser Thr Val
 405 410 415
 Ile Ser Ser Ile Arg Ala Ile Ser Gln Lys Leu Glu Glu Asp Asp Arg
 420 425 430
 Glu Cys Asp Val Ser Cys Ala Ile Gln Glu Leu Thr Lys Arg Leu Ser
 435 440 445
 Ser Ala Tyr Gln Ser Leu Asp Phe Ile Glu Asp
 450 455

(2) INFORMATIONS POUR LA SEQ ID NO: 191:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(194690..195046)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 191:

Gly Gly Phe Met Gly Ile Lys Pro His Asp Tyr Gly Cys Trp Gly Ser
 1 5 10 15
 Arg Gly Asn Val Phe Thr Leu Gln Asp Leu Asn Thr Gln Gln Ala Asn
 20 25 30
 Gln Ser Ala Ala Ala Ser Ser Ser Ser Val Leu Lys Ser Glu Cys Ala
 35 40 45
 Ala Lys Val Ala Arg Tyr Ala Leu Gly Phe Leu Phe Gly Leu Gly Phe
 50 55 60
 Ile Leu Ser Ile Val Thr Phe Ile Ala Ala Ala Ala Thr Leu Pro Leu
 65 70 75 80
 Gly Thr Thr Thr Ile Leu Ile Met Val Thr Gln Ile Ala Phe Ala Ala
 85 90 95
 Ala Leu Ala Phe Lys Leu Tyr Asp Leu Phe Lys His Asp Val Pro Thr
 100 105 110
 Cys Ser Ile Thr Ser Lys Ala
 115

(2) INFORMATIONS POUR LA SEQ ID NO: 192:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 616 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 195184..197031

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 192:

Glu Ala Ser Met Tyr Phe Asp Arg Thr Lys Ile Asn Val Glu Ser Met
 1 5 10 15
 Lys Gln Ala Ile Leu Glu Arg Val Tyr Cys Gly Val Val Gln Thr Pro

20 25 30
 Gln Ser Ala Ser Thr Arg Asp Ile Phe Ile Ala Val Ala Lys Thr Val
 35 40 45
 Leu Glu Trp Met Ala Lys Gly Trp Leu Lys Thr Gln Ser Ser Tyr Tyr
 50 55 60
 Asp Asn Asp Val Lys Arg Val Tyr Tyr Ile Ser Met Glu Phe Leu Leu
 65 70 75 80
 Gly Arg Ser Leu Lys Ser Asn Leu Leu Asn Leu Gly Leu Leu Asp Leu
 85 90 95
 Val Lys Glu Ala Leu Phe Asp Leu Gly Tyr Asp Phe Asp Gln Leu Val
 100 105 110
 Glu Met Glu His Asp Ala Gly Leu Gly Asn Gly Gly Leu Gly Arg Leu
 115 120 125
 Ala Ala Cys Phe Leu Asp Ser Met Ala Thr Leu Glu Ile Pro Ala Tyr
 130 135 140
 Gly Tyr Gly Leu Arg Tyr Asp Tyr Gly Ile Phe Asp Gln Lys Ile Glu
 145 150 155 160
 Asn Gly Phe Gln Val Glu Ser Pro Ile Glu Trp Leu Arg Tyr Gly Asn
 165 170 175
 Pro Trp Glu Ile Cys Arg Gly Glu Tyr Leu Tyr Pro Val His Phe Tyr
 180 185 190
 Gly Lys Val Lys His Ser Ile Asp Ser Arg Gly Arg Asp Val Ala Glu
 195 200 205
 Leu Val Asp Ser Gln Glu Val Leu Ala Met Ala Tyr Asp Val Pro Val
 210 215 220
 Pro Gly Phe Asn Asn Asp Thr Val Asn Ser Leu Arg Leu Trp Gln Ala
 225 230 235 240
 Gln Ser Arg His Gly Phe Glu Phe Ser Tyr Phe Asn His Gly Asn Tyr
 245 250 255
 Ile Arg Ala Ile Glu Asp Ile Ala Leu Ala Gly Asn Ile Thr Arg Val
 260 265 270
 Leu Tyr Pro Asn Asp Ser Ile Ser Glu Gly Gln Glu Leu Arg Leu Lys
 275 280 285
 Gln Glu Tyr Phe Leu Val Ser Ala Thr Ile Gln Asp Ile Leu Arg Arg
 290 295 300
 Tyr Thr Lys Thr His Leu Ser Leu Asp Lys Leu Ser Glu Lys Val Ser
 305 310 315 320
 Val Gln Leu Asn Asp Thr His Pro Ala Leu Gly Ile Ala Glu Met Met
 325 330 335
 Arg Leu Leu Val Asp Arg Glu Glu Leu Asp Trp Asp Val Ala Trp Asp
 340 345 350
 Ala Thr Thr Lys Ile Phe Asn Tyr Thr Asn His Thr Ile Leu Pro Glu
 355 360 365
 Ala Leu Glu Arg Trp Ser Leu Asp Leu Phe Ser Lys Val Leu Pro Arg
 370 375 380
 His Leu Glu Ile Ile Tyr Glu Ile Asn Ala Arg Trp Leu Ala Lys Val
 385 390 395 400
 Ser Gln Lys Tyr Pro Gly Asp Asn Asp Lys Arg Arg Ala Leu Ser Ile
 405 410 415
 Ile Glu Glu Gly Ser Ser Lys Phe Val Asn Met Ala Asn Leu Ala Val
 420 425 430
 Val Gly Thr Asn Lys Val Asn Gly Val Ser Thr Phe His Ser Gln Leu
 435 440 445
 Ile Lys Ser Thr Leu Phe Lys Asp Phe Val Glu Phe Phe Pro Asp Lys
 450 455 460
 Phe Ile Asn Val Thr Asn Gly Ile Thr Pro Arg Arg Trp Leu Ala Leu
 465 470 475 480
 Ser Asn Lys Lys Leu Ser Ser Leu Leu Asn Arg Thr Ile Gly Thr Glu
 485 490 495

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Tyr Leu Thr Asn Leu Thr His Leu His Lys Val Ile Pro Leu Ala Glu
      500                      505          510
Asp Ser Gly Phe Arg Glu Glu Trp Arg Asn Ile Lys Ile Gln Asn Lys
      515                      520          525
Glu Glu Leu Ala Ala Arg Ile Tyr Lys Glu Leu Gly Val Thr Val Asn
      530                      535          540
Pro Gln Ser Ile Phe Asp Cys His Ile Lys Arg Ile His Glu Tyr Lys
545                      550          555          560
Arg Gln Leu Thr Asn Ile Leu Arg Val Ile Tyr Phe Tyr Asn Glu Ile
      565                      570          575
Arg Asn Gly Ser Gly Glu Ile Val Pro Thr Thr Val Ile Phe Gly Gly
      580                      585          590
Lys Ala Ala Pro Gly Tyr Ala Met Ala Lys Leu Ile Ile Lys Leu Ile
      595                      600          605
Asn Asn Val Ala Ala Val Val Lys
      610                      615

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(2) INFORMATIONS POUR LA SEQ ID NO: 193:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 197018..197635

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 193:

```

Gln Leu Leu Leu Asn Asn Asp Pro Lys Val Asn Asp Gln Leu Lys Val
1      5      10      15
Ile Phe Trp Pro Asn Tyr Arg Val Ser Leu Ala Glu Ala Ile Ile Pro
      20      25      30
Ala Thr Asp Leu Ser Glu Gln Ile Ser Thr Ala Gly Met Glu Ala Ser
      35      40      45
Gly Thr Gly Asn Met Lys Phe Ala Leu Asn Gly Ala Leu Thr Ile Gly
      50      55      60
Thr Met Asp Gly Ala Asn Ile Glu Met Ala Glu His Ile Gly Lys Glu
65      70      75      80
His Met Phe Ile Phe Gly Leu Leu Glu Glu Glu Ile Ser Glu Leu Arg
      85      90      95
Lys Glu Tyr Tyr Pro Gln Gly Ile Cys Asn Ala Asn Pro Thr Ile Gln
      100     105     110
Glu Ile Leu Asp Met Ile Ala Gln Ala Lys Phe Ser Gln Glu Asp Lys
      115     120     125
Asp Leu Phe Lys Pro Ile Val Asn Arg Leu Leu Asn Glu Gly Asp Pro
      130     135     140
Phe Phe Val Leu Ala Asp Leu Glu Ala Tyr Ile Asn Thr Gln Asn Arg
145     150     155     160
Val Ala Ser Leu Phe Lys Gln Pro Glu Glu Trp Thr Lys Lys Ser Ile
      165     170     175
Tyr Asn Val Gly Gly Ile Gly Phe Phe Ser Ser Asp Arg Ser Ile Ala
      180     185     190
Glu Tyr Ala Ser Asn Ile Trp Xaa Val Ser Arg Pro Thr Ser
      195     200     205

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(xi)	DESCRIPTION DE LA SEQUENCE														
Gly	Asn	Val	Val	Val	Ser	Leu	Leu	Lys	Met	Pro	Lys	Leu	Ser	Pro	Thr
1				5					10					15	
Met	Glu	Ile	Gly	Ile	Leu	Val	Lys	Trp	His	Lys	Lys	Ala	Gly	Asp	Glu
			20					25					30		
Ile	His	Phe	Gly	Asp	Val	Leu	Leu	Glu	Ile	Ser	Thr	Asp	Lys	Ala	Val
		35					40					45			
Leu	Glu	His	Thr	Ala	Ser	Glu	Asp	Gly	Trp	Leu	Leu	Glu	Ile	Leu	Val
	50					55					60				

Lys	Glu	Gly	Thr	Lys	Thr	Pro	Ile	Gly	Thr	Pro	Ile	Ala	Val	Phe	Ser
65					70					75					80
Thr	Glu	Gln	Asn	Ala	Gln	Tyr	Asp	Leu	Lys	Gln	Leu	Leu	Pro	Leu	Glu
				85					90					95	
Glu	Thr	Val	Val	Thr	Asp	Ala	Ala	Thr	Glu	Ala	Ser	Pro	Lys	Asp	Ser
			100					105					110		
Ala	Gln	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Gly	Pro	Ser	Ile	Thr	Met	Met
			115				120					125			
Gly	Phe	Arg	Pro	Glu	Pro	Pro	Leu	Ala	Thr	Pro	Leu	Thr	Ile	Lys	His
	130					135					140				
Ser	Asn	Asp	Pro	Val	Leu	Ala	Ser	Pro	Leu	Ala	Lys	Lys	Leu	Ala	Lys
	145				150					155					160
Glu	Gln	Asn	Leu	Asp	Leu	Ser	Gly	Val	Thr	Gly	Ser	Gly	Pro	Gly	Gly
				165					170					175	
Arg	Ile	Ile	Lys	Lys	Asp	Leu	Glu	Lys	Ala	Pro	Pro	Leu	Arg	Ile	Ala
			180					185					190		
Gly	Phe	Gly	Tyr	Pro	Glu	Ala	Pro	Asn	Val	Asn	Pro	Gly	Ser	Tyr	Ile
		195				200						205			
Glu	Glu	Pro	Leu	Ser	Pro	Val	Arg	Glu	Val	Ile	Ser	Lys	Arg	Leu	Gln
	210					215						220			
Ala	Ala	Lys	Thr	Phe	Ile	Pro	His	Phe	Tyr	Val	Arg	Gln	Arg	Ile	Tyr
	225				230					235					240
Ala	Ser	Pro	Leu	Leu	Ala	Leu	Leu	Lys	Glu	Leu	Gln	Glu	Gln	Asn	Ile
				245					250					255	
Lys	Leu	Ser	Ile	Asn	Asp	Cys	Ile	Val	Arg	Ala	Cys	Ala	Leu	Ala	Leu
			260					265					270		
Lys	Glu	Phe	Pro	Glu	Ile	Asn	Ser	Gly	Phe	Asn	Ser	Val	Asp	Asn	Lys
		275					280					285			
Ile	Ile	Arg	Phe	Ser	Thr	Ile	Asp	Ile	Ser	Ile	Ala	Val	Ala	Ile	Pro
	290					295						300			
Asp	Gly	Val	Ile	Thr	Pro	Ile	Val	Arg	Cys	Ala	Asp	Arg	Lys	Asn	Ile
	305				310					315					320
Gly	Met	Ile	Ser	Ala	Glu	Ile	Lys	Gly	Leu	Ala	Thr	Lys	Ala	Lys	Gln
				325					330					335	
Gln	Ser	Leu	Ala	Glu	Glu	Glu	Tyr	Lys	Gly	Gly	Ser	Phe	Cys	Val	Ser
			340					345					350		
Asn	Leu	Gly	Met	Thr	Gly	Ile	Ser	Asp	Phe	Thr	Ala	Ile	Leu	Asn	Pro
		355					360					365			
Pro	Gln	Ala	Ala	Ile	Leu	Ala	Val	Gly	Ser	Val	Glu	Glu	Gln	Pro	Val
		370				375					380				
Val	Leu	Asn	Gly	Glu	Leu	Ala	Val	Gly	Ser	Thr	Cys	Met	Leu	Thr	Leu
	385				390					395					400
Ser	Val	Asp	His	Arg	Val	Ile	Asp	Gly	Tyr	Pro	Ala	Ala	Met	Phe	Met
			405					410					415		
Lys	Arg	Leu	Gln	Arg	Leu	Leu	Glu	Ala	Pro	Ser	Val	Leu	Leu	Leu	Asn
			420					425					430		

(2) INFORMATIONS POUR LA SEQ ID NO: 196:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 332 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(198962..199957)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 196:

Lys Arg Gly Ser Met Pro Asn Phe Val Thr Leu Glu Ile Arg Glu Ala
 1 5 10 15
 Ile Arg Gln Ala Ile Asp Glu Glu Met Thr Arg Asp Pro Asn Val Cys
 20 25 30
 Ile Leu Gly Glu Glu Val Ala Glu Tyr Asn Gly Ala Tyr Lys Val Thr
 35 40 45
 Lys Asn Leu Leu Asp Lys Trp Gly Pro Thr Arg Val Ile Asp Thr Pro
 50 55 60
 Ile Ser Glu Ala Ala Phe Ser Gly Ile Gly Ile Gly Ala Ala Leu Thr
 65 70 75 80
 Gly Leu Arg Pro Ile Ile Glu Phe Met Ser Trp Asn Phe Ser Leu Val
 85 90 95
 Ala Ala Asp Gln Ile Ile Ser His Ala Ala Lys Met Tyr Tyr Met Thr
 100 105 110
 Gly Gly Lys Phe Ala Val Pro Ile Val Phe Arg Gly Ala Asn Gly Ala
 115 120 125
 Ala Ala Gln Val Ser Cys Gln His Ser His Cys Val Glu Ala Leu Tyr
 130 135 140
 Ala Asn Ile Pro Gly Leu Ile Val Ile Ala Pro Ser Thr Pro Ala Asp
 145 150 155 160
 Ala Lys Gly Leu Leu Lys Ser Ala Ile Arg Asp Asn Asn Pro Val Leu
 165 170 175
 Phe Leu Glu Asn Glu Leu Asp Tyr Asn Leu Lys Gly Glu Val Pro Ser
 180 185 190
 Glu Glu Tyr Leu Ile Pro Ile Gly Lys Ala Arg Ile Val Gln Glu Gly
 195 200 205
 Lys Asp Leu Thr Ile Ile Ser His Ser Arg Met Val Ser Ile Val Glu
 210 215 220
 Gln Ala Ala Lys Thr Ala Lys Gln Arg Trp Gly Leu Ser Ile Glu Thr
 225 230 235 240
 Ile Asp Leu Arg Thr Ile Lys Pro Leu Asp Val Ala Thr Leu Leu Thr
 245 250 255
 Ser Val Lys Lys Thr Gly Asn Cys Leu Val Val Glu Glu Gly His Tyr
 260 265 270
 Phe Cys Gly Ile Ser Ala Glu Val Ile Thr Thr Ile Thr Glu His Ile
 275 280 285
 Phe Asp Tyr Leu Asp His Pro Pro Leu Arg Val Cys Gln Lys Glu Thr
 290 295 300
 Pro Met Pro Tyr Asn Lys Thr Leu Glu Met Ala Thr Leu Pro Asn Ile
 305 310 315 320
 Asn Arg Ile Leu Asp Ala Ile Glu Lys Ile Met Arg
 325 330

(2) INFORMATIONS POUR LA SEQ ID NO: 197:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 129 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(199941..200327)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 197:

Gln	Asn	Pro	Lys	Arg	Phe	Leu	Met	Val	Phe	Leu	Ser	Ile	Thr	Leu	Asn
1				5					10					15	
Gly	Phe	Asp	Leu	Phe	Asn	Ser	Leu	Ile	Gly	Phe	Arg	Glu	Ala	Tyr	His
			20					25					30		
His	Met	Gln	Gln	Thr	Gly	Ser	Pro	Ile	Ile	Val	Glu	Ala	Leu	Cys	Ser
			35				40					45			
Arg	Phe	Arg	Gly	His	Ser	Ile	Ser	Asp	Pro	Asn	Leu	Tyr	Arg	Ser	Lys
	50				55					60					
Glu	Glu	Met	Gln	Cys	Leu	Lys	Arg	Asp	Pro	Ile	Leu	Phe	Ala	Lys	
65					70				75					80	
Glu	Trp	Leu	Ile	Arg	Ala	Asn	Val	Leu	Ser	Glu	Asp	Asp	Phe	Lys	Asp
			85					90						95	
Leu	Arg	Gln	Thr	Ser	Lys	Thr	Ala	Val	Leu	Glu	Ala	Val	Ala	Gln	Ala
			100					105					110		
Arg	Leu	Asp	Pro	Glu	Pro	Ala	Val	Ala	Thr	Leu	Glu	Glu	Gly	Val	Tyr
		115					120					125			
Ala															

(2) INFORMATIONS POUR LA SEQ ID NO: 198:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(200266..200685)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 198:

Leu	Cys	Cys	Trp	Asn	Ile	Pro	Leu	Arg	Gln	Leu	Ala	Ala	Glu	Leu	Leu
1				5					10					15	
Gly	Lys	Glu	Thr	Gly	Cys	Ala	Leu	Gly	Arg	Gly	Gly	Ser	Met	His	Met
			20					25					30		
Cys	Gly	Asp	Arg	Leu	Pro	Gly	Gly	Phe	Gly	Ile	Val	Gly	Gly	Gln	Ile
		35				40						45			
Pro	Leu	Ala	Ala	Gly	Ala	Ala	Phe	Ser	Met	Lys	Tyr	Gln	Asn	Ser	Ser
	50				55					60					
Ser	Ile	Ser	Met	Cys	Phe	Ile	Gly	Asp	Gly	Ala	Val	Ala	Gln	Gly	Val
65				70					75					80	
Phe	His	Glu	Thr	Leu	Asn	Phe	Val	Ala	Leu	His	Ser	Leu	Pro	Leu	Met
			85					90						95	
Leu	Ile	Ile	Glu	Asn	Asn	Gly	Trp	Ser	Met	Gly	Thr	Ala	Leu	His	Arg
			100					105					110		
Ala	Ile	Ala	Lys	Gln	Pro	Ile	Ala	Glu	Ser	Gln	Ala	Ile	Ser	Tyr	Gly
		115					120					125			
Leu	Ser	Phe	Asp	His	Phe	Glu	Trp	Ile	Arg	Phe	Ile				
	130						135				140				

(2) INFORMATIONS POUR LA SEQ ID NO: 199:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 199:

(2) INFORMATION POUR LA SEQ ID NO: 200:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 200:

(xi)	DESCRIPTION OF THE SEQUENCE														
Ser	Trp	Phe	Glu	Val	Leu	Lys	Phe	His	Phe	Pro	Cys	Ser	Glu	Gly	Leu
1				5					10					15	
Ile	Arg	Gly	Phe	Ser	Ile	Glu	Phe	Leu	Cys	Cys	Ile	Leu	Thr	Asp	Lys
			20					25					30		
Lys	Ile	Gln	Tyr	Pro	Leu	Lys	Asn	Phe	Ile	Cys	Val	Glu	Phe	Ile	Val
			35				40					45			
Asn	Ser	Phe	Phe	Gly	Ile	Leu	Pro	Arg	Gly	Ile	Pro	Asn	Val	Gly	Gly
	50					55					60				
Leu	Ser	Glu	Val	Ala	Gly	Glu	Asn	Lys	Gln	Ser	Leu	Glu	Glu	Arg	Glu
65					70					75					80
Gln	Asp	Lys	Glu	Leu	Lys	Leu	Glu	Lys	Lys	Leu	Leu	Ala	Ile	Arg	Lys
				85					90					95	
Arg	Ile	Lys	Cys	Phe	Cys	Pro	Gln	Gln	Pro	Glu	Ile	Ser	Val	Gln	Ala
			100					105					110		
Ala	Pro	Leu	Lys	His	Thr	Gly	Thr	Phe	Pro	Cys	Ser	Glu	Glu	Glu	Leu
		115					120					125			
Arg	Asp	Ile	Ser	Asp	Leu	Phe	Ser	Ser	Leu	Lys	Ser	Phe	Arg	Gln	Gln
	130					135					140				

```

Leu Ala Gln Leu Phe Phe Tyr Thr Pro Pro Leu Asn Leu Glu Trp Glu
145          150          155          160
Asp Phe Leu Lys Phe Phe Phe Ala Phe Glu Lys Arg Glu Leu Gly Gly
          165          170          175
Ile Leu Phe Ser Ala Gly Pro Phe Glu Ser Phe Asp Arg Tyr Leu Tyr
          180          185          190
Gln Val Asn Lys Ala Arg Pro Val Pro Val Leu Ile Ala Thr Thr Val
          195          200          205
Ser Tyr Ala Leu Gln Ala Tyr Cys Ser Tyr Ile Asn Arg Ala Pro Phe
210          215          220
Gln Glu Lys Glu Asn Phe Phe Gln Leu Gly Glu Ala Val Gly Ile Phe
225          230          235          240
Leu Lys Glu Arg Lys Val Ser Ile Ala Leu Met Tyr Lys Glu Ile Leu
          245          250          255
Asp Leu Asp Asn Lys Gln Tyr Ser Glu Leu Cys Arg Gly Leu Gln Lys
          260          265          270
Ser Gln Ile Val Gln Gly Glu Val Phe His Ser Ser Thr Gln Glu Arg
          275          280          285
Asp Gly Leu Asn Pro Ile Ser Val Asn Tyr Asp Leu Met Gly Thr Ile
290          295          300
Ala Ala Leu Ser Val Asn Ile Asp Arg Ser Cys Leu Arg Phe Ser Gly
305          310          315          320
Ser His Ile Phe His Asp Asp Glu Met Ala Ile Glu Thr Leu His Lys
          325          330          335
Gly Gly Asp Val Phe Thr Phe Ser Ser Leu Ala Glu Phe Gln Phe Ser
          340          345          350
Glu Lys Arg Leu Leu His Leu Val Ser Thr Gly Arg Val Cys Pro Glu
          355          360          365
Ile Ile Arg Lys Lys Leu Ile Lys Val Leu Leu Leu Lys Lys Arg Ala
          370          375          380
Leu Cys Lys Pro Phe Cys Arg His Ile Gln Ile Thr Ser Glu Thr Ala
385          390          395          400
Gln Leu Asn

```

(2) INFORMATIONS POUR LA SEQ ID NO: 201:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 354 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(202380..203441)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 201:

```

Met Ser Gln Ser Thr Tyr Ser Leu Glu Gln Leu Ala Asp Phe Leu Lys
1          5          10          15
Val Glu Phe Gln Gly Asn Gly Ala Thr Leu Leu Ser Gly Val Glu Glu
          20          25          30
Ile Glu Glu Ala Lys Thr Ala His Ile Thr Phe Leu Asp Asn Glu Lys
          35          40          45
Tyr Ala Lys His Leu Lys Ser Ser Glu Ala Gly Ala Ile Ile Ile Ser
          50          55          60
Arg Thr Gln Phe Gln Lys Tyr Arg Asp Leu Asn Lys Asn Phe Leu Ile

```

65 70 75 80
 Thr Ser Glu Ser Pro Ser Leu Val Phe Gln Lys Cys Leu Glu Leu Phe
 85 90 95
 Ile Thr Pro Val Asp Ser Gly Phe Pro Gly Ile His Pro Thr Ala Val
 100 105 110
 Ile His Pro Thr Ala Ile Ile Glu Asp His Val Cys Ile Glu Pro Tyr
 115 120 125
 Ala Val Val Cys Gln His Ala His Val Gly Ser Ala Cys His Ile Gly
 130 135 140
 Ser Gly Ser Val Ile Gly Ala Tyr Ser Thr Val Gly Gln His Ser Tyr
 145 150 155 160
 Ile His Pro Arg Val Val Ile Arg Glu Arg Val Ser Ile Gly Lys Arg
 165 170 175
 Val Ile Ile Gln Pro Gly Ala Val Ile Gly Ser Cys Gly Phe Gly Tyr
 180 185 190
 Val Thr Ser Ala Phe Gly Gln His Lys His Leu Lys His Leu Gly Lys
 195 200 205
 Val Ile Ile Glu Asp Asp Val Glu Ile Gly Ala Asn Thr Thr Ile Asp
 210 215 220
 Arg Gly Arg Phe Lys His Ser Val Val Arg Glu Gly Ser Lys Ile Asp
 225 230 235 240
 Asn Leu Val Gln Ile Ala His Gln Val Glu Val Gly Gln His Ser Met
 245 250 255
 Ile Val Ala Gln Ala Gly Ile Ala Gly Ser Thr Lys Ile Gly Asn His
 260 265 270
 Val Ile Ile Gly Gly Gln Ala Gly Ile Thr Gly His Ile Cys Ile Ala
 275 280 285
 Asp His Val Ile Met Met Ala Gln Thr Gly Val Thr Lys Ser Ile Thr
 290 295 300
 Ser Pro Gly Ile Tyr Gly Gly Ala Pro Ala Arg Pro Tyr Gln Glu Ile
 305 310 315 320
 His Arg Gln Val Ala Lys Val Arg Asn Leu Pro Arg Leu Glu Glu Arg
 325 330 335
 Ile Ala Ala Leu Glu Lys Leu Val Gln Lys Leu Glu Ala Leu Ser Glu
 340 345 350
 Gln His

(2) INFORMATIONS POUR LA SEQ ID NO: 202:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(203471..203998)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 202:

Glu Arg Ile Met Lys Lys Phe Leu Leu Leu Ser Leu Met Ser Leu Ser
 1 5 10 15
 Ser Leu Pro Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val
 20 25 30
 Asn Leu Arg Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser
 35 40 45

Ala	Glu	Phe	Glu	Lys	Met	Lys	Asn	Gln	Phe	Ser	Asn	Ser	Met	Gly	Lys
50						55					60				
Met	Glu	Glu	Glu	Leu	Ser	Ser	Ile	Tyr	Ser	Lys	Leu	Gln	Asp	Asp	Asp
65					70					75					80
Tyr	Met	Glu	Gly	Leu	Ser	Glu	Thr	Ala	Ala	Ala	Glu	Leu	Arg	Lys	Lys
				85					90					95	
Phe	Glu	Asp	Leu	Ser	Ala	Glu	Tyr	Asn	Thr	Ala	Gln	Gly	Gln	Tyr	Tyr
			100					105					110		
Gln	Ile	Leu	Asn	Gln	Ser	Asn	Leu	Lys	Arg	Met	Gln	Lys	Ile	Met	Glu
		115					120					125			
Glu	Val	Lys	Lys	Ala	Ser	Glu	Thr	Val	Arg	Ile	Gln	Gly	Leu	Ser	
	130					135					140				
Val	Leu	Leu	Asn	Glu	Asp	Ile	Val	Leu	Ser	Ile	Asp	Ser	Ser	Ala	Asp
145					150					155					160
Lys	Thr	Asp	Ala	Val	Ile	Lys	Val	Leu	Asp	Asp	Ser	Phe	Gln	Asn	Asn
				165					170					175	

(2) INFORMATIONS POUR LA SEQ ID NO: 203:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 781 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(204059..206401)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 203:

Leu	Ala	Val	Leu	Leu	Leu	Leu	Thr	Phe	Ser	Gln	Ser	Ser	Phe	Cys	Ser
1				5					10					15	
Thr	Ser	Glu	Gly	Arg	Met	Val	Val	Glu	Ser	Ile	Thr	Ile	Thr	Thr	Gln
			20					25					30		
Gly	Glu	Asn	Thr	Gln	Asn	Lys	Arg	Ala	Ile	Pro	Lys	Ile	Lys	Thr	Lys
		35					40					45			
Gln	Gly	Thr	Leu	Phe	Ser	Gln	Ala	Asp	Phe	Asp	Glu	Asp	Leu	Arg	Thr
	50					55					60				
Leu	Ser	Lys	Asn	Phe	Asp	Arg	Val	Glu	Pro	Ile	Val	Glu	Phe	Arg	Asn
65					70					75					80
Gly	Gln	Ala	Val	Ile	Ser	Leu	Ile	Leu	Thr	Ala	Lys	Ser	Val	Ile	Arg
			85						90					95	
Glu	Ile	Asn	Ile	Ser	Gly	Asn	Glu	Ala	Ile	Pro	Thr	His	Lys	Ile	Leu
		100						105					110		
Lys	Thr	Leu	Glu	Leu	Tyr	Lys	Asn	Asp	Leu	Phe	Asp	Arg	Glu	Leu	Phe
		115					120					125			
Phe	Lys	Asn	Phe	Asp	Ala	Leu	Arg	Thr	Leu	Tyr	Leu	Lys	Arg	Gly	Tyr
	130					135					140				
Tyr	Asp	Ser	Gln	Leu	Ser	Tyr	Ser	His	Asn	His	Asn	Glu	Lys	Glu	Gly
145					150					155					160
Phe	Ile	Asp	Ile	Ser	Ile	Glu	Ile	Lys	Glu	Gly	Arg	His	Gly	Arg	Ile
			165						170					175	
Lys	Lys	Leu	Thr	Ile	Ser	Gly	Ile	Thr	Arg	Thr	Glu	Ala	Ser	Asp	Leu
		180						185					190		
Gly	Asp	Ile	Val	Leu	Thr	Lys	Gln	Tyr	Ser	Thr	Thr	Thr	Ser	Trp	Phe
	195						200					205			
Thr	Gly	Ala	Gly	Val	Tyr	His	Pro	Asp	Met	Val	Glu	Gln	Asp	Leu	Phe

210 215 220
 Ala Ile Thr Asn Tyr Phe Gln Asn Lys Gly Tyr Ala Asp Ala Lys Val
 225 230 235
 Ser Lys Glu Val Ser Thr Asp Ala Lys Gly Asn Ile Thr Leu Leu Ile
 245 250 255
 Val Val Asp Lys Gly Pro Leu Tyr Thr Leu Gly His Val His Ile Glu
 260 265 270
 Gly Phe Thr Ala Leu Ser Lys Arg Leu Leu Asp Lys Gln Leu Leu Val
 275 280 285
 Gly Pro Asn Ser Leu Tyr Cys Pro Asp Lys Ile Trp Thr Gly Ala Gln
 290 295 300
 Lys Ile Arg Ser Ala Tyr Ala Arg Tyr Gly Tyr Val Asn Thr Asn Val
 305 310 315 320
 Asp Val Ser Phe Ser Ala His Pro Thr Leu Pro Val Tyr Asp Val Thr
 325 330 335
 Tyr Arg Val Ser Glu Gly Ser Pro Tyr Lys Ile Gly Leu Ile Lys Ile
 340 345 350
 Lys Gly Asn Thr His Thr Lys His Asp Val Ile Leu His Glu Thr Ser
 355 360 365
 Leu Phe Pro Gly Asp Thr Phe Tyr Arg Leu Lys Leu Glu Asp Thr Glu
 370 375 380
 Thr Arg Leu Arg Asn Thr Gly Tyr Phe Lys Ser Val Ser Val Tyr Thr
 385 390 395 400
 Val Arg Ser Gln Leu Asp Pro Leu Asp Ser Asn Asp Leu Tyr Arg Asp
 405 410 415
 Val Phe Ile Glu Val Lys Glu Thr Glu Thr Gly Asn Leu Gly Leu Phe
 420 425 430
 Leu Gly Phe Ser Ser Ile Asp His Leu Phe Gly Gly Ala Glu Ile Ala
 435 440 445
 Glu Ser Asn Phe Asp Leu Phe Gly Ala Arg Asn Phe Leu Lys Lys Gly
 450 455 460
 Phe Lys Ser Leu Arg Gly Gly Gly Glu Tyr Leu Phe Leu Lys Ala Asn
 465 470 475 480
 Leu Gly Asp Lys Val Thr Asp Tyr Thr Val Lys Trp Thr Lys Pro His
 485 490 495
 Phe Leu Asn Thr Pro Trp Ile Leu Gly Val Glu Leu Asp Lys Ser Ile
 500 505 510
 Asn Lys Ala Leu Ser Lys Asp Tyr Ser Val Asp Thr Tyr Gly Gly Asn
 515 520 525
 Ile Ser Thr Thr Tyr Ile Leu Asn Asp Lys Leu Lys Tyr Gly Met Tyr
 530 535 540
 Tyr Arg Gly Ser Gln Thr Ser Leu Ser Leu Arg Lys Lys Thr Ser Ser
 545 550 555 560
 Ser Asn Arg Leu Gly Pro Asp Leu Asp Ser Asn Lys Gly Phe Val Ser
 565 570 575
 Ala Ala Gly Leu Asn Val Leu Tyr Asp Ser Ile Asp Asn Pro Arg Lys
 580 585 590
 Pro Thr Met Gly Ile Arg Ser Phe Leu Asn Xaa Glu Leu Ser Gly Leu
 595 600 605
 Gly Gly Thr Tyr Gln Phe Thr Lys Leu Thr Ala Ser Gly Ser Ile Tyr
 610 615 620
 Arg Leu Leu Thr Lys Lys Gly Val Leu Lys Xaa Arg Ala Glu Ala Xaa
 625 630 635 640
 Phe Ile Lys Pro Phe Gly Thr Thr Thr Ala Gln Gly Ile Pro Val Ser
 645 650 655
 Glu Arg Phe Phe Leu Gly Gly Glu Thr Thr Val Arg Gly Tyr Lys Pro
 660 665 670
 Phe Ile Ile Gly Pro Lys Phe Ser Pro Thr Glu Pro Gln Gly Gly Leu
 675 680 685

Ser	Ser	Leu	Leu	Leu	Thr	Glu	Glu	Phe	Gln	Tyr	Pro	Leu	Ile	Ser	Gln
690						695					700				
Pro	Cys	Ile	Asn	Ala	Phe	Val	Phe	Leu	Asp	Ser	Gly	Phe	Ile	Gly	Ile
705					710					715					720
Glu	Glu	His	Thr	Ile	Arg	Leu	Lys	Asp	Leu	Cys	Ser	Ser	Ala	Gly	Phe
				725					730					735	
Gly	Leu	Arg	Phe	Asp	Met	Met	Asn	Asn	Val	Pro	Ile	Met	Leu	Gly	Trp
			740					745					750		
Gly	Trp	Pro	Phe	Arg	Pro	Thr	Glu	Ile	Leu	Asn	Asn	Glu	Lys	Ile	Asp
		755					760					765			
Val	Ser	Gln	Arg	Phe	Phe	Phe	Ala	Leu	Gly	Gly	Val	Phe			
	770					775					780				

(2) INFORMATIONS POUR LA SEQ ID NO: 204:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 205 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(206811..207425)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 204:

Ile	Gly	Leu	Lys	Asp	Met	Leu	Lys	Tyr	Pro	Asp	Tyr	Ile	Ser	Lys	Leu
1			5					10						15	
Ile	Ser	Phe	Leu	Lys	Lys	Leu	Pro	Gly	Ile	Gly	Phe	Lys	Ser	Ala	Glu
		20						25					30		
Lys	Ile	Ala	Phe	Glu	Leu	Leu	Glu	Trp	Asp	Pro	Ser	Gln	Ile	Glu	Ala
		35					40					45			
Met	Ala	Leu	Ala	Leu	Gln	Glu	Phe	Ser	Thr	Ser	His	Ala	Thr	Cys	Ser
	50					55					60				
Asn	Cys	Phe	Cys	Leu	Lys	Ile	Ser	Gln	Thr	Ser	Pro	Cys	Asn	Phe	Cys
65					70					75					80
Ser	Glu	Ser	Arg	Asp	Ser	Ser	Ser	Leu	Cys	Ile	Val	Ala	Thr	Pro	Lys
			85					90						95	
Asp	Val	Phe	Ala	Leu	Glu	Lys	Ser	Lys	Ile	Phe	Lys	Gly	His	Tyr	Phe
			100					105					110		
Val	Leu	Gly	Asn	Leu	Leu	Ser	Pro	Ile	Thr	Gly	Lys	His	Leu	Ser	Leu
		115					120					125			
Glu	Lys	Leu	Ala	Ile	Leu	Lys	Gln	Arg	Ile	Glu	Ala	Cys	Ser	Pro	Lys
		130				135					140				
Glu	Met	Ile	Ile	Ala	Leu	Asp	Ala	Thr	Leu	Glu	Gly	Asp	Ala	Thr	Ala
145					150					155					160
Leu	Phe	Leu	Lys	Gln	Glu	Phe	Ser	Tyr	Leu	Pro	Ile	Lys	Ile	Ser	Arg
			165					170						175	
Leu	Ala	Leu	Gly	Met	Pro	Val	Gly	Leu	Ser	Phe	Asp	Phe	Val	Asp	Ala
			180				185						190		
Asn	Thr	Leu	Ala	Arg	Ala	Phe	Ser	Gly	Arg	Asn	Cys	Phe			
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 205:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 327 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 207548..208528

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 205:

```

Val Arg Ala Ser Ile Trp Gly Thr Gly Ser Tyr Leu Pro Lys Lys Ile
1          5          10          15
Leu Thr Asn Ala Asp Leu Glu Lys Ile Val Glu Thr Ser Asp Glu Trp
20          25          30
Ile Ser Thr Arg Thr Gly Ile Lys Glu Arg Arg Ile Ala Ser Ala Glu
35          40          45
Glu Phe Ser Ser Phe Met Gly Ala Lys Ala Ala Glu Lys Ala Ile Glu
50          55          60
Ala Ala Lys Ile Ser Lys Ser Gln Val Asp Cys Ile Val Phe Ser Thr
65          70          75          80
Ala Ala Pro Asp Tyr Ile Phe Pro Ser Ser Ala Ala Leu Ala Gln Ala
85          90          95
Tyr Leu Gly Ile Lys Glu Ile Pro Ala Phe Asp Cys Leu Ala Ala Cys
100          105          110
Thr Gly Phe Leu Tyr Gly Leu Ser Ile Ala Lys Ala Tyr Val Glu Ser
115          120          125
Gly Met Tyr Gln Cys Val Leu Val Ile Ala Ala Asp Lys Leu Ser Ser
130          135          140
Phe Val Asn Tyr Gln Asp Arg Asn Thr Cys Val Leu Phe Gly Asp Gly
145          150          155          160
Gly Ser Ala Cys Ile Val Gly His Ser Arg Pro Gly Ala Leu Glu Ile
165          170          175
Ser Lys Val Asn Leu Gly Ala Asp Gly Lys Gln Gly Asp Leu Leu Arg
180          185          190
Leu Pro Ala Gly Gly Ser Arg Cys Pro Ala Ser Gln Asp Thr Val Gln
195          200          205
Asn His Gln His Phe Ile Thr Met Glu Gly Lys Glu Val Phe Lys His
210          215          220
Ala Val Arg Arg Met Glu Phe Ala Ala Lys Thr Cys Ile Thr Glu Ala
225          230          235          240
Gly Leu Gln Glu Lys Asp Ile Asp Trp Leu Val Pro His Gln Ala Asn
245          250          255
Glu Arg Ile Ile Asp Ala Ile Ala Lys Arg Phe Ala Val Lys Asp Ser
260          265          270
Arg Val Phe Lys Thr Leu Ala Lys Tyr Gly Asn Thr Ala Ala Ser Ser
275          280          285
Val Gly Ile Ala Leu Asp Glu Leu Leu Arg Thr His Asp Ile His Val
290          295          300
Ala Glu Arg Leu Leu Leu Val Ala Phe Gly Gly Gly Leu Ser Trp Gly
305          310          315          320
Ala Val Ile Leu Gln Val
325

```

(2) INFORMATIONS POUR LA SEQ ID NO: 206:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 308 acides aminés

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 206:

(2) INFORMATION POUR LA SEQ ID NO: 207:

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 248 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 209471..210214

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 207:

```

Met Xaa Gly Leu Leu Val Asn Lys Thr Ala Ile Val Thr Gly Gly Ser
1      5      10      15
Arg Gly Ile Gly Phe Ser Ile Ala Lys Leu Phe Ala Glu Gln Gly Ala
20      25      30
Asn Val Gln Ile Trp Gly Ile Asn Gly Glu Ala Gly Gln Ala Ala Ala
35      40      45
Gln Thr Leu Ser Glu Gln Thr Gly Arg Gln Val Ser Phe Ala Leu Val
50      55      60
Asp Val Ser Lys Asn Asp Met Val Ser Ala Gln Val Gln Asn Phe Leu
65      70      75      80
Ser Glu Tyr Asn Thr Ile Asp Val Ile Val Asn Asn Ala Gly Ile Thr
85      90      95
Arg Asp Ala Leu Leu Met Arg Met Ser Glu Glu Glu Trp Ser Ser Val
100      105      110
Ile Asn Thr Asn Leu Gly Ser Ile Tyr Asn Val Cys Ser Ala Val Ile
115      120      125
Arg Pro Met Ile Lys Ala Arg Ser Gly Ala Ile Ile Asn Ile Ser Ser
130      135      140
Ile Val Gly Leu Arg Gly Ser Pro Gly Gln Thr Asn Tyr Ala Ala Ala
145      150      155      160
Lys Ala Gly Ile Ile Gly Phe Ser Lys Ala Leu Ser Lys Glu Val Gly
165      170      175
Ser Lys Asn Ile Arg Val Asn Cys Ile Ala Pro Gly Phe Ile Asp Thr
180      185      190
Asp Met Thr Lys Ser Leu Asn Asp Asn Leu Lys Asn Glu Trp Leu Lys
195      200      205
Gly Val Pro Leu Gly Arg Val Gly Met Pro Glu Glu Ile Ala Lys Ala
210      215      220
Ala Leu Phe Leu Xaa Ser Asp Gly Ser Ser Tyr Ile Thr Gly Gln Val
225      230      235      240
Leu Ser Val Asp Gly Gly Met Ala
245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 208:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 77 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 210586..210816

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 208:

```

Met Ser Leu Glu Asp Asp Val Lys Ala Ile Ile Val Asp Gln Leu Gly
1      5      10      15
Val Ser Pro Glu Asp Val Lys Val Asp Ser Ser Phe Ile Glu Asp Leu
20      25      30

```

```

Asn Ala Asp Ser Leu Asp Leu Thr Glu Leu Ile Met Thr Leu Glu Glu
      35              40              45
Lys Phe Ala Phe Glu Ile Ser Glu Asp Asp Ala Glu Gln Leu Arg Thr
      50              55              60
Val Gly Asp Val Ile Lys Tyr Ile Gln Glu His Gln Asn
      65              70              75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 209:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(210883..211332)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 209:

```

Leu Val Pro Ser Phe Lys Ser Leu Val Gly Gly Thr Ser Leu Asn Leu
1              5              10              15
Ile Asp Lys Ala Phe Leu Leu Lys Lys Thr Xaa Leu Phe Ala Ser Leu
      20              25              30
Asp Met Asp Val Leu Leu Ser Ile Ala Asp Lys Ser Glu Val Met Leu
      35              40              45
Phe Lys Ala Gly Ser Glu Ile Phe Ser Glu Gly Gln Pro Ser Phe Ser
      50              55              60
Leu Tyr Val Ile Ala Glu Gly Cys Val Arg Ile Phe Ala Lys Glu Pro
65              70              75              80
Thr Ile Asn Val Arg Leu Lys Pro Leu Asp Cys Phe Gly Glu Glu Ser
      85              90              95
Phe Phe Asn Asn Lys Val Arg Glu Tyr Ser Ala Glu Ala Ile Thr Leu
      100              105              110
Val Lys Thr Leu Ile Leu Asn Lys Gly Gln Phe Leu Ser Ile Ile Glu
      115              120              125
Glu Cys Pro Ser Val Ser Leu Val Leu Leu Glu Phe Tyr Ser Lys Gln
      130              135              140
Ile Val Phe Arg Asp Gln
145              150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 210:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 535 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(211374..212978)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 210:

```

Asn Leu Leu Leu Ser Cys Gly Asp Val His Leu Arg Thr Thr Met Phe

```

1
 Ile His Pro Ala Pro Ile Arg Thr Leu Tyr Tyr His Phe Arg Arg Val
 20 25 30
 Tyr Ser Phe Ser Asn Ile Xaa Arg Thr His Tyr Ser Lys Ala Ile Leu
 35 40 45
 Arg Asn Leu Ser Leu Glu Ser Ile His Arg Arg Arg Ser Ile Arg Glu
 50 55 60
 Trp Phe Ala Asp Met Asn Asp Thr Glu Lys Arg Gln Ala Glu Ile Leu
 65 70 75 80
 Ser Val Thr His Leu Lys Asn Pro Gln Glu Arg Asn Gln Met Phe Ala
 85 90 95
 Phe Gln His Leu Leu Asn Leu Lys Asn Arg Ala Val Leu Pro Asn Leu
 100 105 110
 Leu Leu His Met Asn Lys Leu Gly Leu Ser Gly Lys Leu Lys Thr Leu
 115 120 125
 Asn Met Leu Lys Asn Ser Val Trp Ala Lys Asp Phe Leu Thr Leu Glu
 130 135 140
 Leu Leu Lys Arg Trp Ser Ser Leu Pro Gln His Pro Thr Ile Ala Ala
 145 150 155 160
 Ala Leu His Leu Tyr Phe Val Glu His Asp Phe Leu Tyr Val Ser Asp
 165 170 175
 Ile Ala Asp Asp Leu Tyr Asp Gln Ser Gly Asp Arg Leu Phe Thr Ala
 180 185 190
 Val Leu Ile Val Arg Lys His Lys Pro Gly Gly Glu Tyr Gln Ala Leu
 195 200 205
 Ala Glu Lys His Leu Ser Glu Ile Leu Glu Ser Glu Asp Pro Glu Leu
 210 215 220
 Ile Ile Lys Gly Leu Ser Ile Leu Ala Leu Glu Arg Ser Pro Ser Asn
 225 230 235 240
 Phe Pro Ile Ile Leu Pro Phe Leu Thr His Pro Asn Glu Gln Val Phe
 245 250 255
 Leu Gln Ala Cys Leu Ser Leu Glu Thr Cys Ala Asp Lys Gln Tyr Ala
 260 265 270
 Gln Tyr Gly Arg Thr Val Leu Asn Thr Leu Lys Lys Thr Lys Asp Thr
 275 280 285
 Gln Ala Ala Gln Ala Leu Leu Asn Thr Leu Ala Ala Leu Leu Asp Ala
 290 295 300
 Ser Leu Val Tyr Glu Phe Val Leu Ala Ser Val Gln Leu Lys Ser Val
 305 310 315 320
 Leu Arg Lys Leu Ala Glu Thr Ile Asp Ala Ser Leu Pro Lys Glu Cys
 325 330 335
 Ile Pro Ile Leu Ile Glu Met Val Ala Asp His Ser Leu His Asn Ser
 340 345 350
 Cys Arg Ile Met Ala Ala Lys Ala Leu Ser His Ile Asp Ser Arg Gln
 355 360 365
 Leu Lys Arg Leu Ala Leu Lys Ile Leu Lys Ser Lys Ala Ala Lys Ala
 370 375 380
 Leu Phe Tyr Asp Tyr His Lys Asn Phe Ile Gln Lys Arg Tyr Pro Arg
 385 390 395 400
 Tyr Asp Leu His Leu Leu Ile Glu Ser Leu Glu Ala Asn Tyr Gln Ala
 405 410 415
 Glu Val Asn Phe Met Leu Ala Phe Leu Ala Ile Val Gly Ser Ser Asp
 420 425 430
 Tyr Ala Asp Val Leu Ile Arg Ser Leu Thr Gly Lys Asn Leu Lys Ala
 435 440 445
 Arg Ala Gln Ala Leu Glu Ser Leu Glu Lys Asp Cys Glu Asn His Leu
 450 455 460
 Phe Thr Leu Val Thr Pro Phe Val Tyr Arg Asp Lys His Thr Ser Asp
 465 470 475 480

Glu Lys Tyr Tyr Met Lys Lys Gly Val Glu Pro Leu Ala Ile Glu Glu
 485 490 495
 Leu Leu Asn Arg Leu Glu Gln Thr Pro Phe Leu Phe Ser Lys Leu Ile
 500 505 510
 Ala Gln Gln Leu Lys Glu Gly Ala Phe Ser Leu Arg Cys Arg Val Leu
 515 520 525
 Phe Cys Ser Thr Lys Leu Cys
 530 535

(2) INFORMATIONS POUR LA SEQ ID NO: 211:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 402 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(212875..214080)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 211:

Ser Leu Arg Ala Leu Arg Phe Leu Leu Ser Leu Arg Arg Gly Glu Glu
 1 5 10 15
 Lys Arg Ala Leu Leu Phe Leu Leu Leu Gly Leu Ile Trp Ser Val Ala
 20 25 30
 Cys Tyr Gly Ser Leu Ala Leu Gly Glu Ser Xaa Phe Leu Glu Glu Ile
 35 40 45
 Gly Ala Glu Lys Leu Pro Phe Ala Tyr Leu Gly Ala Ser Phe Phe Leu
 50 55 60
 Cys Phe Ile Ser Cys Leu Ile Leu Tyr Asn Leu Ser Arg Lys Arg Val
 65 70 75 80
 Ser Pro Lys Ala Leu Phe Leu Ser Phe Ile Ser Cys Val Leu Ile Cys
 85 90 95
 Asn Leu Tyr Leu Phe Trp His Leu Ala Ile His Lys Gly Val Ser Gly
 100 105 110
 Thr Pro Thr Phe Leu Tyr Arg Ile Leu Ile Trp Gly Leu Thr Ile Leu
 115 120 125
 Cys Tyr Ala Asn Phe Trp Gly Phe Ile Asp Gln Phe Phe Asn Ile Gln
 130 135 140
 Asp Ala Lys Arg His Phe Cys Ile Phe Asn Ala Ile Thr Phe Cys Gly
 145 150 155 160
 Asp Phe Leu Gly Ala Arg Ile Val Asn Gln Ile Gln Tyr Leu Gly Ala
 165 170 175
 Glu Leu Ile Leu Leu Ala Phe Ile Val Ile Thr Phe Ile Phe Pro
 180 185 190
 Leu Val His Tyr Ile Ser Ser Ser Leu Lys Glu Leu Ser Glu Asp His
 195 200 205
 Asp Leu Phe Leu Asp Thr Gly Tyr Pro Pro Ser Thr Lys Gln Thr Leu
 210 215 220
 Lys Leu Cys Leu Lys Asp Lys Tyr Thr Phe Tyr Leu Val Ser Phe Tyr
 225 230 235 240
 Phe Leu Met Gln Leu Leu Val Val Phe Thr Glu Phe Asn Tyr Leu Lys
 245 250 255
 Ile Phe Asp Ala Gln Phe Gly Asn Ala Glu Thr Cys Glu Leu Thr Glu
 260 265 270
 Asn Phe Thr Lys Tyr Ser Ser Trp Ile Ser Leu Gly Asn Met Phe Phe

275 280 285
 Ala Leu Phe Ala Tyr Ser Arg Val Ile Thr Arg Phe Gly Ile Asn Asn
 290 295 300
 Ile Ile Leu Phe Ala Pro Ile Cys Phe Phe Ser Leu Phe Cys Cys Trp
 305 310 315
 Ser Ile Lys Thr Ser Val Phe Ile Ala Thr Met Gly Met Ile Ala Arg
 325 330 335
 Glu Gly Leu Ala Tyr Ala Leu Asp Asp Asn Asn Leu Gln Leu Leu Ile
 340 345 350
 Tyr Gly Ile Pro Asn Lys Ile Arg Asn Gln Val Arg Ile Ala Ile Glu
 355 360 365
 Ser Phe Val Glu Leu Arg Gly Cys Ser Ser Ala His Tyr Tyr Val Tyr
 370 375 380
 Ser Ser Arg Thr Asn Thr Tyr Ser Val Leu Ser Phe Pro Pro Cys Val
 385 390 395 400
 Phe Phe

(2) INFORMATIONS POUR LA SEQ ID NO: 212:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(214168..214710)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 212:

Gly Asn Val Met Thr Tyr Ser Met Ser Asp Ile Ala His Lys Phe Asp
 1 5 10 15
 Ile Ser Asn Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe
 20 25 30
 Pro Pro Gln Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe
 35 40 45
 Ser Thr Trp Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln
 50 55 60
 Gln Leu Ala Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val
 65 70 75 80
 Ser Ala Leu Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser
 85 90 95
 Leu Gly Leu Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr
 100 105 110
 Ile Leu Ala Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Gly
 115 120 125
 Val Leu Pro Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile
 130 135 140
 Trp Ala Ile Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser
 145 150 155 160
 Ile Ala Cys Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln
 165 170 175
 Thr Leu Tyr Val Ser
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 213:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(214754..215143)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 213:

Phe	Thr	Glu	Gly	Asn	Met	Val	His	Ser	Val	Tyr	Asn	Ser	Leu	Ala	Pro
1				5					10					15	
Glu	Gly	Phe	Ser	Gln	Val	Ser	Ile	Gln	Pro	Ser	Gln	Ile	Pro	Thr	Ser
			20					25					30		
Lys	Lys	Val	Met	Ile	Ala	Ile	Met	Thr	Leu	Phe	Ala	Leu	Thr	Ala	Ile
		35					40					45			
Ala	Ala	Ile	Val	Leu	Ser	Ile	Val	Thr	Val	Cys	Gly	Gly	Phe	Pro	Phe
	50					55				60					
Leu	Leu	Ala	Ala	Leu	Asn	Thr	Val	Thr	Ile	Gly	Ala	Cys	Val	Ser	Leu
65					70					75					80
Pro	Ile	Phe	Thr	Cys	Ile	Ala	Thr	Thr	Leu	Leu	Leu	Leu	Cys	Leu	Arg
				85					90					95	
Asn	Ile	Glu	Leu	Leu	Gly	Gln	Thr	Ala	Ser	Ile	Asp	Pro	Leu	His	Ser
			100					105					110		
Ile	Gln	Pro	Asn	Lys	Thr	Ser	Arg	Asn	Arg	Val	Val	Ala	Gln	Gln	Lys
		115					120					125			
Met	Ser														
															130

(2) INFORMATIONS POUR LA SEQ ID NO: 214:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 490 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(215236..216705)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 214:

Met	Asn	Lys	Lys	Asn	Thr	Val	Phe	Ser	Ser	Arg	Leu	Gly	Phe	Ile	Leu
1				5					10					15	
Ser	Met	Met	Gly	Val	Ala	Ile	Gly	Ala	Gly	Asn	Ile	Trp	Arg	Phe	Pro
			20					25					30		
Arg	Met	Val	Ala	Gln	Asn	Gly	Gly	Gly	Thr	Phe	Ile	Leu	Leu	Trp	Leu
		35					40					45			
Leu	Phe	Leu	Ile	Ile	Trp	Ser	Ile	Pro	Leu	Ile	Ile	Val	Glu	Leu	Ser
	50					55				60					
Ile	Gly	Lys	Leu	Thr	Arg	Lys	Ala	Pro	Ile	Gly	Ala	Leu	Ile	Arg	Thr
65				70						75				80	
Ala	Gly	Pro	Lys	Ser	Ala	Trp	Leu	Gly	Gly	Phe	Ile	Val	Leu	Val	Ala

85 90 95
 Thr Cys Ile Leu Gly Tyr Tyr Ser Asn Ile Val Gly Trp Gly Phe Ser
 100 105 110
 Tyr Phe Phe Tyr Ser Leu Ser Gly Lys Ile Val Pro Gly Asn His Phe
 115 120 125
 Pro Gln Leu Trp Ala His His Cys Gln Ser Trp Met Pro Leu Ser Cys
 130 135 140
 His Cys Leu Ala Leu Phe Leu Ala Tyr Cys Ile Ile Arg Lys Gly Ile
 145 150 155 160
 Val Asn Gly Ile Glu Thr Cys Asn Lys Ile Leu Ile Pro Phe Phe
 165 170 175
 Ile Cys Ala Leu Val Leu Leu Ala Arg Ala Val Ser Leu Pro His Ala
 180 185 190
 Trp Glu Gly Ile Arg Leu Leu Phe Val Phe Asn Lys Ala Ser Leu Cys
 195 200 205
 Asp Tyr Lys Val Trp Ile Glu Ala Leu Thr Gln Asn Ala Trp Asp Thr
 210 215 220
 Gly Ala Gly Trp Gly Leu Leu Leu Val Tyr Ala Gly Phe Ala Ser Lys
 225 230 235 240
 Gln Thr Ser Leu Val Thr Asn Gly Ala Ile Thr Ala Ile Thr Asn Asn
 245 250 255
 Phe Ile Ser Phe Leu Met Ala Val Ile Val Phe Ser Ala Cys Ala Ser
 260 265 270
 Leu Asp Ser Thr Glu Met Leu Gly Leu Arg Glu Gly Val Gly Ala Ser
 275 280 285
 Asn Ile Gly Met Ala Phe Ile Tyr Leu Pro Glu Leu Phe Thr Arg Leu
 290 295 300
 Pro His Ala His Ile Leu Ser Thr Phe Phe Ser Ala Ile Phe Phe Leu
 305 310 315 320
 Ala Phe Ser Met Ala Ala Leu Ser Ser Met Ile Ser Met Leu Phe Leu
 325 330 335
 Leu Ser Gln Thr Leu Thr Glu Phe Gly Ile Lys Lys His Ile Ala Glu
 340 345 350
 Ser Ser Ala Thr Ile Ala Ala Phe Leu Ile Gly Val Pro Ser Ala Leu
 355 360 365
 Asn Leu Gln Phe Phe Asp Asn Gln Asp Ile Val Trp Gly Ile Ala Leu
 370 375 380
 Ile Leu Asn Gly Met Ile Phe Ile Tyr Ser Ala Leu Ser Tyr Gly Ile
 385 390 395 400
 Lys Arg Leu Arg Gln Asp Val Ile Asn Ser Val Pro Gly Asp Tyr Lys
 405 410 415
 Leu Lys Thr Tyr Phe Asp Met Leu Val Lys Phe Leu Leu Pro Leu Glu
 420 425 430
 Gly Val Leu Leu Leu Ala Trp Tyr Phe Tyr Glu Gly Ala Met Leu Pro
 435 440 445
 Gln Ala Tyr Trp Trp Asn Pro Phe Val Ser Tyr Asn Ile Ser Ser Leu
 450 455 460
 Leu Met Gln Trp Gly Leu Gly Gly Gly Val Leu Phe Leu Leu Asn Arg
 465 470 475 480
 Lys Leu Tyr Thr Lys Phe Tyr Leu Asn Asn
 485 490

(2) INFORMATIONS POUR LA SEQ ID NO: 215:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 342 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(216892..217917)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 215:

```

Lys Ser Met Val Ser Val Val Arg Ser Ser Leu Tyr Tyr Thr Leu Leu
1      5      10      15
Thr Thr Leu Ile Ser Ala Ala Ile Ala Leu Val Leu Phe Ile Phe Ile
20      25      30
Lys Pro Ser Val Pro Leu Ser Gly Phe Asn Ala Ala Thr Glu Thr Asn
35      40      45
Ala Thr Gly Tyr Leu Ser Val Leu Ser Lys Thr Ile Pro Gly Asn Ile
50      55      60
Leu Glu Pro Phe Leu Glu Ser Asn Val Ile Ala Ala Ala Phe Leu Ser
65      70      75      80
Ala Leu Leu Ala Thr Phe Ser Leu Ser Leu Pro Glu Asn Glu Arg Leu
85      90      95
Phe Val Arg Asn Ala Phe Asn Thr Leu Phe Ser Leu Leu Leu Ser Ile
100     105     110
Ser Lys Gly Ile Leu Lys Met Leu Pro Leu Ala Thr Phe Ala Phe Ser
115     120     125
Leu Leu Phe Val Arg Glu Met Arg Thr Gly Asn Leu Glu Leu Ser Ser
130     135     140
Phe Gly Glu Tyr Leu Phe Cys Ile Val Thr Ala Asn Cys Leu Gln Gly
145     150     155     160
Phe Leu Val Leu Pro Leu Leu Leu Lys Met Lys Gly Ile Ser Pro Leu
165     170     175
Arg Thr Phe Lys Leu Met Ser Arg Pro Leu Ala Thr Ala Phe Phe Ser
180     185     190
Lys Ser Ser Ala Val Thr Leu Pro Leu Thr Met Glu Val Ala Glu Glu
195     200     205
Asn Leu His Ile Arg Pro Thr Ile Ser Arg Phe Val Phe Pro Leu Cys
210     215     220
Ser Val Ile Asn Met Asn Ala Cys Ala Ala Phe Ile Leu Thr Thr Val
225     230     235     240
Leu Phe Val Gly Val Ser Asn Gly Ile Val Phe Ser Pro Leu Ser Leu
245     250     255
Ile Ser Trp Val Phe Ile Ala Thr Leu Ala Ala Val Gly Asn Ala Gly
260     265     270
Val Pro Met Gly Cys Tyr Phe Leu Thr Ser Ser Leu Leu Ala Ser Met
275     280     285
Asn Val Pro Leu Gly Leu Leu Gly Leu Ile Leu Pro Ala Tyr Ala Leu
290     295     300
Leu Asp Met Leu Glu Thr Leu Ile Asn Val Trp Ser Asp Cys Cys Ile
305     310     315     320
Val Ser Val Ile Asn Lys Lys Phe Ser Glu Thr Glu Asp Leu Pro Pro
325     330     335
Cys Ser Tyr Thr Asn Glu
340

```

(2) INFORMATIONS POUR LA SEQ ID NO: 216:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 216:

(2) INFORMATION POUR LA SEQ ID NO: 217:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 217:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 218:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 218695..219009

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 218:

Arg	Ser	Phe	Glu	Glu	Glu	Tyr	Lys	Ala	Leu	Ser	Glu	Val	Tyr	Arg	Ala	1	5	10	15
Asn	Leu	Glu	Ala	Arg	Arg	Ala	Val	Ser	Lys	Tyr	Cys	Gln	Glu	Leu	Glu	20	25	30	
Glu	Lys	Ile	Leu	Asp	Leu	Cys	Lys	Arg	His	Ala	Ala	Thr	Ile	Cys	Ser	35	40	45	
Ile	Glu	Glu	Asp	Ala	Lys	Gln	Glu	Ile	Arg	His	Gln	Thr	Glu	Arg	Phe	50	55	60	
Lys	Gln	Arg	Leu	Gln	Gln	Asn	Gln	Asn	Thr	Cys	Ser	Gln	Ile	Thr	Ala	65	70	75	80
Glu	Leu	Cys	Lys	Leu	Arg	Ser	Glu	Asn	Lys	Ala	Leu	Ser	Glu	Arg	Leu	85	90	95	
Gln	Val	Gln	Ala	Ser	Arg	Arg	Lys	Lys								100	105		

(2) INFORMATIONS POUR LA SEQ ID NO: 219:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 219179..219748

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 219:

Arg	Arg	Arg	Phe	Phe	Phe	Thr	Val	Ala	Asn	Ser	Phe	Leu	Arg	Arg	Asp	1	5	10	15
Lys	Ile	Tyr	Phe	Val	Phe	Asn	Lys	Arg	Glu	Tyr	Leu	Phe	Gln	Asn	Phe	20	25	30	
Gly	Tyr	Ser	Phe	Ser	Tyr	Arg	Arg	Arg	Phe	Ser	Cys	Cys	Arg	Trp	Gly	35	40	45	
Ile	Ser	Phe	Gly	Phe	Val	Arg	Tyr	Asn	Val	Ile	Phe	Thr	Val	Ile	Gly	50	55	60	
Ile	Pro	Ala	Leu	Ile	Ile	Gly	Ser	Ala	Cys	Val	Gly	Ala	Gly	Ile	Ser	65	70	75	80
Arg	Leu	Met	Tyr	Arg	Ser	Ser	Tyr	Ala	Ser	Leu	Glu	Ala	Lys	Asn	Val	85	90	95	
Leu	Ala	Glu	Gln	Arg	Leu	Arg	Asn	Leu	Ser	Glu	Glu	Lys	Asp	Ala	Leu	100	105	110	
Ala	Ser	Val	Ser	Phe	Ile	Asn	Lys	Met	Phe	Leu	Arg	Gly	Leu	Thr	Asp				

115 120 125
 Asp Leu Gln Ala Leu Glu Ala Lys Val Met Glu Phe Glu Ile Asp Cys
 130 135 140
 Leu Asp Arg Leu Glu Lys Asn Glu Gln Ala Leu Leu Ser Asp Val Arg
 145 150 155
 Leu Val Leu Ser Ser Tyr Thr Arg Trp Leu Asp Ser Ala Glu Lys Glu
 165 170 175
 Lys Ala Ala Leu Lys Ala Ser Ile Asp Ala Asn Gln Ala Ser
 180 185 190

(2) INFORMATIONS POUR LA SEQ ID NO: 220:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 180 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 219891..220430

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 220:

Thr Glu Pro Cys Phe Arg Ile Leu Phe Tyr Thr Leu Val Ser Arg Asp
 1 5 10 15
 Glu Arg Arg Val Lys Val Phe Tyr Val Lys Asn Ile Cys Val Phe Leu
 20 25 30
 Pro Ser Arg Val Leu Ser Arg Pro Phe Phe Gly Pro Glu Ser Thr Met
 35 40 45
 Ser Tyr Leu Phe Cys Ser Ser Cys Ala Pro Thr Leu Glu Ser Pro Ala
 50 55 60
 Glu Leu Cys Leu Tyr Lys Thr His Ile Tyr Cys Lys Arg Arg Gly Asn
 65 70 75 80
 Ile Glu Phe Ala Val Ser Leu Gly Ile Phe Ala Ile Leu Ser Cys Val
 85 90 95
 Ala Leu Leu Cys Leu Leu Cys Arg Gly Ser Ser Leu Val Phe Ala Gly
 100 105 110
 Leu Gly Ile Gly Ala Ile Met Ile Gly Ser Val Ala Leu Gly Val Gly
 115 120 125
 Leu Thr Phe Leu Tyr Trp Ser Cys Ser Arg Gly Leu Gln Asn Arg Ile
 130 135 140
 Arg Thr Asn Ile Leu Ala Ser Ser Asp Ser Ser Ser Leu Ser Ser
 145 150 155 160
 Lys Ser Asp Phe Ser Leu Glu Phe Glu Leu Asn Glu Ala Asp Val Thr
 165 170 175
 Ile Ser Val Ser
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 221:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 192 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 220499..221074

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 221:

Leu	Pro	Leu	Lys	Tyr	Ile	Lys	Ile	Phe	Thr	Leu	Ile	Ser	Phe	Pro	Val
1				5					10					15	
Ala	Cys	Arg	Pro	Phe	Leu	Arg	Asn	Arg	Gly	Ala	Met	Phe	Asn	Ile	Ser
			20					25					30		
Phe	Cys	Cys	Asn	Ser	Ser	Lys	Pro	Leu	Arg	Ala	Asp	His	Thr	Glu	Thr
		35					40					45			
Ile	Gly	Ala	Gln	Thr	Thr	Thr	Ser	Arg	Lys	Glu	Gln	Leu	Leu	Ala	Ile
	50					55					60				
Gly	Ala	Leu	Val	Leu	Gly	Val	Leu	Ala	Val	Leu	Gly	Gly	Ala	Leu	Leu
65					70					75					80
Leu	Leu	Phe	Ser	Gly	Ser	Val	Leu	Ser	Leu	Phe	Ala	Pro	Ile	Leu	Ser
				85					90					95	
Leu	Leu	Ala	Met	Thr	Leu	Gly	Ser	Ala	Cys	Ile	Gly	Gly	Ser	Leu	Val
			100					105					110		
Tyr	Met	Tyr	Gly	Phe	Ser	Leu	Lys	Pro	Thr	Arg	Leu	Pro	Ser	Glu	Ser
		115					120					125			
Ser	Gly	Leu	Ala	Pro	Glu	Ala	Val	Thr	Pro	Gly	Leu	Val	Leu	Ser	Tyr
	130					135					140				
Gln	Glu	Leu	Leu	Tyr	Glu	Ala	Glu	Glu	Asp	Leu	Lys	Glu	Val	Glu	Gly
145					150					155					160
Leu	Leu	Ala	Gln	Lys	Ser	Lys	Asp	Leu	Glu	Leu	Ala	Gln	Lys	Lys	Ile
				165					170					175	
Glu	Gln	Leu	Gln	Ser	Gly	Leu	Lys	Cys	Val	Leu	Glu	Glu	Ser	Leu	Arg
			180					185					190		

(2) INFORMATIONS POUR LA SEQ ID NO: 222:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 135 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 221137..221541

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 222:

Gly	Ile	Val	Val	Gln	Gln	Lys	Leu	Arg	Tyr	Ser	Glu	Asn	Val	Ala	Asn
1				5					10					15	
Asn	Ser	Phe	Ile	His	Arg	Ser	Lys	Arg	Tyr	Gln	Leu	Phe	Val	Val	Val
			20					25					30		
Leu	Thr	Ser	Leu	Leu	Ala	Ala	Leu	Gly	Gly	Val	Phe	Leu	Cys	Leu	Gly
		35					40					45			
Gly	Val	Tyr	Ser	Ser	Leu	Val	Leu	Gly	Val	Val	Gly	Gly	Ala	Ala	Ile
	50					55					60				
Ile	Gly	Ser	Cys	Ile	Gly	Ala	Phe	Gly	Leu	Val	Ser	Tyr	Leu	Leu	Ser
65					70					75					80
Val	Ile	Arg	Asn	Ser	Asp	Gln	Leu	Leu	Gln	Glu	Ala	Lys	Glu	Ser	Asp
				85					90					95	
Arg	Lys	Ile	Ser	Ser	His	Tyr	Arg	Val	Leu	Glu	Thr	Gln	Lys	Asn	Arg

Glu Ile Gly Leu Leu Glu Glu Arg Val Asn Met Leu Asp Gly Phe Tyr
 100 105 110
 115 120 125
 Ala Lys Phe His Gly Trp Asp
 130 135

(2) INFORMATIONS POUR LA SEQ ID NO: 223:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 164 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 221601..222092

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 223:

Arg Lys Ala Ser Leu Leu Ile Thr Asp Leu Phe Tyr Leu Lys Trp Asp
 1 5 10 15
 Ala Met Ser Phe Val Gly Asp Ser Val Pro Leu Arg Ser Tyr Met Pro
 20 25 30
 Glu Ala Pro Leu Val Asp Ser Ala Ser Lys Ala Arg Val Ser Cys Cys
 35 40 45
 Ser Glu Arg Ile Ala Val Leu Ala Leu Gly Ile Leu Ser Ile Leu Phe
 50 55 60
 Ile Val Thr Gly Ala Ala Leu Phe Ile Gly Ala Gly Trp Thr Thr Leu
 65 70 75 80
 Pro Met Ile Asn Val Val Thr Leu Val Val Phe Gly Ser Val Met
 85 90 95
 Leu Gly Ala Val Leu Thr Arg Ile Ser Gly Tyr Gly Gly Glu Pro Lys
 100 105 110
 Lys Val Ser Leu Asp Arg Phe Val Leu Glu Asn Glu Arg Gln Gly Phe
 115 120 125
 Leu Asp Lys Gln Arg Leu Ala Asp Ile Ser Lys Glu Glu Ile Ala Leu
 130 135 140
 Ala Lys Gln Gln Ile Glu Glu Glu Lys Glu Ala Ile Leu His Ser Ile
 145 150 155 160
 Phe Pro Asn Asp

(2) INFORMATIONS POUR LA SEQ ID NO: 224:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 273 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 222472..223290

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 224:


```

Arg Lys Gly Gly Lys Met Val Ser Leu Ala Leu Gly Thr Ser Asn Arg
1      5      10      15
Val Glu Ala Asn Asn Gly Ile Asn Asp Leu Ser Pro Ala Pro Glu Ala
20      25      30
Lys Lys Thr Gly Phe Gly Leu Cys Tyr Lys Ile Ser Ala Val Ala Ala
35      40      45
Leu Val Leu Gly Leu Leu Ala Ala Ala Gly Gly Ala Val Val Leu Ala
50      55      60
Leu Phe Cys Thr Phe Thr Pro Pro Leu Phe Phe Tyr Ala Gly Val Ala
65      70      75      80
Leu Val Ala Leu Gly Ala Val Ile Leu Gly Val Gly Val Ser Asn Thr
85      90      95
Cys Ser Cys Cys Leu Arg Ser Lys Arg Ile Glu Ala Arg Glu Gln Leu
100     105     110
Leu Leu Gln Gln Lys Glu Glu Ile Ser Gln Leu Glu Gln Gln Leu Ala
115     120     125
Lys Ala Leu Gly Glu Leu Asp Thr Lys Cys Ala Ser Leu Leu Glu Arg
130     135     140
Arg Asp Leu Arg Glu Asn Leu Lys Ala Trp Gln Ala Tyr Cys Leu Asn
145     150     155     160
Leu Glu Glu Asp Val Arg Asp Leu Leu Lys Lys Leu Glu Gly Tyr Gln
165     170     175
Glu Arg Leu Lys Val Leu Pro Ala Lys Glu Lys Gln Ile Glu Glu Leu
180     185     190
Lys Ala Met Leu Glu His Tyr Ser Arg Ile Cys Tyr Glu Arg Gly Asp
195     200     205
Leu Ile Arg Met Leu Lys Thr Ala Asn Lys Lys Leu Ser Lys Glu Cys
210     215     220
Glu Lys Leu Leu Leu Asn Tyr Lys Ala His Leu Asp Val Cys Leu Gly
225     230     235     240
Glu Lys Val Leu Ala Lys Ser Val Asn Leu Ile Asp Leu Asp Leu Lys
245     250     255
Ser Asp Ser Ser Asp Gly Asp Asp Tyr Asp Phe Asn Tyr Gly Ser Arg
260     265     270
Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 225:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 223435..223818

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 225:

```

Met Arg Cys Cys Cys Val Arg Thr Asn Cys Glu Glu Val Arg Ser Ser
1      5      10      15
Ser Thr Gly Asp Gln Val Val Ser Ala Val Lys Glu Arg Lys Cys Asp
20      25      30
Ser Ser Leu Arg Arg Lys Ile Ala Ser Val Ala Phe Thr Leu Ile Gly
35      40      45
Ala Leu Leu Leu Gly Ile Gly Met Val Leu Ser Phe Ala Leu Leu Gly

```

50 55 60
 Ser Ser Ala Gly Leu Ile Gly Val Gly Val Leu Ser Ala Leu Gly Ala
 65 70 75 80
 Val Cys Leu Ser Leu Gly Leu Tyr Lys Leu Phe Leu Arg Met Lys Arg
 85 90 95
 Val Ser Leu Asp Lys Ala Glu Gln Lys Met Leu Glu Asp Gln Val Glu
 100 105 110
 Leu Leu Arg Gln Glu Asn Gln Glu Leu Lys Ala Ile Ser Val Phe His
 115 120 125

(2) INFORMATIONS POUR LA SEQ ID NO: 226:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 224278..225171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 226:

Met Ala His Thr Ile Arg Phe Thr Lys Phe Ser Phe Pro Leu Tyr Phe
 1 5 10 15
 Ser Lys Thr Leu Ser Trp Phe Ile Ile Gly Gly Phe Leu Ala Ala Cys
 20 25 30
 Val Val His Met Ile Leu Ala Pro Asn Asp Leu Ile Asp Gly Gly Ile
 35 40 45
 Val Gly Leu Ser Met Ile Ala Ala His Ser Phe Gly His Gln Phe Leu
 50 55 60
 Pro Val Phe Leu Val Leu Phe Asn Leu Pro Phe Ile Ile Leu Ala Tyr
 65 70 75 80
 Lys Arg Ile Gly Lys Tyr Phe Val Val Gln Met Ile Thr Ala Val Ile
 85 90 95
 Ile Phe Ser Cys Trp Leu Trp Leu Ile Glu Val Leu Pro Glu Trp Leu
 100 105 110
 Gly Ile Gln Pro Phe Ile Phe Asp Gly Ser Glu Ile Glu Thr Ile Val
 115 120 125
 Leu Gly Gly Val Val Leu Gly Ala Gly Gly Gly Leu Ile Ile Arg His
 130 135 140
 Gly Gly Ala Thr Asp Gly Thr Glu Ile Leu Gly Ile Ile Val Asn Lys
 145 150 155 160
 Lys Arg Gly Tyr Thr Val Gly Gln Val Ile Leu Phe Val Asn Phe Phe
 165 170 175
 Ile Phe Ser Leu Gly Gly Ile Val Tyr Arg Asn Trp His Thr Ala Phe
 180 185 190
 Met Ser Leu Leu Thr Tyr Ala Val Ala Ile Lys Val Met Asp Met Val
 195 200 205
 Ile Leu Gly Phe Glu Asp Thr Lys Ser Val Thr Ile Ile Thr Ser Ser
 210 215 220
 Pro Arg Lys Leu Gly Asn Ile Leu Met Glu Thr Leu Gly Val Gly Leu
 225 230 235 240
 Thr Tyr Leu His Ala Glu Gly Gly Phe Ser Gly Glu Pro Arg Asn Leu
 245 250 255
 Leu Tyr Ile Val Val Glu Arg Leu Gln Leu Ser Gln Leu Lys Glu Ile
 260 265 270

Val His Arg Glu Asp Pro Ser Ala Phe Ile Ala Ile Glu Asn Leu His
 275 280 285
 Glu Val Ile Asn Glu Lys Arg Thr Ser His
 290 295

(2) INFORMATIONS POUR LA SEQ ID NO: 227:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 185 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(225174..225728)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 227:

Ile	Ser	Gly	Ala	Ser	Gly	Ile	Xaa	Leu	Ala	Val	Thr	Leu	Val	Ser	Glu	1	5	10	15
Leu	Ala	Arg	Leu	Gly	His	His	Ile	Asp	Val	Ile	Ile	Ser	Pro	Ser	Ala	20	25	30	
Gln	Lys	Thr	Leu	Tyr	Tyr	Glu	Leu	Asp	Thr	Lys	Ser	Phe	Leu	Ser	Thr	35	40	45	
Ile	Pro	Gln	Asn	Phe	His	Asn	Gln	Ile	Val	Leu	His	His	Ile	Ser	Ser	50	55	60	
Ile	Glu	Ser	Ser	Val	Ser	Ser	Gly	Ser	Asn	Thr	Val	Asp	Ala	Thr	Ile	65	70	75	80
Ile	Val	Pro	Cys	Ser	Val	Ala	Thr	Val	Ala	Ala	Ile	Ser	Cys	Gly	Leu	85	90	95	
Ala	Asp	Asn	Leu	Leu	Arg	Arg	Val	Ala	Asp	Val	Ala	Leu	Lys	Glu	Lys	100	105	110	
Arg	Pro	Leu	Ile	Leu	Val	Pro	Arg	Glu	Ala	Pro	Leu	Ser	Ala	Ile	His	115	120	125	
Leu	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Gln	Asn	Gly	Ala	Val	Ile	Leu	Pro	130	135	140	
Pro	Met	Pro	Ile	Trp	Tyr	Phe	Lys	Pro	Gln	Thr	Ala	Glu	Asp	Ile	Ser	145	150	155	160
Asn	Asp	Ile	Val	Gly	Lys	Ile	Leu	Ala	Ile	Leu	Gln	Leu	Asp	Ser	Pro	165	170	175	
Leu	Ile	Lys	Arg	Trp	Glu	Asn	Pro	Arg								180	185		

(2) INFORMATIONS POUR LA SEQ ID NO: 228:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 72 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 225334..225549

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 228:

Lys Phe Ser Lys Cys Ile Ala Asp Arg Gly Ala Ser Arg Gly Thr Arg
 1 5 10 15
 Ile Arg Gly Leu Phe Ser Phe Arg Ala Thr Ser Ala Thr Leu Leu Lys
 20 25 30
 Arg Leu Ser Ala Lys Pro His Glu Ile Ala Ala Thr Val Ala Thr Leu
 35 40 45
 Gln Gly Thr Ile Ile Val Ala Ser Thr Val Phe Glu Pro Asp Asp Thr
 50 55 60
 Glu Leu Ser Ile Glu Asp Ile Trp
 65 70

(2) INFORMATIONS POUR LA SEQ ID NO: 229:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 288 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(225749..226612)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 229:

Tyr Ala Leu Phe Ala Ala Leu Phe Leu Ala Ser Ser Thr Leu Phe Cys
 1 5 10 15
 Phe Ser Leu Pro Cys Thr Pro Phe Ser Leu Phe Ser Leu Gly Ser Ile
 20 25 30
 Lys Thr Ile Ser Leu Gly Gly Ser Ala Phe Phe Ile Ala Arg Ala Leu
 35 40 45
 Gly Met Ile Val Asn Gln Val Val Asp Cys Ala Ile Asp Lys Arg Asn
 50 55 60
 Pro Arg Thr Gln Ser Arg Val Leu Pro Ala Glu Leu Leu Ser Ile Lys
 65 70 75 80
 His Ser Met Leu Leu Leu Thr Leu Cys Leu Ile Leu Phe Leu Ser Thr
 85 90 95
 Cys Trp Leu Phe Asn Pro Leu Cys Phe Ser Leu Ala Val Leu Ser Thr
 100 105 110
 Leu Ile Met Ile Ile Tyr Pro Tyr Thr Lys Arg Phe Thr Phe Leu Cys
 115 120 125
 His Trp Ile Leu Gly Leu Val Tyr Tyr Leu Ala Ile Leu Met Asn Phe
 130 135 140
 Phe Ala Ile Ile Glu Thr Pro Ser Phe Ser Leu Phe Cys Met Ser Ser
 145 150 155 160
 Leu Leu Gly Ile Ser Phe Gly Met Ile Ile Ala Ala Asn Asp Ile Ile
 165 170 175
 Tyr Ala Leu Gln Asp Val Glu Phe Asp Gln Lys Glu Gly Leu Phe Ser
 180 185 190
 Ile Pro Ala Arg Phe Gly Thr Lys Gln Ala Ile Thr Ile Ala Ser Ala
 195 200 205
 Asn Leu Ile Xaa Ser Ala Ile Ala Tyr Leu Leu Ile Gly Tyr Phe Val
 210 215 220
 Pro Asn Lys Thr Ile Phe Tyr Leu Cys Ser Leu Val Pro Leu Thr Gly
 225 230 235 240
 Ile Leu Arg Thr Ile Lys His Tyr Ser Leu Ile Asp Pro Arg Ala Lys
 245 250 255

Ser Thr Leu Gln Gln Asn Phe Phe Leu Gly Asn Leu Ser Leu Gly Ile
 260 265 270
 Ala Phe Phe Ala Asn Met Ile Gly Leu Phe Leu Leu Arg Gly Ile Leu
 275 280 285

(2) INFORMATION POUR LA SEQ ID NO: 230:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(226769..227299)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 230:

Trp Glu Lys Phe Arg Thr Leu Pro Leu Leu Leu Cys His Cys Arg Ser
 1 5 10 15
 Tyr Lys Arg Ser Glu Ser Pro Trp Asn Ser Cys Asp Ser Leu Ser Gln
 20 25 30
 Ser Glu Asn Ile Ala Phe Phe Gln Glu Ala His Met Ala Ser Leu Ile
 35 40 45
 Arg Ser Leu Cys Glu Phe Thr Val Ala Tyr Lys His Thr Asp Pro Leu
 50 55 60
 Gly Leu Asn Val Asn Phe Pro Ala Ser Ala Asp Asp Ser Pro Trp Lys
 65 70 75 80
 Gly Ile Arg Phe Thr Leu Ser Gly Asn Glu Phe Leu Phe Gly Ile Pro
 85 90 95
 Arg Leu Val Arg Thr Glu Gly Asn Arg Arg Tyr Tyr Thr Leu Tyr Asp
 100 105 110
 Met Arg Asp Lys Val Ser Glu Glu Phe Ser Glu Glu Tyr Leu Ala Leu
 115 120 125
 Ala Asn Asn Tyr Ile Ser Ala Ala Pro Leu Val Ser Lys Asn Thr Pro
 130 135 140
 Arg Ala Thr Leu Ser Glu Glu Glu Leu Ala Phe Leu Lys Asp Ser Phe
 145 150 155 160
 Glu Gln Ser Val Leu Trp Lys Ala Ser Leu Asn Leu Glu Glu Asp Leu
 165 170 175
 Ala

(2) INFORMATION POUR LA SEQ ID NO: 231:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 152 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(227161..227616)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 231:

Met Thr Glu Thr Arg Arg Leu Arg Ile Leu Ile Thr Asn Asp Asp Gly
 1 5 10 15
 Ile Lys Ala Lys Gly Ile Ser Leu Leu Ile Ser Leu Leu Arg Glu Ala
 20 25 30
 Asp Phe Ala Asp Leu Tyr Val Val Ala Pro Leu Glu Glu Gln Ser Gly
 35 40 45
 Arg Ser Met Ala Phe Ser Leu Val Glu Pro Thr Ala Leu Glu Pro Phe
 50 55 60
 Asp Tyr Pro Gln Arg Val Gln Glu Ala Trp Ala Val Thr Gly Thr Pro
 65 70 75 80
 Val Asp Cys Val Lys Leu Ala Ile Gly Glu Leu Phe Lys Glu Asn Ala
 85 90 95
 Leu Asp Leu Ile Leu Ser Gly Ile Asn Asn Gly Lys Asn Ser Gly Arg
 100 105 110
 Cys Leu Tyr Tyr Ser Ala Thr Val Gly Ala Ile Arg Glu Ala Asn Leu
 115 120 125
 His Gly Ile Pro Ala Ile Val Phe Leu Lys Val Arg Ile Ser Leu Phe
 130 135 140
 Ser Lys Lys Leu Ile Trp Pro Pro
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 232:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 236 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(227750..228457)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 232:

Lys Phe Ser Ala Gln Ser Val Tyr Thr His Ala Met Leu Gln Lys His
 1 5 10 15
 Thr Arg Ile Ala Val Ala Leu Ser Gly Gly Lys Asp Ser Leu Ser Leu
 20 25 30
 Leu Leu Met Leu Lys Ala Ile Ser Gly Arg Gly Phe Pro Glu Leu Thr
 35 40 45
 Ile His Ala Ile His Ile Gly Gly Lys Tyr Ser Cys Gly Ala Ala Val
 50 55 60
 Ser Gly Asn Tyr Leu Ser Ser Ile Cys Asp Lys Ile Gln Val Pro Leu
 65 70 75 80
 Ile Ser Ile Pro Ser Pro Tyr Glu Thr Glu Asn Pro Glu Cys Tyr Thr
 85 90 95
 Cys Ser Arg Ile Arg Arg Arg Leu Leu Phe Asp Thr Ala Lys Ala Val
 100 105 110
 Gly Ala Thr Ala Val Ala Phe Gly His His Arg Asp Asp Val Val Gln
 115 120 125
 Thr Thr Leu Met Asn Leu Leu His Lys Ala Glu Phe Ala Gly Met Leu
 130 135 140
 Pro Val Val Asp Met Val Asn Phe Gly Ile Thr Ile Leu Arg Pro Leu
 145 150 155 160
 Ile Phe Ile Pro Glu Asp Leu Ile Arg Lys Phe Ala Lys Glu Ser Gly
 165 170 175

Phe	Ala	Arg	Ile	Thr	Cys	Arg	Cys	Pro	Val	Ile	Ser	Leu	Arg	Thr	Lys
			180					185					190		
Thr	Glu	Glu	Ala	Leu	Lys	Thr	Leu	Glu	Thr	Ile	Phe	Pro	Gln	Ala	Arg
		195					200					205			
His	Asn	Ile	Ala	Leu	Ala	Val	Arg	Glu	Thr	Gly	Leu	Ser	Lys	Ala	Asn
	210					215					220				
Arg	Val	Glu	Gln	Tyr	Asp	Ser	Leu	Leu	Thr	Glu	Thr				
225					230					235					

(2) INFORMATIONS POUR LA SEQ ID NO: 233:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 465 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(228607..230001)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 233:

Ala	Ser	Ser	Gln	Ile	Phe	Tyr	Pro	Ile	Gly	Tyr	Phe	Tyr	Cys	Arg	Asp
1			5					10					15		
Val	Ile	Pro	Cys	Ser	Ser	Tyr	Gln	Phe	Thr	Lys	Pro	Ser	Phe	Asn	Ser
			20					25					30		
Lys	Thr	Trp	Leu	Ile	Tyr	Ser	Ile	Leu	Leu	Ser	Val	Ala	Val	Ala	Cys
		35					40					45			
Phe	Met	Ile	Pro	Tyr	Ala	Leu	Ile	Ala	Ala	Glu	Leu	Ala	Ser	Phe	Lys
	50					55				60					
Pro	Gln	Gly	Ile	Tyr	Val	Trp	Thr	Arg	Asp	Ala	Leu	Gly	Lys	Arg	Trp
65					70				75					80	
Gly	Phe	Phe	Ala	Ile	Trp	Met	Gln	Trp	Phe	His	Asn	Met	Thr	Trp	Tyr
			85					90					95		
Pro	Ala	Met	Leu	Ala	Phe	Ile	Ala	Ser	Thr	Leu	Val	Tyr	Gln	Ile	Ser
			100					105					110		
Pro	Asp	Leu	Ala	Asn	Asn	Arg	Leu	Tyr	Leu	Ser	Ser	Val	Ile	Leu	Leu
		115					120					125			
Gly	Phe	Trp	Gly	Leu	Thr	Phe	Phe	Asn	Phe	Leu	Gly	Ile	Gly	Thr	Ser
	130					135				140					
Ala	Leu	Phe	Ser	Ser	Ile	Cys	Val	Ile	Val	Gly	Thr	Leu	Ile	Pro	Gly
145					150					155				160	
Ala	Ile	Leu	Val	Ala	Phe	Ala	Ala	Tyr	Trp	Ile	Gln	Gly	Gly	Asn	Pro
			165						170					175	
Ile	Ala	Ile	Asn	Phe	Ser	Trp	Ser	Glu	Leu	Leu	Pro	Asp	Phe	Ser	Ser
			180					185					190		
Pro	Ser	Ser	Phe	Val	Leu	Leu	Ser	Gly	Met	Leu	Leu	Ala	Leu	Cys	Gly
		195					200					205			
Leu	Glu	Ala	Asn	Ala	Asn	Leu	Ala	Ser	Asp	Met	Glu	Asp	Pro	Lys	Arg
	210					215					220				
Asn	Tyr	Pro	Lys	Ala	Val	Phe	Ile	Gly	Ala	Val	Ser	Thr	Leu	Ala	Ile
225					230					235					240
Leu	Val	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ile	Val	Ile	Pro	Lys	Glu	Glu
			245						250					255	
Ile	Ser	Leu	Val	Ser	Gly	Leu	Ile	Arg	Ala	Phe	Ser	Leu	Phe	Phe	Glu
			260					265					270		
Lys	Tyr	Asn	Leu	Ser	Trp	Met	Thr	Gly	Ile	Ile	Val	Ala	Met	Thr	Ile

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                275                280                285
Ala Gly Ser Leu Gly Glu Leu Asn Ala Trp Met Phe Ala Gly Thr Lys
    290                295                300
Gly Leu Phe Ile Ser Thr Gln Asn Asp Cys Leu Pro Lys Ile Phe Lys
305                310                315
Lys Thr Asn Ser Arg Asp Val Pro Thr Asn Leu Met Leu Phe Gln Ala
    325                330                335
Ile Val Val Thr Leu Phe Thr Phe Ile Phe Val Tyr Val Asp Ser Ala
    340                345                350
Asp Leu Ala Tyr Trp Ile Leu Ser Ala Leu Ser Leu Gln Met Tyr Leu
    355                360                365
Val Met Tyr Ile Cys Leu Phe Ile Val Gly Pro Val Leu Arg Ile Lys
    370                375                380
Glu Pro Lys Ala Gln Arg Leu Tyr Ser Val Pro Gly Lys Leu Val Gly
385                390                395
Met Cys Val Leu Ser Thr Leu Gly Ile Leu Ser Cys Leu Phe Ala Leu
    405                410                415
Gly Ile Ser Phe Leu Pro Pro Gln Glu Val Val Ser Phe Ser Thr Met
    420                425                430
Gly Gly Asn Phe Gly Tyr Thr Ala Leu Leu Leu Leu Ala Phe Val Ile
    435                440                445
Asn Cys Cys Ile Pro Phe Gly Met Tyr Tyr Ser His Lys Lys Leu Ile
    450                455                460
Lys
465

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(2) INFORMATIONS POUR LA SEQ ID NO: 234:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 308 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(230151..231074)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 234:

```

Glu His Leu Arg Met Thr Thr Ile Phe Asp Leu Leu Gly Lys Asp Ala
1          5          10          15
Asp Tyr Leu Leu Asn His Lys Cys Val Ile Lys Lys Glu Ala Leu Thr
    20          25          30
Leu Pro Ser Gly Asp Phe Val Ser Arg Val Phe Ala Glu Ser Asp Arg
    35          40          45
Asn Asn Arg Val Leu Arg Ser Leu Gln Gln Met Phe Ser Tyr Gly Arg
    50          55          60
Leu Gly Gly Thr Gly Tyr Leu Ser Ile Leu Pro Val Asp Gln Gly Val
65          70          75          80
Glu His Thr Ala Gly Ala Ser Phe Ala Lys Asn Pro Met Tyr Phe Asp
    85          90          95
Pro Glu Asn Ile Val Arg Leu Ala Met Glu Ala Gly Cys Ser Ala Val
    100         105         110
Ala Ser Ser Tyr Gly Val Leu Ser Ile Leu Ala Arg Arg Tyr Ala His
    115         120         125
Lys Ile Pro Phe Leu Leu Lys Leu Asn His Asn Glu Leu Leu Ser Tyr
    130         135         140

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Pro Thr Thr Tyr His Gln Ile Phe Phe Ser Gln Val Glu Asp Ala Tyr
145                      150                      155                      160
Asn Met Gly Ala Val Ala Val Gly Ala Thr Ile Tyr Phe Gly Ser Glu
                      165                      170                      175
Ser Ser Ser Glu Glu Ile Val Ala Val Ala Glu Ala Phe Ala Arg Ala
                      180                      185                      190
Arg Glu Leu Gly Leu Ala Thr Val Leu Trp Cys Tyr Leu Arg Asn Pro
                      195                      200                      205
His Phe Val Val Asn Asn Val Asp Tyr His Thr Ala Ala Asp Leu Thr
                      210                      215                      220
Gly Gln Ala Asp His Leu Gly Ala Thr Leu Gly Ala Asp Ile Val Lys
225                      230                      235                      240
Gln Lys Leu Pro Thr Leu Gln Gly Gly Phe Lys Thr Ile Asn Phe Ser
                      245                      250                      255
Lys Thr Asp Asp Leu Val Tyr Ser Glu Leu Ser Ser Asn His Pro Ile
                      260                      265                      270
Asp Leu Cys Arg Tyr Gln Val Leu Asn Ser Tyr Cys Gly Lys Val Gly
                      275                      280                      285
Leu Ile Asn Ser Gly Ala Leu Leu Gly Lys Met Thr Leu Leu Lys Gln
                      290                      295                      300
Leu Lys Gln Gln
305

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(2) INFORMATIONS POUR LA SEQ ID NO: 235:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 553 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 231348..233006

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 235:

```

Lys Glu Lys Ile Val Phe Met Arg Thr Asp Ser Pro Leu Asn Pro Pro
1                      5                      10                      15
Asp Ser Thr Arg Gly Val Phe Gln Phe Leu Glu Thr Gln Cys Asp Arg
                      20                      25                      30
Ala Met Ala Arg Ser Arg Gln Ser Gln Phe Ile Gly Leu Val Ser Ala
                      35                      40                      45
Val Ala Ala Ala Ala Leu Leu Leu Leu Leu Val Val Ala Leu Ser Val
                      50                      55                      60
Pro Gly Phe Pro Val Ala Ala Ser Ile Val Val Gly Val Leu Phe Ala
65                      70                      75                      80
Leu Ser Ile Val Ala Leu Thr Ala Ser Phe Leu Val Tyr Ile Ala Asn
                      85                      90                      95
Ala Lys Leu Val Ala Ile Arg Ile Lys Phe Leu Ser Ser Gly Leu Gln
                      100                     105                     110
Asp His Phe Ser Glu Ser Pro Ile Leu Gly Thr Leu Arg Lys Gly Arg
                      115                     120                     125
Gly Ala Ser Ile Pro Leu Ile Ser Gly Gln Ala Asp Asp Ser Leu Pro
                      130                     135                     140
Asn Arg Ile Gly Ile Lys Lys Ser Ala Glu Met Arg Val Leu Gln Lys
145                      150                      155                      160
Gly Ile Gly Thr Asp Tyr Lys Lys Tyr Lys Gln His Leu Asp Arg Val

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                                165                                170                                175
Asn Asn Asp Phe Thr Phe Val Cys Glu Gly Ile Ser Ala Leu Ile Pro
                                180                                185                                190
Thr Glu Lys Asp Ala Pro Phe Pro Ile Glu Pro Ser His Leu Ala Gly
                                195                                200                                205
Val Phe Leu Val Ser Phe Ser Pro Asp Lys Asn Pro Ile Leu Lys Ile
                                210                                215                                220
Thr Arg His Ala Glu Lys Met Leu Gln Pro Pro Gln Gly Gly Phe Pro
225                                230                                235                                240
Asn Gly Leu Val Trp Leu Cys Gly Ala Leu Ser Asp Pro Lys Lys Phe
                                245                                250                                255
Ala Ala Pro Phe Leu Ser Leu Ile Glu Lys Thr His Gln Gly Ile Leu
                                260                                265                                270
Val Ser Lys Asp Leu Lys Asp Asn Lys Glu Arg Lys Leu Ala Leu Glu
                                275                                280                                285
Ala Ser Leu Leu Ser Leu Asn Ile Phe Phe Ser Gly Trp Cys Leu Gly
                                290                                295                                300
Asn Pro Glu Tyr Asn Gln Tyr Ile Thr Thr Ala Val Ala Glu Lys Tyr
305                                310                                315                                320
Lys Asp Val Ser Val Arg Asn Arg Ile Tyr Asp Phe Leu Asp Thr Gly
                                325                                330                                335
Asn Val Ile Ser Ala Leu Ala Leu Ala Ser Xaa Tyr Ser Gln Asp Ser
                                340                                345                                350
Ala Trp Ala Ala Gly Leu Gln Lys Val Leu Arg Glu Glu Asp Lys Lys
                                355                                360                                365
Thr Lys Lys Lys Ser Arg Glu Glu Val Ser Cys Leu Tyr Arg Asp Ile
                                370                                375                                380
Asp Pro Gly Cys Cys Leu Arg Ala Leu Pro Lys Arg Phe Glu Ser Lys
385                                390                                395                                400
Ser Ser Gly Ser Gln Gly Ser Pro Lys Glu Gln Leu Ser Ser Leu Leu
                                405                                410                                415
Lys Ala Leu Asp Gln Lys Ile Pro Ser Gly Val Leu Gly Leu Ile Ala
                                420                                425                                430
Lys Ala Ser Ser Ala Asp Leu Lys Ala Asp Phe Ala Gly Met Leu Glu
                                435                                440                                445
Val Ile Lys Gln Leu Gln Ala Leu Phe Asp Ser Tyr Pro Pro Leu Cys
                                450                                455                                460
Glu Asp Asn Ile Leu Leu Trp Leu Ser Ala Ser Leu Glu Gln Val Gly
465                                470                                475                                480
Leu Gln Lys Lys Leu Arg Thr Phe Leu Pro Ser Ser Glu Lys Lys Leu
                                485                                490                                495
Leu Glu Arg Val Leu Ser Thr Phe Leu Leu Gly Leu Tyr Thr Arg Gly
                                500                                505                                510
Val Phe Ser Val Gly Gln Val Asn Gln Leu Ala Thr Ile Cys Asn Thr
                                515                                520                                525
Gln Asp Ser Thr Glu Phe Cys Gln Arg Val Ser Asp Leu Ser Leu Ile
                                530                                535                                540
Lys Arg Ala Leu Pro Ala Leu Phe Gly
545                                550

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(2) INFORMATIONS POUR LA SEQ ID NO: 236:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 232 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 233134..233829

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 236:

Ser	Asp	Lys	Phe	Phe	Pro	Ile	Lys	Gln	Lys	Leu	Ala	Leu	Glu	Ala	Val
1				5				10					15		
Ala	Leu	Val	Glu	Pro	Gly	Met	Cys	Val	Gly	Leu	Gly	Ser	Gly	Ser	Thr
			20				25					30			
Ala	Arg	Glu	Phe	Ile	Leu	Ala	Leu	Gly	Asp	Arg	Val	Arg	Thr	Glu	Arg
		35				40				45					
Leu	Val	Ile	Thr	Ala	Val	Ala	Ser	Ser	Arg	Ile	Ser	Gln	Leu	Leu	Ala
	50					55				60					
Glu	Ala	Val	Gly	Ile	Pro	Leu	Leu	Asp	His	Ser	Leu	Leu	Gln	Asp	Val
65				70				75					80		
Asp	Leu	Val	Val	Asp	Gly	Ala	Asp	Glu	Val	Asp	Pro	Cys	Leu	Arg	Met
			85					90					95		
Ile	Lys	Gly	Gly	Gly	Gly	Ala	Leu	Phe	Arg	Glu	Lys	Ile	Leu	Leu	Gln
		100					105					110			
Ser	Gly	Lys	Arg	Asn	Val	Ile	Leu	Val	Asp	Glu	Arg	Lys	Leu	Val	Pro
	115					120				125					
Thr	Leu	Gly	Lys	Phe	Ser	Leu	Pro	Ile	Glu	Ile	Ala	Pro	Phe	Gly	Cys
	130					135				140					
Ser	Ser	Val	Gln	Arg	Ile	Leu	Asn	Lys	Gln	Gly	Tyr	Phe	Gly	Glu	Trp
145				150				155						160	
Arg	Glu	Thr	Ser	Ala	Gly	Glu	Arg	Phe	Ile	Thr	Asp	Asn	Gly	Asn	Tyr
			165					170					175		
Ile	Tyr	Asp	Val	Arg	Thr	Pro	Asp	Ser	Tyr	Ala	Asn	Pro	Glu	Glu	Asp
	180						185					190			
Met	Ile	Arg	Leu	Leu	Gln	Ile	Arg	Gly	Ile	Ile	Asp	Val	Gly	Phe	Val
	195					200					205				
Ile	Ala	Lys	Ala	Glu	Val	Trp	Val	Gly	Tyr	Ala	Asp	Gly	Ser	Ile	Val
	210				215					220					
Arg	Lys	Lys	Glu	His	Asn	Glu	Tyr								
225				230											

(2) INFORMATIONS POUR LA SEQ ID NO: 237:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 233855..234265

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 237:

Ser	Leu	Ile	Leu	Ile	Asn	Phe	Tyr	Lys	Leu	Val	Ser	Phe	Arg	Asn	Tyr
1				5				10					15		
Ala	Gly	Ile	Ile	Leu	Gly	Thr	Asp	Glu	Lys	Gln	Phe	Ala	Ile	Tyr	Gly
		20					25					30			
His	Ala	Ser	Met	Asp	Thr	Ala	Phe	Lys	Lys	Arg	Glu	Asp	Leu	Ala	Ala
	35					40				45					
Glu	Glu	Glu	Arg	Ser	Arg	Pro	Ser	Thr	His	Asp	Val	Leu	Asn	Phe	Val

```

      50              55              60
Leu Thr Ser Phe Asp Leu Ser Val Val Arg Val Val Ile Thr Glu Tyr
65              70              75              80
Lys Asp Asn Val Phe Tyr Ser Arg Leu Phe Leu Glu Gln Lys Arg Gly
      85              90              95
Asp Arg Leu Tyr Ile Ala Asp Ile Asp Ala Arg Pro Ser Asp Ser Ile
      100              105              110
Pro Leu Ala Ile Lys Tyr Gln Val Pro Ile Leu Cys Val Lys Ser Ile
      115              120              125
Phe Asp Glu Ala Ile Pro Tyr Glu Asp
      130              135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 238:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 191 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 234282..234854

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 238:

```

Asp Val Met Thr Lys Leu Pro Tyr Ala Leu Leu Asp Lys Gly Ser Leu
1              5              10              15
Leu Val Ala Ser Pro Asp Val Asn Gly Gly Ile Phe Ser Arg Ser Val
      20              25              30
Val Leu Leu Cys Glu His Ser Pro Asn Gly Ser Phe Gly Leu Ile Leu
      35              40              45
Asn Lys Ile Leu Glu Ile Asp Ser Pro Glu Glu Ile Phe Pro Leu Asp
      50              55              60
His Phe Asp Glu Ser Lys Val Arg Phe Cys Met Gly Gly Pro Leu Gln
65              70              75              80
Ala Asn Gln Ile Met Leu Leu His Thr Ser Pro Asp Ser Ala Asn Ser
      85              90              95
Ser Ile Glu Ile Cys Pro Ser Val Phe Leu Gly Gly Asp Phe Ser Phe
      100              105              110
Ala Gly Glu Lys Glu Gly Arg Thr Arg Asp Asp Lys Met Leu Leu Cys
      115              120              125
Phe Gly Tyr Ser Gly Trp Gln Gly Gly Gln Leu Glu Lys Glu Phe Leu
      130              135              140
Glu Gly Leu Trp Phe Leu Ala Pro Ser Ser Gln Glu Ile Ile Phe Thr
145              150              155              160
Asp Ala Pro Glu Arg Met Trp Ser Asp Val Leu Gln His Leu Gly Gly
      165              170              175
Arg Phe Ala Ser Leu Ser Thr Ile Pro Glu Asn Leu Leu Leu Asn
      180              185              190

```

(2) INFORMATIONS POUR LA SEQ ID NO: 239:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 297 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(235227..236117)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 239:

Met	Ser	His	Leu	Phe	Ser	Lys	Ala	Cys	Gln	Tyr	Phe	Pro	Gly	Gly	Val	1	5	10	15
Asn	Ser	Pro	Val	Arg	Ala	Cys	Arg	Ala	Val	Asn	Ile	Thr	Pro	Pro	Ile	20	25	30	
Val	Ala	Arg	Ala	Ser	Lys	Glu	Val	Phe	Ile	Asp	Ser	Leu	Asp	Lys	Thr	35	40	45	
Phe	Ile	Asp	Phe	Cys	Gly	Ser	Trp	Gly	Ser	Leu	Ile	His	Gly	His	Ser	50	55	60	
His	Pro	Lys	Ile	Cys	Ala	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Gly	Ser		65	70	75	80
Ser	Tyr	Gly	Leu	Thr	Ser	Glu	Gln	Glu	Ile	Leu	Phe	Ala	Glu	Glu	Ile	85	90	95	
Phe	Ser	Tyr	Leu	Gly	Leu	Glu	Thr	Asn	Tyr	Lys	Ile	Arg	Phe	Met	Ser	100	105	110	
Thr	Gly	Ser	Glu	Ala	Thr	Met	Thr	Ala	Val	Arg	Leu	Ala	Arg	Gly	Ile	115	120	125	
Thr	Gly	Arg	Pro	Ile	Ile	Ile	Lys	Phe	Leu	Gly	Cys	Tyr	His	Gly	His	130	135	140	
Ala	Asp	Thr	Phe	Leu	Gln	Glu	Lys	Pro	Phe	Ser	His	Thr	Ser	Leu	Asp	145	150	155	160
Thr	Leu	Asp	Leu	Ala	His	Pro	Leu	Thr	Leu	Ser	Leu	Pro	Phe	Asn	Asp	165	170	175	
Phe	Pro	Leu	Phe	Gln	Thr	Val	Met	Asn	Ser	Leu	Gly	His	Lys	Val	Ala	180	185	190	
Gly	Val	Ile	Phe	Glu	Pro	Val	Cys	Ala	Asn	Met	Gly	Val	Ile	Leu	Pro	195	200	205	
Val	Pro	Asp	Phe	Ile	Glu	Gly	Val	Ile	Gln	Thr	Cys	Gln	Gln	Thr	Gly	210	215	220	
Ser	Phe	Ser	Ile	Met	Asp	Glu	Val	Val	Thr	Gly	Phe	Arg	Val	Ala	Gln	225	230	235	240
Gly	Gly	Ala	Ala	Ala	Leu	Tyr	His	Val	Lys	Pro	Asp	Ile	Leu	Val	Phe	245	250	255	
Gly	Lys	Ile	Leu	Gly	Gly	Gly	Leu	Pro	Ala	Ser	Ala	Val	Val	Ala	Pro	260	265	270	
Lys	Asp	Ile	Met	Asp	His	Leu	Ala	Pro	Glu	Glu	Lys	Ser	Ser	Lys	Leu	275	280	285	
Glu	His	Phe	Gln	Glu	Ile	Leu	Trp	Leu								290	295		

(2) INFORMATIONS POUR LA SEQ ID NO: 240:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 632 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 236314..238209

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 240:

```

Met Arg Tyr Asp Pro Gly Leu Ile Glu Glu Lys Trp Gln Lys Phe Trp
1      5      10      15
Lys Asn Glu Gln Val Phe Lys Ala Glu Glu Asp Glu Thr Lys Thr Lys
20      25      30
Tyr Tyr Val Leu Asp Met Phe Pro Tyr Pro Ser Gly Ala Gly Leu His
35      40      45
Val Gly His Leu Ile Gly Tyr Thr Ala Thr Asp Ile Val Ala Arg Cys
50      55      60
Lys Arg Ala Gln Gly Phe Ser Val Leu His Pro Met Gly Trp Asp Ser
65      70      75      80
Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Arg Thr Gly Thr His Pro
85      90      95
Arg Glu Thr Thr Glu Lys Asn Ile Ala Asn Phe Lys Lys Gln Leu Thr
100      105      110
Ala Met Gly Phe Ser Tyr Asp Glu Ser Arg Glu Phe Ala Thr Ser Asp
115      120      125
Pro Glu Tyr Tyr Lys Trp Thr Gln Lys Leu Phe Leu Ile Leu Tyr Glu
130      135      140
Lys Gly Leu Ala Tyr Met Ala Asp Met Ala Val Asn Tyr Cys Pro Glu
145      150      155      160
Leu Gly Thr Val Leu Ser Asn Glu Glu Ile Glu Asn Gly Phe Ser Val
165      170      175
Asp Gly Gly Tyr Pro Val Glu Arg Arg Met Leu Arg Gln Trp Val Leu
180      185      190
Arg Ile Thr Ala Phe Ala Asp Gln Leu Leu Glu Gly Leu Asp Glu Leu
195      200      205
Asp Trp Pro Glu Ser Val Lys Gln Leu Gln Lys Asn Trp Ile Gly Lys
210      215      220
Ser Ser Gly Ala Ser Val Asn Phe Ala Thr Glu His Gly Ala Ile Glu
225      230      235      240
Val Phe Thr Thr Arg Pro Asp Thr Leu Ile Gly Val Ser Phe Leu Ala
245      250      255
Leu Ala Pro Glu His Pro Leu Val Asp Leu Leu Thr Ser Asp Glu Gln
260      265      270
Lys Ala Val Val Ala Gln Tyr Ile Lys Glu Thr Gln Ser Lys Ser Glu
275      280      285
Arg Asp Arg Ile Ser Glu Met Lys Thr Lys Ser Gly Val Phe Thr Gly
290      295      300
Ser Tyr Ala Lys His Pro Val Thr His Glu Leu Ile Pro Ile Trp Ile
305      310      315      320
Ala Asp Tyr Val Leu Met Gly Phe Gly Ser Gly Ala Val Met Gly Val
325      330      335
Pro Ala His Asp Glu Arg Asp Leu Leu Phe Ala Glu Gln Phe Asn Leu
340      345      350
Pro Val Val Ser Val Leu Asn Glu Glu Gly Val Cys Ile Asn Ser Cys
355      360      365
Cys Glu Gly Phe His Leu Asp Gly Leu Ser Gly Glu Glu Ala Lys Gln
370      375      380
Tyr Val Ile Asn Phe Leu Glu Glu Asn His Leu Gly Ala Ala Lys Ile
385      390      395      400
Ala Tyr Lys Leu Arg Asp Trp Leu Phe Ser Arg Gln Arg Tyr Trp Gly
405      410      415
Glu Pro Ile Pro Ile Ile His Phe Glu Asp Gly Ser Cys Arg Pro Leu
420      425      430
Arg Asp Asp Glu Leu Pro Leu Leu Pro Pro Glu Ile Gln Asp Tyr Arg
435      440      445

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```

Pro Glu Gly Val Gly Gln Gly Pro Leu Ala Lys Val Arg Glu Trp Val
 450                               455                               460
Gln Val Phe Asp Thr Glu Thr Gln Arg Ala Gly Lys Arg Glu Thr His
465                               470                               475                               480
Thr Met Pro Gln Trp Ala Gly Ser Cys Trp Tyr Tyr Leu Arg Phe Cys
                               485                               490                               495
Asp Ala His Asn Ser Ala Ala Pro Trp Ala Lys Glu Lys Glu Gln Tyr
                               500                               505                               510
Trp Met Pro Val Asp Leu Tyr Ile Gly Gly Ala Glu His Ala Val Leu
                               515                               520                               525
His Leu Leu Tyr Ala Arg Phe Trp His Gln Val Phe Tyr Glu Ala Gly
 530                               535                               540
Ile Val Ser Thr Pro Glu Pro Phe Lys Lys Leu Val Asn Gln Gly Leu
545                               550                               555                               560
Val Leu Ala Thr Ser Tyr Arg Ile Pro Gly Lys Gly Tyr Ile Tyr Pro
                               565                               570                               575
Glu Thr Ala Lys Glu Glu Asn Gly Lys Trp Val Ala Pro Ser Gly Glu
                               580                               585                               590
Glu Leu Asp Val Arg Gln Glu Lys Met Ser Lys Ser Lys Leu Asn Gly
 595                               600                               605
Val Asp Pro Gln Ile Leu Ile Asp Glu Phe Gly Leu Thr Leu Phe Gly
 610                               615                               620
Cys Thr Gln Cys Phe Gln Gly Leu
625                               630

```

(2) INFORMATIONS POUR LA SEQ ID NO: 241:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 202 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 238164..238769

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 241:

```

Ile Trp Thr Asp Ala Val Arg Met Tyr Ala Met Phe Ser Gly Pro Leu
1                               5                               10                               15
Asp Lys Asn Lys Leu Trp Ser Asn Gln Gly Val Ala Gly Cys Arg Arg
 20                               25                               30
Phe Leu Asn Arg Phe Tyr Glu Met Val Ser Ser Asp Arg Val Lys Glu
 35                               40                               45
Asp Asn Asn Phe Glu Gly Leu Ser Leu Ala His Lys Leu Val Gln Arg
 50                               55                               60
Val Thr Asp Ala Ile Glu Lys Leu Ser Leu Asn Thr Ile Pro Ser Ser
 65                               70                               75                               80
Phe Met Glu Phe Ile Asn Asp Phe Val Lys Leu Ala Val Tyr Pro Lys
 85                               90                               95
Ser Ala Val Glu Met Ala Val Arg Ala Leu Ala Pro Ile Ala Pro His
 100                              105                              110
Ile Ser Glu Glu Leu Trp Val Leu Leu Gly Asn Ser Pro Gly Val Gln
 115                              120                              125
Lys Ser Gly Trp Pro Ser Val Leu Pro Glu Tyr Leu Glu Glu Gln Thr
 130                              135                              140
Val Thr Ile Val Val Gln Val Asn Gly Lys Leu Arg Ala Arg Leu Asp

```

```

145          150          155          160
Ile Met Lys Asp Ala Ser Lys Glu Glu Val Leu Ala Leu Ala Arg Glu
          165          170          175
Ser Ala Ser Lys Tyr Leu Glu Gly Cys Glu Val Lys Lys Ala Ile Phe
          180          185          190
Val Pro Ala Arg Leu Val Asn Phe Val Val
          195          200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 242:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 431 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 238769..240061

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 242:

```

Met Ile Arg Arg Trp Leu Thr Ser Arg Leu Tyr Asp Ala Phe Leu Val
1          5          10          15
Cys Ala Phe Phe Val Ser Ala Pro Arg Ile Phe Tyr Lys Val Phe Phe
          20          25          30
His Gly Lys Tyr Ile Asp Ser Trp Lys Ile Arg Phe Gly Val Gln Lys
          35          40          45
Pro Phe Val Lys Gly Glu Gly Pro Leu Val Trp Phe His Gly Ala Ser
          50          55          60
Val Gly Glu Val Ser Leu Leu Ala Pro Leu Leu Asn Arg Trp Arg Glu
65          70          75          80
Glu Phe Pro Glu Trp Arg Phe Val Val Thr Cys Ser Glu Ala Gly
          85          90          95
Val His Thr Ala Arg Arg Leu Tyr Glu Ser Leu Gly Ala Thr Val Phe
          100          105          110
Val Leu Pro Leu Asp Leu Ser Cys Ile Ile Lys Ser Val Val Arg Lys
          115          120          125
Leu Ala Pro Asp Ile Val Ile Phe Ser Glu Gly Asp Cys Trp Leu His
          130          135          140
Phe Leu Thr Glu Ser Lys Arg Leu Gly Ala Lys Ala Phe Leu Ile Asn
145          150          155          160
Gly Lys Leu Ser Glu His Ser Cys Lys Arg Phe Ser Phe Leu Lys Arg
          165          170          175
Leu Gly Arg Asn Tyr Phe Ala Pro Leu Asp Leu Leu Ile Leu Gln Asp
          180          185          190
Glu Leu Tyr Lys Gln Arg Phe Met Gln Ile Gly Ile Ser Ser Asp Lys
          195          200          205
Ile His Val Thr Gly Asn Met Lys Thr Phe Ile Glu Ser Ser Leu Ala
          210          215          220
Thr Asn Arg Arg Asp Phe Trp Arg Ala Lys Leu Gln Ile Ser Ser Gln
225          230          235          240
Asp Arg Leu Ile Val Leu Gly Ser Met His Pro Lys Asp Val Glu Val
          245          250          255
Trp Ala Glu Val Val Ser His Phe His Asn Ser Ser Thr Lys Ile Leu
          260          265          270
Trp Val Pro Arg His Leu Glu Lys Leu Lys Glu His Ala Lys Leu Leu
          275          280          285

```


Glu	Lys	Ala	Gly	Ile	Leu	Phe	Gly	Leu	Trp	Ser	Gln	Gly	Ala	Ser	Phe
290						295					300				
Arg	Gln	Tyr	Asn	Ser	Leu	Ile	Met	Asp	Ala	Met	Gly	Val	Leu	Lys	Asp
305					310					315					320
Ile	Tyr	Ser	Ala	Ala	Asp	Ile	Ala	Phe	Val	Gly	Gly	Thr	Phe	Asp	Pro
				325					330					335	
Ser	Val	Gly	Gly	His	Asn	Leu	Leu	Glu	Pro	Leu	Gln	Lys	Glu	Ala	Pro
			340					345					350		
Leu	Met	Phe	Gly	Pro	Tyr	Ile	Tyr	Ser	Gln	Ser	Val	Leu	Ala	Glu	Arg
		355					360					365			
Leu	Arg	Glu	Lys	Glu	Ala	Gly	Leu	Ser	Val	Asn	Lys	Glu	Thr	Leu	Leu
	370					375					380				
Asp	Val	Val	Thr	Asp	Leu	Leu	Gln	Asn	Glu	Lys	Asn	Arg	Gln	Ala	Tyr
385					390					395					400
Ile	Glu	Lys	Gly	Lys	Ser	Phe	Leu	Lys	Gln	Glu	Glu	Asn	Ser	Phe	Gln
				405					410					415	
Gln	Thr	Trp	Glu	Ile	Leu	Lys	Ser	Gln	Ile	Thr	Cys	Met	Lys	Ile	
			420					425					430		

(2) INFORMATIONS POUR LA SEQ ID NO: 243:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 556 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(240313..241980)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 243:

Lys	Thr	Ser	Ile	Ile	Gly	His	Thr	Met	Glu	Leu	Leu	Ser	Val	Asn	Lys
1				5					10					15	
Ser	Tyr	Phe	Glu	Leu	Gln	Arg	Leu	His	Tyr	Arg	Pro	Asp	Thr	Leu	Ser
			20					25					30		
Leu	Leu	Asn	Ser	Leu	Cys	Ser	Met	His	Ile	Gln	Glu	Lys	Pro	Ser	Ser
		35					40					45			
Glu	Pro	Ala	Ser	Asp	Leu	Leu	Ala	Lys	His	Ile	Pro	His	Leu	Cys	Ala
	50					55				60					
Leu	Pro	Asp	Leu	Thr	Leu	Gln	Lys	Asp	Ala	Pro	Ser	Ser	Ser	Glu	Pro
65					70					75					80
Leu	Arg	Ile	Gly	Val	Leu	Leu	Ser	Gly	Gly	Gln	Ala	Pro	Gly	Gly	His
			85						90					95	
Asn	Val	Val	Ile	Gly	Leu	Phe	Glu	Gly	Leu	Arg	Ala	Phe	Asn	Lys	Glu
			100					105					110		
Thr	Lys	Leu	Phe	Gly	Phe	Ile	Lys	Gly	Pro	Leu	Gly	Leu	Ile	Arg	Gly
		115					120					125			
Leu	Tyr	Lys	Asp	Leu	Asp	Ile	Ser	Val	Ile	Tyr	Asp	Tyr	Tyr	Asn	Ala
	130					135					140				
Gly	Gly	Phe	Asp	Met	Leu	Ser	Ser	Ser	Arg	Glu	Lys	Ile	Lys	Thr	Lys
145					150					155					160
Glu	Gln	Lys	Ser	Ala	Ile	Leu	Ala	Thr	Val	Lys	Lys	Met	Lys	Leu	His
				165					170					175	
Gly	Leu	Leu	Ile	Val	Gly	Gly	Asp	Asn	Ser	Asn	Thr	Asp	Thr	Ala	Met
			180					185					190		
Leu	Ala	Glu	Tyr	Phe	Ile	Glu	His	Asn	Cys	Pro	Thr	Ala	Val	Ile	Gly

```

          195                200                205
Val Pro Lys Thr Ile Asp Gly Asp Leu Lys Asn Ala Trp Ile Glu Thr
      210                215                220
Pro Leu Gly Phe His Thr Ser Cys Arg Thr Tyr Ser Glu Met Ile Gly
225                230                235                240
Asn Leu Glu Lys Asp Val Leu Ser Thr Arg Lys Tyr His His Phe Val
      245                250                255
Lys Leu Met Gly Glu Gln Ala Ser His Ser Thr Leu Glu Cys Gly Leu
      260                265                270
Gln Thr Leu Pro Asn Ile Thr Leu Ile Gly Glu Glu Val Ala Val Gln
      275                280                285
His Ala Ser Leu Gln Ser Leu Ser Leu Ser Ile Ala Gln Gly Leu Ile
      290                295                300
Glu Arg Phe His Arg Gly Lys Asp Tyr Ser Thr Ile Leu Ile Pro Glu
305                310                315                320
Gly Leu Ile Lys Gln Ile Pro Asp Thr Lys Arg Leu Ile Gln Glu Leu
      325                330                335
Asn Thr Leu Ile Ala Glu Glu Gln Phe Ser Val His Asn Leu Asp Gln
      340                345                350
Gln Leu Ser Pro Met Ala Ile Glu Thr Phe Ser Ser Leu Pro Glu Asn
      355                360                365
Ile Arg Asp Gln Leu Leu Leu Asp Arg Asp Ser Tyr Gly Asn Ile Arg
      370                375                380
Val Ser Lys Ile Ala Ile Glu Glu Leu Leu Ala Ser Leu Val Ser Lys
385                390                395                400
Glu Ile Ser Lys Leu Glu Pro Thr Met Ser Phe Ser Pro Val Thr His
      405                410                415
Phe Leu Gly Tyr Glu Ser Arg Ala Ser Phe Pro Ser Asn Phe Asp Ser
      420                425                430
Asn Tyr Gly Leu Ala Leu Gly Ile Ala Ala Ser Leu Phe Leu Val Arg
      435                440                445
Gly Lys Thr Gly Tyr Met Val Thr Ile Gly Asn Leu Ala Glu Thr Tyr
      450                455                460
Thr Glu Trp Thr Ile Ala Ala Thr Pro Leu Tyr Lys Met Met His Leu
465                470                475                480
Glu Lys Arg Phe Asn Gln Glu Thr Pro Val Ile Lys Thr Asp Ser Val
      485                490                495
Ser Pro Asp Ala Pro Met Ala Lys Tyr Leu His Lys Met Lys Glu Ile
      500                505                510
Cys Leu Leu Glu Asp Ser Tyr Arg Phe Pro Gly Pro Leu Gln Tyr Phe
      515                520                525
Glu Glu Gln Ala Leu Val Asp Gln Arg Pro Leu Thr Leu Leu Trp Glu
      530                535                540
Lys Gly Lys Leu Ser Glu Asn Asn Ala Thr Lys Phe
545                550                555

```

(2) INFORMATIONS POUR LA SEQ ID NO: 244:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 302 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(241941..242846)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 244:

Met	Ala	Lys	Thr	Leu	Phe	Tyr	Leu	Phe	Arg	Asn	Pro	Arg	Ser	Gly	Leu	1	5	10	15
Leu	Thr	Ile	Ser	Met	Asp	Ile	Thr	Lys	Glu	Leu	Pro	Phe	Ile	Met	Met	20	25	30	
Gln	Gln	Pro	His	Tyr	Phe	Xaa	His	Ser	Lys	Lys	Ile	Phe	Glu	Ile	Pro	35	40	45	
Leu	Leu	Asp	Asn	Val	Thr	Ser	Leu	Gly	Val	Leu	His	Ile	Pro	His	Ser	50	55	60	
Gln	Glu	Lys	Thr	Phe	Pro	Leu	Val	Ile	Val	Leu	His	Gly	Leu	Ala	Ser	65	70	75	80
Ser	Lys	Ile	Gly	Thr	Lys	Arg	Ser	Tyr	Leu	His	Leu	Ala	Asn	Gln	Leu	85	90	95	
Val	Gln	Glu	Gly	Ile	Gly	Val	Leu	Arg	Val	Asp	Leu	Pro	Gly	His	Gly	100	105	110	
Asp	Ser	Glu	Gly	Phe	Ile	His	Glu	Phe	Ser	Leu	Thr	Asp	Tyr	Ile	Gln	115	120	125	
Ala	Ser	Gln	Lys	Ile	Ile	Gln	Phe	Gly	Leu	Ser	Leu	Pro	Gln	Ala	Asn	130	135	140	
His	Ser	Val	Ala	Leu	Phe	Gly	Ser	Ser	Leu	Gly	Gly	Ser	Leu	Ser	Leu	145	150	155	160
Leu	Asn	Leu	Pro	Tyr	Phe	Pro	Glu	Ile	Gln	His	Ala	Ala	Ile	Trp	Thr	165	170	175	
Pro	Thr	Ile	Gln	Gly	Ala	Leu	Trp	Leu	Glu	Asp	Thr	Met	Gln	Ser	Met	180	185	190	
Ser	Pro	Ser	Leu	Gln	Leu	Pro	Pro	Asp	Asn	Phe	Ser	Tyr	Gln	Gly	Ile	195	200	205	
Pro	Leu	Gly	Lys	Lys	Phe	Cys	Ser	Gln	Phe	Ile	Glu	Leu	Asp	Thr	Val	210	215	220	
Asp	Ala	Leu	Ser	Lys	Ile	Thr	Gln	Glu	Val	Ser	Ile	Leu	Tyr	Leu	Gln	225	230	235	240
Gly	Glu	Asp	Asp	Ala	Val	Val	Ser	Leu	Arg	His	Gln	Ala	Leu	Phe	Ala	245	250	255	
Lys	Thr	Phe	Thr	Gly	Lys	Ala	Ser	Tyr	Arg	Thr	Tyr	Pro	Lys	Met	Thr	260	265	270	
His	Gln	Leu	Cys	Ile	Tyr	Ser	Glu	Ala	Phe	Gln	Asp	Leu	Val	Asp	Trp	275	280	285	
Leu	Lys	His	Gln	Leu	Leu	Gly	Thr	Pro	Trp	Ser	Tyr	Ser	Leu			290	295	300	

(2) INFORMATIONS POUR LA SEQ ID NO: 245:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 561 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(242798..244480)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 245:

Ala	Asn	Val	Phe	Glu	Gln	Lys	Leu	Met	Ser	Ser	Asn	Lys	His	Ala	Ser	1	5	10	15
Leu	Cys	Gln	Lys	Thr	Pro	Ser	Leu	Cys	Arg	Glu	Leu	Gln	Lys	Ala	Pro				

20 25 30
 Ala Leu Leu Leu Thr Glu Asp Ile Arg Phe Lys Ala Leu Leu Asn Glu
 35 40 45
 Arg Ile Asp Ser Val Ala Glu Leu Phe Pro Cys Thr Tyr Asn Ser Pro
 50 55 60
 Tyr Tyr Lys Phe Ile Ser Lys Ser Asp Leu Ser Ala Glu Thr Phe Pro
 65 70 75 80
 Leu Lys Val Gly Val Met Leu Ser Gly Gly Pro Ala Pro Gly Gly His
 85 90 95
 Asn Val Ile Leu Gly Leu Leu His Ser Ile Lys Lys Leu His Pro Asp
 100 105 110
 Ser Gln Leu Leu Gly Phe Ile Arg Asn Gly Glu Gly Leu Leu Asn Asn
 115 120 125
 Asn Thr Val Glu Ile Thr Asp Glu Phe Ile Glu Glu Phe Arg Asn Ser
 130 135 140
 Gly Gly Phe Asn Cys Ile Gly Thr Gly Arg Thr Asn Ile Ile Thr Glu
 145 150 155 160
 Glu Asn Lys Ala Arg Cys Leu Gln Thr Ala Asn Glu Leu Asp Leu Asp
 165 170 175
 Gly Leu Val Ile Ile Gly Gly Asp Gly Ser Asn Thr Ala Thr Ala Ile
 180 185 190
 Leu Ala Glu Tyr Phe Ala Lys His Gln Ala Lys Thr Val Leu Val Gly
 195 200 205
 Val Pro Lys Thr Ile Asp Gly Asp Leu Gln His Leu Phe Leu Asp Leu
 210 215 220
 Thr Phe Gly Phe Asp Thr Ala Thr Lys Phe Tyr Ser Ser Ile Ile Ser
 225 230 235 240
 Asn Ile Ser Arg Asp Ala Leu Ser Cys Lys Gly His Tyr His Phe Ile
 245 250 255
 Lys Leu Met Gly Arg Ser Ser Ser His Ile Thr Leu Glu Cys Ala Leu
 260 265 270
 Gln Thr His Pro Asn Ile Ala Leu Ile Gly Glu Glu Ile Ala Glu Lys
 275 280 285
 Ser Ile Ser Leu Glu Thr Leu Ile His Asp Ile Cys Glu Ile Ile Ala
 290 295 300
 Asp Arg Ala Ala Met Gly Lys Tyr His Gly Val Ile Leu Ile Pro Glu
 305 310 315 320
 Gly Val Ile Glu Phe Ile Pro Glu Ile Gln Ser Leu Val Lys Glu Ile
 325 330 335
 Glu Ser Ile Pro Glu Gln Glu Asn Leu Tyr Gln Ala Leu Ser Leu Ser
 340 345 350
 Ser Gln Gln Leu Leu Cys Gln Phe Pro Glu Asp Ile Cys His Gln Leu
 355 360 365
 Leu Tyr Asn Arg Asp Ala His Gly Asn Val Tyr Val Ser Lys Ile Ser
 370 375 380
 Val Asp Lys Leu Leu Ile His Leu Val Arg Gln His Leu Glu Thr His
 385 390 395 400
 Phe Arg Gln Val Pro Phe Asn Xaa Ser Ala His Phe Leu Gly Tyr Glu
 405 410 415
 Gly Arg Ser Gly Thr Pro Thr His Phe Asp Asn Val Tyr Ser Tyr Asn
 420 425 430
 Leu Gly Tyr Gly Ala Gly Val Leu Val Phe Asn Arg Cys Asn Gly Tyr
 435 440 445
 Leu Ser Thr Ile Glu Gly Leu Thr Ser Pro Ile Glu Lys Trp Arg Leu
 450 455 460
 Arg Ala Leu Pro Ile Val Arg Met Leu Thr Thr Lys Gln Gly Lys Asp
 465 470 475 480
 Ser Lys His Tyr Pro Leu Ile Lys Lys Arg Leu Val Asp Ile Ala Ser
 485 490 495

Pro	Val	Phe	Asn	Lys	Phe	Ser	Leu	Tyr	Arg	Lys	Ile	Trp	Ala	Leu	Glu
			500					505					510		
Asp	Ser	Tyr	Arg	Phe	Val	Gly	Pro	Leu	Gln	Ile	His	Ser	Pro	Glu	Asp
		515					520					525			
Ala	His	Ser	Asp	Asp	Phe	Pro	Pro	Leu	Ile	Leu	Phe	Leu	Asn	His	Asn
	530					535					540				
Glu	Trp	Gln	Lys	Arg	Cys	Ser	Ile	Cys	Leu	Glu	Ile	Pro	Asp	Gln	Asp
545					550					555					560
Tyr															

(2) INFORMATIONS POUR LA SEQ ID NO: 246:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 473 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(244479..245897)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 246:

Gly	Ala	Met	Asn	Lys	His	Lys	Arg	Phe	Leu	Ser	Leu	Val	Leu	Leu	Thr
1				5					10					15	
Phe	Ile	Leu	Leu	Gly	Ile	Trp	Phe	Cys	Pro	His	Ser	Asp	Leu	Ile	Asp
			20					25					30		
Ser	Lys	Ala	Trp	His	Leu	Phe	Ala	Ile	Phe	Thr	Thr	Thr	Ile	Ile	Gly
		35					40					45			
Ile	Ile	Val	Gln	Pro	Ala	Pro	Met	Gly	Ala	Ile	Val	Ile	Met	Gly	Ile
		50				55					60				
Ser	Leu	Leu	Leu	Val	Thr	Lys	Thr	Leu	Thr	Leu	Asp	Gln	Ala	Leu	Ser
65					70					75					80
Gly	Phe	His	Ser	Pro	Ile	Ala	Trp	Leu	Val	Phe	Leu	Ser	Phe	Ser	Ile
			85					90						95	
Ala	Lys	Gly	Val	Ile	Lys	Thr	Gly	Leu	Gly	Glu	Arg	Val	Ala	Tyr	Phe
			100					105					110		
Phe	Val	Lys	Ile	Leu	Gly	Lys	Ser	Pro	Leu	Gly	Leu	Ser	Tyr	Gly	Leu
		115					120					125			
Val	Leu	Thr	Asp	Phe	Leu	Leu	Ala	Pro	Ala	Ile	Pro	Ser	Leu	Thr	Ala
	130					135					140				
Arg	Ala	Gly	Gly	Ile	Leu	Phe	Pro	Val	Val	Met	Gly	Leu	Ser	Glu	Ser
145					150					155					160
Phe	Gly	Ser	Ser	Val	Glu	Lys	Gly	Thr	Glu	Lys	Leu	Leu	Gly	Ser	Phe
			165						170					175	
Leu	Ile	Lys	Val	Ala	Tyr	Gln	Ser	Ser	Val	Ile	Thr	Ser	Ala	Met	Phe
		180						185					190		
Leu	Thr	Ala	Met	Ala	Gly	Asn	Pro	Ile	Ile	Ser	Ala	Leu	Ala	Ser	His
		195					200					205			
Ser	Gly	Val	Thr	Leu	Thr	Trp	Ala	Ile	Trp	Ala	Lys	Ala	Ala	Ile	Leu
	210					215					220				
Pro	Gly	Ile	Ile	Ser	Leu	Ala	Cys	Met	Pro	Phe	Val	Leu	Phe	Lys	Leu
225					230					235					240
Phe	Pro	Pro	Gln	Ile	Thr	Ser	Cys	Glu	Glu	Ala	Val	Ala	Thr	Ala	Lys
			245						250					255	
Thr	Arg	Leu	Lys	Glu	Met	Gly	Pro	Leu	Asn	Gln	Gly	Glu	Arg	Ile	Ile

260 265 270
 Leu Leu Ile Phe Ser Leu Leu Ile Ser Leu Trp Thr Phe Gly Asp Ser
 275 280 285
 Ile Gly Ile Ser Ala Thr Thr Thr Phe Ile Gly Leu Ser Leu Leu
 290 295 300
 Ile Leu Thr Asn Ile Leu Asp Trp Gln Lys Asp Val Leu Ser Asn Thr
 305 310 315 320
 Thr Ala Trp Glu Thr Phe Val Trp Phe Gly Ala Leu Ile Met Met Ala
 325 330 335
 Ser Phe Leu Ser Ala Phe Gly Phe Ile His Phe Val Gly Asp Ser Val
 340 345 350
 Ile Gly Ser Val Gln Gly Leu Ser Trp Lys Ile Gly Phe Pro Ile Leu
 355 360 365
 Phe Leu Ile Tyr Phe Tyr Ser His Tyr Leu Phe Ala Ser Asn Thr Ala
 370 375 380
 His Ile Ala Ala Met Tyr Pro Ile Phe Leu Thr Val Ser Ile Ser Leu
 385 390 395 400
 Gly Ala Asn Pro Met Phe Ala Ala Leu Ala Leu Ala Phe Ala Ser Asn
 405 410 415
 Leu Phe Gly Gly Leu Thr His Tyr Gly Ser Gly Pro Ala Pro Leu Tyr
 420 425 430
 Phe Gly Ser His Phe Val Ser Val Gln Glu Trp Trp Arg Ser Gly Phe
 435 440 445
 Ile Leu Ser Ile Val Asn Leu Thr Ile Trp Leu Gly Leu Gly Ser Trp
 450 455 460
 Trp Trp Tyr Cys Leu Gly Leu Ile Arg
 465 470

(2) INFORMATIONS POUR LA SEQ ID NO: 247:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 318 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(245924..246877)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 247:

Cys Gly Leu Asp Ser Pro Tyr Leu Leu Arg Leu Arg Ala Pro Trp Ser
 1 5 10 15
 Leu Leu Ala Thr Ala Cys Ser Phe Ser Glu Ser Pro Ser Phe Arg Glu
 20 25 30
 Arg Leu Glu Gly Leu His Ser Tyr Arg Val Val Asp Arg Arg Phe Leu
 35 40 45
 Ala Cys Tyr Asp Gln Glu Thr Ile Asp Tyr Ser Gln Ile Phe Arg Thr
 50 55 60
 Gly Val Thr Leu Thr Met Glu Ile Ser His Ile Leu Glu Asp Leu Val
 65 70 75 80
 Tyr Asp Asn Gly Val Leu Pro Arg Glu Ala Ile Glu Ala Ala Ile Val
 85 90 95
 Lys His His Gln Ile Thr Pro Tyr Leu Leu Lys Ile Leu Glu Gly
 100 105 110
 Ile Asp His Val Ser Asp Ile Ile Asp Asp Asp Cys Tyr Gln Gly His
 115 120 125

```

Leu Tyr Ala Met Tyr Leu Leu Ala Gln Phe Arg Glu Thr Arg Ala Leu
130          135          140
Pro Leu Ile Ile Lys Leu Phe Ser Phe Glu Gln Asp Ile Pro His Ala
145          150          155          160
Ile Ala Gly Asp Val Leu Thr Glu Asp Leu Ser Arg Ile Leu Ala Ser
          165          170          175
Val Cys Asp Asp Val Ala Leu Ile Gln Glu Leu Ile Glu Thr Pro His
          180          185          190
Val Asn Pro Tyr Val Gln Ala Ala Ile Ser Ser Leu Val Ala Leu
          195          200          205
Val Gly Val His Lys Leu Ser Arg Glu Thr Ala Ile Arg Tyr Phe Gly
210          215          220
Glu Leu Leu Asn Tyr Arg Leu Glu Lys Lys Pro Ser Phe Ala Trp Asp
225          230          235          240
Ser Leu Val Ala Ser Ile Cys Ala Leu Tyr Pro Lys Glu Leu Phe Tyr
          245          250          255
Pro Ile Ser Lys Ala Phe Ser Ala Gly Leu Ile Asp Thr Ser Phe Ile
          260          265          270
Ser Met Glu Asp Val Glu Thr Ile Ile His Glu Glu Ser Ile Asp Ser
          275          280          285
Cys Leu Lys Glu Val Phe Ser Ser Thr Asp Leu Ile Asn Asp Thr Leu
290          295          300
Glu Glu Met Glu Lys Trp Leu Glu Arg Phe Pro Phe Glu Ser
305          310          315

```

(2) INFORMATIONS POUR LA SEQ ID NO: 248:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 249 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(246985..247731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 248:

```

Leu Ala Met Ser Thr Leu Val Ser Ile Lys Asp Leu Ser Leu Thr Ile
1          5          10          15
Arg Lys Gln Pro Ile Leu Arg Asn Val His Leu Glu Ile Cys Arg Gly
          20          25          30
Glu Cys Leu Thr Ile Val Gly Ala Ser Gly Ser Gly Lys Thr Ser Leu
          35          40          45
Ala Leu Ala Ile Leu Gly Leu Leu Pro Pro Asp Ala Gln Asp Ser Ile
50          55          60
Asp Phe His Leu Pro Pro Lys Thr Pro Arg Thr Lys Ala Val Gln Met
65          70          75          80
Ile Trp Gln Asp Val Tyr Ser Ser Leu Asn Pro Met Met Thr Ile Gln
          85          90          95
Glu Ile Ile Ala Glu Pro Leu His Ile Met Gly Gly Leu Ser Lys Ser
          100          105          110
Xaa Gln Gln Glu Glu Ile Ala His Ala Leu Lys Leu Val His Leu Pro
          115          120          125
Lys Ser Phe Leu Ser Leu Arg Pro Ile Lys Leu Ser Gly Gly Gln Arg
130          135          140
Gln Arg Ile Ala Ile Ala Lys Ala Leu Val Cys Lys Pro Glu Leu Ile

```

```

145          150          155          160
Ile Cys Asp Glu Pro Leu Ser Ala Leu Asp Thr Met Asn Gln Lys Leu
165          170          175
Ile Leu Asp Leu Phe Gln Thr Ile Lys Asn Gln Tyr Asn Asn Ala Phe
180          185          190
Leu Phe Ile Thr His Asp Met Ser Ala Ala Tyr Thr Leu Ala Asp Lys
195          200          205
Ile Ala Val Met Asp Arg Gly Tyr Leu Val Glu Ile Ala Ser Lys Gln
210          215          220
Glu Ile Phe Ser Ser Pro Lys His Ile Lys Thr Arg Glu Leu Leu Asp
225          230          235          240
Ala Ile Pro Ala Phe Thr Phe Ser Phe
245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 249:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 281 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(247743..248585)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 249:

```

Arg Lys Ile Pro Leu Ser Glu Asp Leu Leu Lys Ile Asp Asn Leu Val
1      5      10      15
Val Ser Val Lys Asn Ser Asn Gln Arg Leu Val Asn His Leu Ser Leu
20     25     30
Thr Ile Lys Arg Cys Gln Ser Met Ala Leu Val Gly Glu Asn Gly Ser
35     40     45
Gly Lys Thr Thr Val Ser Lys Ala Val Leu Gly Phe Leu Pro Asp Asn
50     55     60
Cys Tyr Ile Gln Ser Gly Arg Ile Leu Tyr Ser Ser Thr Asp Ile Thr
65     70     75     80
Arg Leu Ser Arg Arg Gln Leu Gln Thr Ile Arg Gly Lys Lys Ile Ala
85     90     95
Thr Ile Phe Gln Asn Ala Met Gly Thr Leu Thr Pro Ser Met Arg Val
100    105    110
Gly Ala Gln Ile Val Glu Thr Leu Arg His His Phe Asp Met Ser Lys
115    120    125
Glu Glu Ala Phe Ser Lys Ala Arg Glu Leu Leu Glu Ser Val His Ile
130    135    140
Glu Ser Pro Asp Arg Cys Leu Gln Leu Tyr Pro Phe Glu Leu Ser Gly
145    150    155    160
Gly Met Cys Gln Arg Val Ser Ile Ala Ile Ala Leu Ala Thr Asn Pro
165    170    175
Glu Leu Ile Ile Ala Asp Glu Pro Ser Thr Ala Leu Asp Ser Ile Ser
180    185    190
Gln Ala Gln Val Leu Arg Val Leu Thr Gln Ile His Gln Asn His Ser
195    200    205
Thr Ala Leu Leu Leu Ile Thr His Asn Leu Ala Leu Val Ser Glu Leu
210    215    220
Cys Glu Glu Met Ala Ile Ile Arg Tyr Gly Glu Ile Val Glu Gln Gly
225    230    235    240

```



```

Pro Val Gln Glu Leu Leu His Ser Pro Ser His Pro Tyr Thr Gln Gln
                245                      250                255
Leu Ile Arg Ala Ile Pro Arg Ile Pro Ser Pro Ser Tyr Leu Ser Pro
                260                      265                270
Thr Glu Pro Leu Ala Thr Thr Ala Tyr
                275                      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 250:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(248569..249420)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 250:

```

Asn Lys Leu Met Phe Arg Ser Ser Ser Ser His Thr Trp Arg Tyr Ile
1      5      10      15
Arg Thr Asn Lys Met Leu Val Leu Gly Cys Leu Thr Leu Ala Val Leu
      20      25      30
Val Leu Ala Ala Thr Phe Leu Pro Tyr Leu Tyr Pro Asp Tyr Glu Arg
      35      40      45
Thr Phe Pro Glu His Ala Leu Gln Ser Pro Ser Lys Ala Phe Pro Phe
50      55      60
Gly Thr Asp Asn Leu Gly Arg Cys Met Leu Ala Arg Thr Leu Gln Gly
65      70      75      80
Ile Arg Leu Ser Leu Leu Ile Ala Val Ser Ala Thr Ile Ile Asp Val
      85      90      95
Cys Leu Gly Leu Leu Trp Ser Thr Leu Ala Leu Ala Ser Gly Lys Lys
      100     105     110
Val Ala Asp Ile Met Ser Arg Ile Thr Glu Ile Leu Phe Ser Ile Pro
      115     120     125
Arg Ile Pro Val Ile Ile Leu Leu Leu Val Ile Phe Asn His Gly Ile
130     135     140
Leu Pro Leu Ile Leu Ala Met Thr Ile Thr Gly Trp Ile Pro Ile Ala
145     150     155     160
Arg Ile Ile Tyr Gly Gln Phe Leu Leu Leu Glu Asn Lys Glu Phe Val
      165     170     175
Leu Ser Ala Arg Ala Leu Gln Ala Ser Thr Phe His Ile Leu Arg Lys
      180     185     190
His Leu Leu Pro Asn Ser Leu Gly Pro Ile Ile Ser Thr Leu Ile Phe
195     200     205
Thr Ile Pro Asn Ala Val Tyr Thr Glu Ala Phe Ile Ser Phe Leu Gly
210     215     220
Leu Gly Xaa Gln Pro Pro Tyr Ala Ser Leu Gly Thr Leu Val Lys Glu
225     230     235     240
Gly Ile His Ser Leu Ala Tyr His Pro Trp Leu Phe Phe Ile Pro Ser
      245     250     255
Phe Phe Met Ile Ile Val Ser Val Ser Phe Asn Cys Ile Gly Glu Gly
260     265     270
Leu Gln Thr Lys Leu Leu Glu Glu Asn Thr Leu Val
275     280

```

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 206 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(249766..250383)

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 214 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(250545..251186)

Thr Lys Lys Leu Leu Pro Pro Trp Leu Leu Xaa Xaa Pro Ala Lys His
1 5 10 15

```

Leu Leu Pro Ala His Leu His Thr Tyr Pro Glu Gln Pro Ser Tyr Lys
      20      25      30
Gln Gln Glu Ala Ile Thr Leu Ala Lys Ser Leu Leu Glu Glu Ala Leu
      35      40      45
Thr Glu Leu Asn Met Thr Ile Lys Asp Leu Glu Lys Tyr Pro Leu Thr
      50      55      60
Phe Ser Ala Thr Ser Thr Val Asn Ser Gln Ile Ala Gln Met Leu Arg
      65      70      75      80
Asp Gln Trp Arg Arg Ser Leu Gly Ile Thr Phe Pro Ile Cys Gly Lys
      85      90      95
Glu Tyr Ala Leu Leu Gln Asn Asp Leu Ile Gly Asn Thr Phe Phe Met
      100      105      110
Ser Ile Gly Gly Trp Phe Ala Asp Phe Ser Asp Pro Leu Ala Phe Leu
      115      120      125
Ser Ile Phe Ser Ser Lys Gly Val Lys Pro Tyr Ala Leu Gln Asp Pro
      130      135      140
Gln Phe Asp Gln Leu Ile Leu Ser Ile Glu Thr Glu Lys Asn Pro Gln
      145      150      155      160
Lys Arg Ser Ala Leu Ile Ser Glu Ala Ser Leu Tyr Ile Glu Arg Gln
      165      170      175
Asn Val Ile Glu Pro Leu Tyr His Asp Val Phe His Tyr Thr Thr Asn
      180      185      190
Asn Lys Leu Ser Phe Val Arg Leu His Pro Ser Gly Leu Val Asp Met
      195      200      205
Arg Tyr Ala Lys Asn Ser
      210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 253:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(251095..252111)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 253:

```

Gly Gly His Ser Met Arg Lys Ile Ser Val Gly Ile Cys Leu Leu Leu
1      5      10      15
Ala Leu Ala Thr Ser Gly Cys Ser Lys Ser Ser Ser Asn Ala Thr His
      20      25      30
Arg Ser Pro Ala Thr His Thr Val Ala Val Ser Val Lys Asp Asp Pro
      35      40      45
Arg Thr Phe Asp Pro Arg Glu Val Arg Leu Leu Ser Asp Ile Asn Leu
      50      55      60
Ile His His Leu Tyr Glu Gly Leu Val Gln Glu Thr Pro Ser Gly Glu
      65      70      75      80
Val Phe Pro Ala Leu Ala Glu Ser Phe Phe Leu Ser Glu Asp Lys Lys
      85      90      95
Thr Tyr Thr Phe Asn Leu Lys Lys Ala Phe Trp Ser Asn Gly Asp Leu
      100      105      110
Ile Thr Ala His Asp Phe Val Arg Ser Trp Asn Asp Val Leu Gln Asn
      115      120      125
Arg Val Ala Ser Ile Tyr Ser Phe Ala Phe Leu Pro Ile Asp Val Asn

```

130 135 140
 Lys Asp Ser Gly Phe Phe Ala Lys Asp Asp His Thr Leu Val Ile Asn
 145 150 155 160
 Leu Leu Thr Pro Thr Pro His Phe Leu Lys Leu Leu Thr Leu Pro Val
 165 170 175
 Phe Tyr Pro Val His Ser Gln His Gln Ile Trp Lys Glu Glu Lys Ser
 180 185 190
 Leu Pro Ile Ser Thr Gly Ala Phe Phe Leu Lys Glu Lys Lys Asp Arg
 195 200 205
 Arg Trp Leu Lys Leu Glu Lys Ser Pro Tyr Tyr Tyr Asn Lys Asp Gln
 210 215 220
 Val Ala Val Gln Glu Ile Cys Ile His Ile Ile Pro Asp Gln Gln Thr
 225 230 235 240
 Ala Ser Ala Leu Phe Asn Gln Gly Lys Leu Asp Trp Gln Gly Leu Pro
 245 250 255
 Trp Gly His Ser Ile Pro Gln Glu Thr Leu Ala Thr Ala Asn Lys Arg
 260 265 270
 Arg Ala Pro Gln Ser Phe Asp Ile Ser Gly Thr Ser Trp Leu Thr Phe
 275 280 285
 Asn Thr Ala Lys Lys Pro Phe Ser His Ser Lys Leu Arg Gln Ala Leu
 290 295 300
 Ser Leu Val Leu Asn Lys Glu Ala Leu Ala Ser Leu Ala Phe Val Xaa
 305 310 315 320
 Xaa Cys Lys Thr Ser Pro Ser Cys Thr Phe Ala His Leu Pro Arg Ala
 325 330 335
 Ala Phe Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 254:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 341 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire
 (iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(252066..253088)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 254:

Val Phe Ala Met Leu Thr Leu Gly Leu Glu Ser Ser Cys Asp Glu Thr
 1 5 10 15
 Ser Cys Ser Leu Val Gln Asn Gly Lys Ile Leu Ala Asn Lys Ile Ala
 20 25 30
 Ser Gln Asp Ile His Ala Ser Tyr Gly Gly Val Ile Pro Glu Leu Ala
 35 40 45
 Ser Arg Ala His Leu Gln Thr Phe Pro Glu Leu Leu Thr Ala Ala Thr
 50 55 60
 Gln Ser Ala Gly Val Ser Leu Glu Asp Ile Glu Leu Ile Ser Val Ala
 65 70 75 80
 Asn Thr Pro Gly Leu Ile Gly Ala Leu Ser Ile Gly Val Asn Phe Ala
 85 90 95
 Lys Gly Leu Ala Ser Gly Leu Lys Arg Pro Leu Ile Gly Val Asn His
 100 105 110
 Val Glu Ala His Leu Tyr Ala Ala Cys Met Glu Ala Pro Ala Thr Gln
 115 120 125

```

Phe Pro Ala Leu Gly Leu Ala Ile Ser Gly Ala His Thr Ser Leu Phe
130                      135                      140
Leu Met Pro Asp Ala Thr Thr Phe Leu Leu Ile Gly Lys Thr Arg Asp
145                      150                      155                      160
Asp Ala Ile Gly Glu Thr Phe Asp Lys Val Ala Arg Phe Leu Gly Leu
165                      170                      175
Pro Tyr Pro Gly Gly Gln Lys Leu Glu Glu Leu Ala Arg Glu Gly Asp
180                      185                      190
Ala Asp Ala Phe Ala Phe Ser Pro Ala Arg Val Ser Gly Tyr Asp Phe
195                      200                      205
Ser Phe Ser Gly Leu Lys Thr Ala Val Leu Tyr Ala Leu Lys Gly Asn
210                      215                      220
Asn Ser Ser Ala Lys Ala Pro Phe Pro Glu Val Ser Glu Thr Gln Lys
225                      230                      235                      240
Arg Asn Ile Ala Ala Ser Phe Gln Lys Ala Val Phe Met Thr Ile Ala
245                      250                      255
Gln Lys Leu Pro Asp Ile Val Lys Ala Phe Ser Cys Glu Ser Leu Ile
260                      265                      270
Val Gly Gly Gly Val Ala Asn Asn Ser Tyr Phe Arg Arg Leu Leu Asn
275                      280                      285
Gln Ile Cys Ser Leu Pro Ile Tyr Phe Pro Ser Ser Gln Leu Cys Ser
290                      295                      300
Asp Asn Ala Ala Met Ile Ala Gly Leu Gly Glu Arg Leu Phe Cys Asn
305                      310                      315                      320
Arg Thr His Val Ser Lys Glu Val Ile Pro Cys Ala Arg Tyr Gln Trp
325                      330                      335
Glu Ser Ala Cys Ser
340

```

(2) INFORMATIONS POUR LA SEQ ID NO: 255:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 495 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 255234..256718

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 255:

```

Met Asp Ser Lys Thr Ser His Leu Asp Asp Glu Leu Cys Phe Lys Leu
1      5      10      15
Glu Glu Ala Phe Asp Thr Leu Thr Ala Gly Glu His Ser Gln Asp Leu
20     25     30
Thr Ser Ile Val Ser Val Tyr Asn Pro Ile Asp Leu Ala Tyr Ala Val
35     40     45
Ser Cys Leu Pro Ser Asp Ser Arg Ser Ile Leu Tyr Lys Asn Leu Asp
50     55     60
Ser Ile Ala Ser Lys Ile Ala Phe Ile Ile Asn Thr Asp Ser Ala Ser
65     70     75     80
Arg Trp Ala Ile Phe Arg Asn Leu Ser Asp Gly Glu Ile Cys Ala Leu
85     90     95
Ile Glu Gln Met Pro Pro Asp Glu Ala Ile Trp Val Leu Asp Asp Ile
100    105    110
Pro Asp Arg Arg Tyr Arg Arg Ile Leu Asp Leu Ile Asp Val Lys Lys

```

115 120 125
 Ala Leu Lys Ile Arg Asp Leu Gln Lys His Gly Arg Asn Thr Ala Gly
 130 135 140
 Arg Leu Met Thr Asn Glu Phe Phe Ala Phe Leu Met Glu Thr Thr Val
 145 150 155 160
 Lys Glu Val Ala Thr Cys Ile Arg Asn Asn Pro Gly Ile Asp Leu Thr
 165 170 175
 Arg Leu Val Phe Val Leu Asp Phe Lys Gly Glu Leu Gln Gly Phe Val
 180 185 190
 Thr Asp Arg Ser Leu Ile Ile Ala Ser Pro Glu Met Pro Leu Lys Gln
 195 200 205
 Ile Met Arg Pro Ile Glu His Lys Val Leu Ala Asp Thr Thr Arg Glu
 210 215 220
 Glu Val Val Asp Leu Val Glu Arg Tyr Lys Val Ala Val Leu Pro Val
 225 230 235 240
 Val Asp Glu Glu Asn Phe Leu Ile Gly Ala Ile Thr Tyr Glu Asp Val
 245 250 255
 Val Glu Thr Ile Glu Asp Ile Ala Asp Glu Thr Ile Ala Arg Met Ala
 260 265 270
 Gly Thr Thr Glu Asp Val Gly Tyr His Asp Cys His Val Val Gln Arg
 275 280 285
 Phe Leu Leu Arg Ala Pro Trp Leu Leu Ile Thr Leu Cys Ala Gly Leu
 290 295 300
 Val Ser Ala Ser Val Met Ala Tyr Phe Gln Lys Ile Ala Pro Thr Leu
 305 310 315 320
 Leu Ala Met Val Ile Phe Phe Ile Pro Leu Val Asn Gly Leu Ser Gly
 325 330 335
 Asn Val Gly Val Gln Cys Ser Thr Ile Leu Val Arg Ser Met Ala Thr
 340 345 350
 Gly Thr Leu Ser Phe Gly Arg Arg Arg Glu Thr Ile Leu Lys Glu Met
 355 360 365
 Ser Ile Gly Leu Leu Thr Gly Val Ala Leu Gly Ile Leu Cys Gly Leu
 370 375 380
 Val Val Cys Cys Met Gly Cys Leu Gly Leu Gly Leu Phe Ala Thr Gly
 385 390 395 400
 Gly Val Gln Leu Gly Val Thr Val Ser Val Gly Ile Leu Gly Ala Ser
 405 410 415
 Leu Thr Ala Thr Thr Leu Gly Val Leu Ser Pro Phe Phe Phe Ala Lys
 420 425 430
 Ile Gly Val Asp Pro Ala Leu Ala Ser Gly Pro Ile Val Thr Ala Leu
 435 440 445
 Asn Asp Ile Val Ser Met Val Ile Phe Leu Leu Ile Thr Gly Thr Leu
 450 455 460
 Asn Val Leu Phe Leu Gln Ile Val Gly Glu Ser Glu Asp Lys Gly Phe
 465 470 475 480
 Leu Arg Ala Phe Phe Thr Met Ser Phe Leu Pro Leu Ser Leu Glu
 485 490 495

(2) INFORMATIONS POUR LA SEQ ID NO: 256:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 361 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 256762..257844

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 256:

Arg	Ser	Gly	Phe	Val	Ala	Leu	Arg	Phe	Glu	Ile	Leu	His	Gln	Ser	Lys	1	5	10	15
Lys	Ser	Arg	Ala	Arg	Val	Gly	Arg	Ile	Glu	Thr	Ala	His	Gly	Tyr	Ile	20	25	30	
Asp	Thr	Pro	Ala	Phe	Val	Pro	Val	Ala	Thr	Asn	Gly	Ala	Leu	Lys	Gly	35	40	45	
Val	Leu	Asp	His	Ser	Asn	Ile	Pro	Leu	Met	Phe	Cys	Asn	Thr	Tyr	His	50	55	60	
Leu	Ile	Val	His	Pro	Gly	Ala	Glu	Ala	Ile	Ala	Ala	Met	Gly	Gly	Leu	65	70	75	80
His	Gln	Phe	Ile	Gly	Arg	Asn	Ala	Pro	Ile	Ile	Thr	Asp	Ser	Gly	Gly	85	90	95	
Phe	Gln	Ile	Phe	Ser	Leu	Ala	Tyr	Gly	Ser	Val	Ala	Glu	Glu	Ile	Lys	100	105	110	
Ser	Cys	Gly	Lys	Lys	Lys	Gly	Gly	Asn	Thr	Ile	Ile	Lys	Val	Asn	Asp	115	120	125	
Asp	Gly	Val	His	Phe	Lys	Ser	Tyr	Arg	Asp	Gly	Arg	Lys	Leu	Phe	Leu	130	135	140	
Ser	Pro	Glu	Ile	Ser	Val	Gln	Ala	Gln	Lys	Asp	Leu	Gly	Ala	Asp	Ile	145	150	155	160
Ile	Leu	Pro	Leu	Asp	Glu	Leu	Leu	Pro	Phe	His	Ala	Asp	Pro	Thr	Tyr	165	170	175	
Phe	His	Gln	Ser	Gln	Arg	Thr	Tyr	Val	Trp	Glu	Lys	Arg	Ser	Leu		180	185	190	
Asp	Tyr	His	Leu	Lys	Asn	Pro	Gly	Ile	Gln	Ser	Met	Tyr	Gly	Val	Ile	195	200	205	
His	Gly	Gly	Thr	Phe	Pro	Asp	Gln	Arg	Lys	Leu	Gly	Cys	Lys	Phe	Val	210	215	220	
Glu	Asp	Leu	Pro	Phe	Asp	Gly	Ser	Ala	Ile	Gly	Gly	Ser	Leu	Gly	Lys	225	230	235	240
Asn	Leu	Gln	Asp	Ile	Val	Glu	Val	Val	Gly	Val	Thr	Ala	Ala	Asn	Leu	245	250	255	
Ser	Ala	Glu	Arg	Pro	Arg	His	Leu	Leu	Gly	Ile	Gly	Asp	Leu	Pro	Ser	260	265	270	
Ile	Trp	Ala	Thr	Val	Gly	Phe	Gly	Ile	Asp	Ser	Phe	Asp	Ser	Ser	Tyr	275	280	285	
Pro	Thr	Lys	Ala	Ala	Arg	His	Gly	Ser	Gly	Ile	Leu	Thr	Ser	Gln	Gly	290	295	300	
Pro	Leu	Lys	Ile	Asn	Asn	Gln	Arg	Tyr	Ser	Ser	Asp	Leu	Asn	Pro	Ile	305	310	315	320
Glu	Pro	Gly	Cys	Ser	Cys	Leu	Ala	Cys	Ser	Gln	Gly	Ile	Thr	Arg	Ala	325	330	335	
Tyr	Leu	Arg	His	Leu	Phe	Lys	Val	His	Glu	Pro	Asn	Ala	Gly	Ile	Trp	340	345	350	
Ala	Ser	Ile	His	Asn	Met	His	His	Met								355	360		

(2) INFORMATIONS POUR LA SEQ ID NO: 257:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 257911..258690

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 257:

Asp	Ser	Phe	Cys	Val	Phe	Ile	Gly	Phe	Ser	Ile	Lys	Pro	Phe	Ala	Val	
1			5					10						15		
Tyr	Leu	Phe	Asp	Leu	Lys	Lys	Thr	Gly	Lys	Glu	Glu	Phe	Val	Gln	Ser	
		20					25						30			
Val	Gly	Gln	Glu	Ala	Ser	Gln	Asn	Thr	Leu	Ser	Trp	Thr	Ile	Arg	Pro	
		35				40						45				
Arg	Ile	Pro	Ser	Ile	Ile	Gln	Gly	Ser	Lys	Glu	Val	Ser	Leu	Ala	Leu	
		50				55					60					
Phe	Val	Leu	Gly	Thr	Val	Leu	Ala	Ile	Val	Gly	Ala	Cys	Ala	Ala	Ala	
65				70					75					80		
Val	Gly	Gly	Ala	Phe	Ser	Val	Cys	Leu	Gly	Ala	Leu	Phe	Leu	Gly	Gly	
			85				90						95			
Val	Val	Leu	Ala	Thr	Gly	Leu	Leu	Leu	Ala	Val	Leu	Glu	Phe	Cys	His	
			100				105						110			
Ile	Arg	Ser	Ser	Arg	Glu	Lys	Tyr	Val	Ile	Leu	Thr	Lys	Gln	Asp	Leu	
		115				120						125				
Phe	Lys	Glu	Pro	Val	Ile	Gln	Glu	Glu	Gln	Ala	Thr	Pro	Leu	Ile	Glu	
		130				135					140					
Glu	Ala	Ser	Tyr	Thr	Cys	Glu	Pro	Gly	Ile	Pro	Leu	Ser	Gly	Pro	Glu	
145					150					155				160		
Glu	Val	Gln	Gln	Glu	Arg	Pro	Val	Ile	Leu	Gln	Lys	Asp	Leu	Asp	Leu	
			165				170						175			
Ser	His	Val	Pro	Lys	Tyr	Ile	Ala	Val	Gly	Ser	His	Val	Val	Glu	Leu	
		180					185					190				
Val	Lys	Ala	Gly	Lys	Ile	Gly	Arg	Asn	Gly	Glu	Leu	Leu	Leu	Glu	Glu	
		195					200					205				
Gly	Ile	Asp	Thr	Asp	Gln	Asn	Phe	Val	Arg	Arg	Ala	Lys	Glu	Ala	Gly	
		210				215					220					
Ser	Ile	Arg	Gln	Arg	Arg	Glu	Val	Val	Arg	Leu	Asp	Gly	Phe	Cys	Cys	
225				230					235					240		
Lys	Val	Leu	Pro	Lys	Thr	Ser	Lys	Ser	Glu	Ser	Ile	Asn	Asp	Leu	Val	
			245					250					255			
Ser	Asn	Asp	Cys													
			260													

(2) INFORMATIONS POUR LA SEQ ID NO: 258:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 258780..259187

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 258:

Glu	Pro	Ser	Ser	Xaa	Ala	Phe	Cys	Glu	Gly	Arg	Cys	Ala	Cys	Ala	Tyr	
1				5					10					15		


```

Arg Arg Ser Val Val Ser Phe Tyr Pro Gln Asn Leu Pro Ser Phe Arg
      20                      25                      30
Arg Arg Lys Pro Ser Arg Thr Asp Ser Pro Ile Lys His Ala Lys His
      35                      40                      45
Phe Leu Arg Asp His Leu Ser His Leu Arg Lys Ile Leu Ala Gly Lys
      50                      55                      60
Pro Gln Glu Val Ile Glu Ala Trp Tyr Glu Ile Leu Gly Lys Lys Tyr
      65                      70                      75                      80
Asn Gly Met Thr Gln Ala Ile Gly Leu Lys Asp Gly Ile Leu Ser Ile
      85                      90                      95
Lys Val Arg Asn Ala Ser Leu Tyr Ala Val Leu Lys Gln Ser Ser Gln
      100                     105                     110
Lys Glu Leu Ile Ser Arg Ile His Ser Ala Val Pro Gly Ala Lys Val
      115                     120                     125
Lys Glu Ile Arg Phe Leu Leu Gly
      130                     135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 259:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 804 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 259193..261604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 259:

```

Met Asp Ala Gln Glu Lys Lys Tyr Asp Ala Ser Ala Ile Thr Val Leu
1      5      10      15
Glu Gly Leu Gln Ala Val Arg Glu Arg Pro Gly Met Tyr Ile Gly Asp
      20      25      30
Thr Gly Val Thr Gly Leu His His Leu Val Tyr Glu Val Val Asp Asn
      35      40      45
Ser Ile Asp Glu Ala Met Ala Gly Phe Cys Thr Glu Val Val Val Arg
      50      55      60
Ile Leu Glu Asp Gly Gly Ile Ser Ile Ser Asp Asn Gly Arg Gly Ile
      65      70      75      80
Pro Ile Gln Ile His Glu Lys Glu Ser Ala Lys Gln Gly Arg Glu Ile
      85      90      95
Ser Ala Leu Glu Val Val Leu Thr Val Leu His Ala Gly Gly Lys Phe
      100     105     110
Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu Xaa Gly Val Gly Val
      115     120     125
Ser Cys Val Asn Ala Leu Ser Glu Lys Phe Ile Ala Lys Val Phe Lys
      130     135     140
Asp Gly Gln Ala Tyr Ser Met Glu Phe Ser Arg Gly Ala Pro Leu Thr
      145     150     155     160
Thr Leu Gln Val Leu Gly Pro Thr Asp Lys Arg Gly Thr Glu Val Leu
      165     170     175
Phe Tyr Pro Asp Pro Ala Ile Phe Ser Thr Cys Val Phe Asp Arg Ala
      180     185     190
Ile Leu Met Lys Arg Leu Arg Glu Leu Ala Phe Leu Asn Arg Gly Ala
      195     200     205
Thr Ile Val Phe Glu Asp Asp Arg Asp Thr Gly Phe Asp Lys Val Val

```

210 215 220
 Phe Phe Tyr Glu Gly Gly Ile Gln Ser Phe Val Ser Tyr Leu Asn Gln
 225 230 235
 Asn Lys Glu Ile Leu Phe Pro Asn Pro Ile Tyr Ile Gln Gly Ser Arg
 245 250 255
 Pro Gly Asp Asp Gly Asp Ile Glu Phe Glu Ala Ala Leu Gln Trp Asn
 260 265 270
 Ser Gly Tyr Ser Glu Leu Ile Tyr Ser Tyr Ala Asn Asn Ile Pro Thr
 275 280 285
 Arg Gln Gly Gly Thr His Leu Thr Gly Phe Ser Thr Ala Leu Thr Arg
 290 295 300
 Ala Val Asn Ser Tyr Ile Lys Ala His Asn Leu Ser Lys Ser Asp Lys
 305 310 315 320
 Leu Ser Leu Thr Gly Glu Asp Ile Lys Glu Gly Leu Val Ala Ile Val
 325 330 335
 Ser Val Lys Val Pro Asn Pro Gln Phe Glu Gly Gln Thr Lys Gln Lys
 340 345 350
 Leu Gly Asn Ser Asp Val Gly Ser Val Ser Gln Gln Ile Ser Gly Glu
 355 360 365
 Val Leu Thr Thr Phe Phe Glu Glu Asn Thr Gln Ile Ala Lys Thr Ile
 370 375 380
 Val Asp Lys Val Phe Val Ala Ala Gln Ala Arg Glu Ala Ala Lys Arg
 385 390 395 400
 Ala Arg Glu Leu Thr Phe Arg Lys Ser Ala Leu Asp Ser Ala Arg Leu
 405 410 415
 Pro Gly Lys Leu Ile Asp Cys Leu Glu Lys Asp Pro Glu Lys Cys Glu
 420 425 430
 Met Tyr Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
 435 440 445
 Arg Asp Arg Arg Phe Gln Ala Ile Leu Pro Ile Arg Gly Lys Ile Leu
 450 455 460
 Asn Val Glu Lys Ala Arg Leu Gln Lys Val Phe Gln Asn Gln Glu Ile
 465 470 475 480
 Gly Ser Ile Ile Ala Ala Leu Gly Cys Gly Ile Gly Lys Asp Asn Phe
 485 490 495
 Asn Leu Ser Lys Leu Arg Tyr Lys Arg Ile Ile Ile Met Thr Asp Ala
 500 505 510
 Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr
 515 520 525
 Arg His Met Ser Ala Leu Ile Glu Asn Glu Cys Val Tyr Ile Ala Gln
 530 535 540
 Pro Pro Leu Tyr Arg Val Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu
 545 550 555 560
 Ser Glu Lys Glu Met Asp Gly Tyr Leu Leu Asn Leu Gly Thr Lys Glu
 565 570 575
 Ser Gln Ile Val Phe Asp Asp Thr Leu Arg Asp Leu Arg Gly Glu Ala
 580 585 590
 Leu Glu Thr Phe Val Asn Leu Ile Leu Glu Val Glu Ser Phe Ile Val
 595 600 605
 Ser Leu Glu Lys Lys Ala Ile Pro Phe Ser Glu Phe Leu Asp Met Phe
 610 615 620
 Arg Asp Gly Ala Tyr Pro Leu Tyr Tyr Tyr Pro Pro Glu Ser Gly Lys
 625 630 635 640
 Gln Gly Gly Ser Tyr Leu Tyr Ser His Glu Lys Glu Ala Ala Ile
 645 650 655
 Ala Ala Asn Glu Glu Ser Ala Ser Arg Ile Leu Glu Leu Tyr Lys Gly
 660 665 670
 Ser Val Leu Glu Glu Leu Gln Arg Asp Leu Gly Asp Tyr Gly Tyr Asp
 675 680 685

```

Ile Arg Asn Tyr Leu His Pro Lys Gly Ser Gly Ile Thr Val Ser Thr
690                               695                               700
Glu Asp Pro Lys Ile Ser Pro Tyr Val Cys Tyr Thr Leu Lys Glu Val
705                               710                               715                               720
Ile Asp Tyr Leu Lys Gly Leu Gly Arg Lys Gly Ile Glu Ile Gln Arg
725                               730                               735
Tyr Lys Gly Leu Gly Glu Met Asn Ala Asp Gln Leu Trp Asp Thr Thr
740                               745                               750
Met Asn Pro Glu Gln Arg Thr Leu Val Arg Val Ser Leu Lys Asp Ala
755                               760                               765
Val Glu Ala Asp His Ile Phe Thr Met Leu Met Gly Glu Glu Val Pro
770                               775                               780
Pro Arg Arg Glu Phe Ile Lys Ser His Ala Leu Ser Ile Arg Met Asn
785                               790                               795                               800
Asn Leu Asp Ile

```

(2) INFORMATIONS POUR LA SEQ ID NO: 260:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 836 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 261622..264129

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 260:

```

Met Leu Asn Lys Glu Glu Ile Ile Val Pro Lys Asn Leu Glu Glu Glu
1                               5                               10                               15
Met Lys Glu Ser Tyr Leu Arg Tyr Ser Met Ser Val Ile Ile Ser Arg
20                               25                               30
Ala Leu Pro Asp Ala Arg Asp Gly Leu Lys Pro Ser Gln Arg Arg Ile
35                               40                               45
Leu Tyr Ala Met Lys Gln Leu Asn Leu Thr Pro Gly Val Lys His Arg
50                               55                               60
Lys Cys Ala Lys Ile Cys Gly Asp Thr Ser Gly Asp Tyr His Pro His
65                               70                               75                               80
Gly Glu Ser Val Ile Tyr Pro Thr Leu Val Arg Met Ala Gln Asp Trp
85                               90                               95
Ala Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Ile
100                              105                              110
Asp Gly Asp Pro Ala Ala Ala Met Arg Tyr Thr Glu Ala Arg Leu Thr
115                              120                              125
His Ser Ala Ile Phe Leu Leu Glu Asp Leu Asp Lys Asp Thr Val Asp
130                              135                              140
Met Val Pro Asn Tyr Asp Glu Thr Lys Tyr Glu Pro Val Val Phe Pro
145                              150                              155                              160
Ser Lys Phe Pro Asn Leu Leu Cys Asn Gly Ser Ser Gly Ile Ala Val
165                              170                              175
Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Gly Glu Leu Ile Glu
180                              185                              190
Ala Thr Leu Leu Val Leu Ala Asn Ser Gln Thr Ser Ile Glu Asp Ile
195                              200                              205
Leu Glu Val Met Pro Gly Pro Asp Phe Pro Thr Gly Gly Ile Ile Cys

```

210 215 220
 Gly Thr Glu Gly Ile Arg Ser Thr Tyr Tyr Thr Gly Arg Gly Lys Leu
 225 230 235 240
 Arg Leu Arg Ala Arg Met His Val Glu Glu Asn Ser Asp Lys Gln Arg
 245 250 255
 Glu Asn Ile Ile Leu Thr Glu Met Pro Tyr Asn Val Asn Lys Ser Pro
 260 265 270
 Leu Ile Glu Gln Ile Ala Glu Leu Ile Asn Glu Lys Thr Leu Thr Gly
 275 280 285
 Ile Ser Asp Val Arg Asp Glu Ser Asp Lys Asp Gly Asn Arg Val Val
 290 295 300
 Leu Glu Leu Lys Lys Gly Glu Ser Ser Glu Val Val Ile Asn Arg Leu
 305 310 315 320
 Tyr Lys Phe Thr Asp Val Gln Val Thr Phe Gly Ala Asn Met Leu Ala
 325 330 335
 Leu Asp Lys Asn Leu Pro Arg Thr Met Asn Ile His Arg Met Ile Ser
 340 345 350
 Ala Trp Ile Arg His Arg Met Asp Val Ile Arg Arg Arg Thr Arg Tyr
 355 360 365
 Glu Leu Asn Lys Ala Glu Ala Arg Ala His Ile Leu Glu Gly Phe Leu
 370 375 380
 Lys Ala Leu Ser Cys Met Asp Glu Val Val Lys Thr Ile Arg Glu Ser
 385 390 395 400
 Ser Asn Lys Glu His Ala Lys Gln Gln Leu Val Glu Leu Phe Ser Phe
 405 410 415
 Ser Glu Ala Gln Ala Leu Ala Ile Leu Glu Leu Arg Leu Tyr Gln Leu
 420 425 430
 Thr Gly Leu Glu Ala Asp Lys Val Gln Lys Glu Tyr Ser Glu Leu Leu
 435 440 445
 Glu Lys Ile Thr Tyr Tyr Arg Lys Val Leu Ala Glu Glu Glu Leu Val
 450 455 460
 Lys Asp Ile Ile Arg Glu Glu Leu Gln Glu Leu His Lys Val His Lys
 465 470 475 480
 Thr Pro Arg Arg Thr Lys Ile Glu Met Asp Thr Gly Asp Val Arg Asp
 485 490 495
 Ile Glu Asp Ile Ile Ser Asp Glu Ser Val Ile Ile Thr Ile Ser Gly
 500 505 510
 Asp Asp Tyr Val Lys Arg Met Pro Val Lys Val Phe Arg Glu Gln Lys
 515 520 525
 Arg Gly Gly Gln Gly Val Thr Gly Phe Asp Met Lys Lys Gly Ser Asp
 530 535 540
 Phe Leu Lys Ala Val Tyr Ser Ala Ser Thr Lys Asp Tyr Leu Leu Ile
 545 550 555 560
 Phe Thr Asn Phe Gly Gln Cys Tyr Trp Leu Lys Val Trp Gln Leu Pro
 565 570 575
 Glu Gly Glu Arg Arg Ala Lys Gly Lys Pro Ile Ile Asn Phe Leu Glu
 580 585 590
 Gly Ile Arg Pro Gly Glu Gln Val Ala Ala Val Leu Asn Val Lys Arg
 595 600 605
 Phe Glu Gln Gly Glu Tyr Leu Phe Leu Ala Thr Lys Lys Gly Val Val
 610 615 620
 Lys Lys Val Ser Leu Asp Ala Phe Gly Ser Pro Arg Lys Lys Gly Ile
 625 630 635 640
 Arg Ala Leu Glu Ile Asp Asp Gly Asp Glu Leu Ile Ala Ala Arg His
 645 650 655
 Ile Ala Asn Asp Glu Glu Lys Val Met Leu Phe Thr Arg Leu Gly Met
 660 665 670
 Ala Val Arg Phe Pro His Asp Lys Val Arg Pro Met Gly Arg Ala Ala
 675 680 685

```

Arg Gly Val Arg Gly Val Ser Leu Lys Asn Glu Gln Asp Phe Val Val
690                               695                               700
Ser Cys Gln Val Val Thr Glu Asp Gln Ser Val Leu Val Val Cys Asp
705                               710                               715                               720
Asn Gly Phe Gly Lys Arg Ser Leu Val Cys Asp Phe Arg Glu Thr Asn
                               725                               730                               735
Arg Gly Ser Val Gly Val Arg Ser Ile Val Ile Asn Gln Arg Asn Gly
740                               745                               750
Asp Val Leu Gly Ala Ile Ser Val Thr Asp Cys Asp Ser Ile Leu Leu
755                               760                               765
Met Ser Ala Gln Gly Gln Ala Ile Arg Ile Asn Met Gln Asp Val Arg
770                               775                               780
Val Met Gly Arg Ala Thr Gln Gly Val Arg Leu Val Asn Leu Arg Glu
785                               790                               795                               800
Gly Asp Thr Leu Val Ala Met Glu Lys Leu Ser Ile Asn Thr Glu Ser
                               805                               810                               815
Val Glu Thr Glu Glu Asn Leu Ala Ala Ser Val Gln Ser Gly Gln Asp
                               820                               825                               830
Thr Ile Glu Glu
835

```

(2) INFORMATIONS POUR LA SEQ ID NO: 261:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 264125..264742

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 261:

```

Arg Asn Ser Val Phe Ile Val Val Glu Gly Gly Glu Gly Ala Gly Lys
1                               5                               10                               15
Thr Gln Phe Ile Gln Ala Leu Ser Lys Arg Leu Ile Glu Glu Gly Arg
                               20                               25                               30
Glu Ile Val Thr Thr Arg Glu Pro Gly Gly Cys Ser Leu Gly Asp Ser
35                               40                               45
Val Arg Gly Leu Leu Leu Asp Pro Glu Gln Lys Ile Ser Pro Tyr Ala
50                               55                               60
Glu Leu Leu Leu Phe Leu Ala Ala Arg Ala Gln His Ile Gln Glu Lys
65                               70                               75                               80
Ile Ile Pro Ala Leu Lys Ser Gly Lys Thr Val Ile Ser Asp Arg Phe
85                               90                               95
His Asp Ser Thr Ile Val Tyr Gln Gly Ile Ala Gly Gly Leu Gly Glu
100                               105                               110
Ser Phe Val Thr Asn Leu Cys Tyr His Val Val Gly Asp Lys Pro Phe
115                               120                               125
Leu Pro Asp Ile Ile Phe Leu Leu Asp Ile Pro Ala Arg Glu Gly Leu
130                               135                               140
Leu Arg Lys Ala Arg Gln Lys His Leu Asp Lys Phe Glu Gln Lys Pro
145                               150                               155                               160
Gln Ile Phe His Gln Ser Val Arg Glu Gly Phe Leu Ala Leu Ala Glu
165                               170                               175
Lys Ala Pro Asp Arg Tyr Lys Val Leu Asp Ala Leu Leu Pro Thr Glu

```

Ala Ser Val Asp Gln Ala Leu Leu Gln Ile Arg Ala Leu Ile
 180 185 190
 195 200 205

(2) INFORMATIONS POUR LA SEQ ID NO: 262:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 296 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 264741..265628

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 262:

Tyr Arg Gln Gly Glu Val Met Glu Ser Ala Ala Trp Glu Ala Leu Ile
 1 5 10 15
 Gln Arg Val Arg Asp Gln Lys Leu Pro Ser Ala Ile Ile Leu His Gly
 20 25 30
 Gln Asp Leu Ser Asn Leu Ser Ala Arg Ala Tyr Glu Tyr Ala Ser Leu
 35 40 45
 Ile Ile Lys Glu Thr Leu Pro Glu Ala Ala Tyr Lys Leu Ala Asn Lys
 50 55 60
 Leu His Pro Asp Ile His Glu Tyr Ser Pro Gln Gly Lys Gly Arg Leu
 65 70 75 80
 His Thr Ile Glu Thr Pro Arg Ala Ile Arg Lys Asp Ile Trp Ile His
 85 90 95
 Pro Tyr Glu Ser Pro Tyr Lys Ile Tyr Ile Ile Tyr Glu Ala Asp Arg
 100 105 110
 Ile Thr Leu Asp Ala Ile Ser Ala Phe Leu Lys Leu Leu Glu Asp Pro
 115 120 125
 Pro Gln Tyr Gly Met Phe Ile Leu Val Ser Ala Leu Pro Gln Arg Leu
 130 135 140
 Pro Pro Thr Ile Arg Ser Arg Cys Val Ser Phe His Ile Pro Met Glu
 145 150 155 160
 Glu Lys Thr Leu Val Ser Lys Lys Asp Ile Ala Phe Leu Ile Gly Leu
 165 170 175
 Ala Gln Gly Lys Glu Ser Val Thr Arg Ile Gly Ser Gln Val Lys Gly
 180 185 190
 Thr Ala Asp Glu Asp Lys Gln Val Leu Arg Asp Lys Thr Lys Ala Met
 195 200 205
 Leu Thr Val Leu Leu Gln Leu Phe Arg Asp Arg Phe Leu Leu Ala Lys
 210 215 220
 Lys Val Pro Val Ser Leu Leu Ala Tyr Pro Asp Leu Leu Asn Glu Ile
 225 230 235 240
 Lys Thr Met Pro Val Tyr Pro Leu Glu Glu Val Leu Ser Ile Ile Thr
 245 250 255
 Arg Ala Val Gln Ala Leu Asp Ser Tyr Ser Ser Ala Pro Ser Cys Leu
 260 265 270
 Glu Trp Ile Cys Leu Gln Leu Trp Ser Phe Lys Asn Arg Gln Gln Met
 275 280 285
 Ala Ile Arg Asn Arg Arg Arg Ser
 290 295

(2) INFORMATIONS POUR LA SEQ ID NO: 263:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 244 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(265631..266362)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 263:

```

Met Leu Ile Ala Asp Ser Gln Glu Glu Phe Leu Gln Ile Ala Cys Tyr
1      5      10      15
Asp Trp Ile Ser Thr Ala Asn Lys Ala Ile His Lys Arg Gly Ala Phe
20      25      30
Tyr Val Ala Leu Ser Gly Gly Lys Thr Pro Leu Gln Ile Phe Gln Glu
35      40      45
Ile Val Lys Lys Arg Ala Ala Ile Ser Asp Cys Ser Lys Ile Val Val
50      55      60
Phe Trp Gly Asp Glu Arg Ala Asn Glu Asp Val Glu Ala Gly Ser Asn
65      70      75      80
Tyr Leu Lys Ala Met Asp Ile Leu Lys Gly Leu Arg Ile Pro Glu Asp
85      90      95
Gln Ile Phe Arg Met Asp Thr Ala Asp Pro Lys Gly Asp Glu Ala Tyr
100     105     110
Glu Ala Leu Ile Gln Lys Tyr Val Pro Asp Ala Ile Phe Asp Met Val
115     120     125
Met Leu Gly Val Gly Glu Asp Gly His Thr Leu Ser Leu Phe Pro Glu
130     135     140
Thr Gln Ala Leu Glu Glu Lys Glu Arg Phe Val Val Phe Asn Glu Val
145     150     155     160
Pro Gln Leu His Thr Arg Arg Met Thr Leu Thr Phe Pro Ile Val Arg
165     170     175
Gln Ala Arg His Leu Val Ala Tyr Val Gln Gly Glu Asn Lys Gln Asp
180     185     190
Leu Phe His Lys Leu Val His Pro Leu Gly Arg Asp Thr Phe Pro Ile
195     200     205
Glu Arg Val Gly Thr Pro Leu Asn Pro Val Gln Trp Val Leu Ser Ser
210     215     220
Asp Ser Cys Arg Lys Thr Asp Leu Ala Asp Ile Pro Ala Asp Cys Lys
225     230     235     240
Leu Glu Met Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 264:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(266426..266938)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 264:

```

Lys Leu Phe Ile Asp Asn Pro Arg Trp Lys Gly Val Pro Phe Tyr Leu
1      5      10
Gln Ala Gly Lys Arg Leu Pro Lys Arg Thr Thr Asp Ile Ala Val Ile
20      25
Phe Lys Lys Ser Ser Tyr Asn Leu Phe Asn Ala Glu Asn Cys Pro Leu
35      40      45
Cys Pro Leu Asp Asn Asp Leu Leu Ile Ile Arg Ile Gln Pro Asp Glu
50      55      60
Gly Val Ala Leu Gln Phe Asn Cys Lys Val Pro Gly Thr Asn Lys Leu
65      70      75      80
Val Arg Pro Val Lys Met Asp Phe Arg Tyr Asp Ser Tyr Phe Asn Thr
85      90      95
Val Thr Pro Glu Ala Tyr Glu Arg Leu Leu Cys Asp Cys Ile Leu Gly
100      105      110
Asp Arg Thr Leu Phe Thr Ser Asn Glu Glu Val Leu Ala Ser Trp Glu
115      120      125
Leu Phe Ser Pro Leu Leu Glu Lys Trp Ser Gln Val His Pro Ile Phe
130      135      140
Pro Asn Tyr Met Ala Gly Ser Leu Arg Pro Gln Glu Ala Asp Glu Leu
145      150      155      160
Leu Ser Arg Asp Gly Lys Ala Trp Arg Pro Tyr
165      170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 265:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 340 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(266942..267961)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 265:

```

Ile Leu Gly Cys Thr Leu Glu Glu Ile Lys Asp Phe Gly Pro Thr Leu
1      5      10
Pro Ala Cys Pro Pro Cys Ile Val Val Ile Phe Gly Ala Thr Gly Asp
20      25
Leu Thr Ser Arg Lys Leu Phe Pro Ala Leu Tyr Asn Leu Thr Lys Glu
35      40      45
Gly Arg Leu Ser Glu Asn Phe Val Cys Val Gly Phe Ala Arg Arg Pro
50      55      60
Lys Ser His Glu Gln Phe Arg Glu Glu Met Lys Leu Ala Val Gln His
65      70      75      80
Phe Ser His Ser Ser Glu Ile Asp Ile Arg Val Trp Glu Ser Leu Glu
85      90      95
Asn Arg Ile Phe Tyr His Gln Ala Asn Phe Ser Asp Ala Glu Gly Tyr
100      105      110
Ser Ala Leu Lys Ala Tyr Leu Glu Gln Leu Asp Gln Gln Tyr Gly Thr
115      120      125
Gln Gly Asn Arg Leu Phe Tyr Leu Ser Thr Pro Pro Asp Tyr Phe Gln
130      135      140

```


Glu	Ile	Ile	Arg	Asn	Leu	Asn	Arg	His	Gln	Leu	Phe	Tyr	His	Glu	Gln
145					150					155					160
Gly	Ala	Gln	Gln	Pro	Trp	Ser	Arg	Leu	Ile	Ile	Glu	Lys	Pro	Phe	Gly
				165					170						175
Val	Asn	Leu	Glu	Thr	Ala	Arg	Glu	Leu	Gln	Gln	Cys	Ile	Asp	Ala	Asn
			180					185					190		
Ile	Asp	Glu	Glu	Ser	Val	Tyr	Arg	Ile	Asp	His	Tyr	Leu	Gly	Lys	Glu
	195						200					205			
Thr	Val	Gln	Asn	Ile	Leu	Thr	Ile	Arg	Phe	Ala	Asn	Thr	Leu	Phe	Glu
	210					215						220			
Ser	Cys	Trp	Asn	Ser	Gln	Tyr	Ile	Asp	His	Val	Gln	Ile	Ser	Val	Ser
225					230					235					240
Glu	Ser	Ile	Gly	Ile	Gly	Ser	Arg	Gly	Asn	Phe	Phe	Glu	Lys	Ser	Gly
			245						250					255	
Met	Leu	Arg	Asp	Met	Val	Gln	Asn	His	Leu	Thr	Gln	Leu	Leu	Cys	Leu
			260					265					270		
Leu	Thr	Met	Glu	Pro	Pro	Ser	Glu	Phe	Ser	Ser	Glu	Glu	Ile	Lys	Lys
		275					280					285			
Glu	Lys	Ile	Lys	Ile	Leu	Lys	Lys	Ile	Leu	Pro	Ile	Arg	Glu	Glu	Asp
	290					295					300				
Ala	Val	Arg	Gly	Gln	Tyr	Gly	Glu	Gly	Ile	Val	Gln	Asp	Val	Ser	Val
305					310					315					320
Leu	Gly	Tyr	Arg	Glu	Glu	Glu	Asn	Val	Asp	Pro	Asn	Ser	Ser	Val	Glu
			325						330					335	
Thr	Tyr	Val	Ala												
			340												

(2) INFORMATIONS POUR LA SEQ ID NO: 266:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268066..268320)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 266:

Phe	Ser	Gly	Asn	Pro	Leu	Pro	Met	Gln	Lys	Ala	Tyr	Ala	Ser	Ser	Val
1			5					10					15		
Gln	Ser	Glu	Ile	Gln	Glu	Leu	Ala	Ala	Leu	Ile	Gln	Glu	Met	Thr	Ala
		20					25					30			
Ile	Glu	Val	Ile	Leu	Trp	Asp	Glu	Arg	Leu	Ser	Ser	Ala	Gln	Ala	Glu
		35				40						45			
Arg	Met	Leu	Lys	Ser	Asp	Cys	Gly	Leu	Asn	Arg	Lys	Gln	Arg	Lys	Asn
	50				55					60					
Ser	Ser	Asp	Ser	Leu	Ala	Thr	Leu	Ile	Leu	Ser	Ser	Phe	Leu	Asp	
65				70					75					80	
Ser	Arg	Lys	Leu	Tyr											
			85												

(2) INFORMATIONS POUR LA SEQ ID NO: 267:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 102 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268205..268510)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 267:

```

Met Asn Ile Ala Lys Gln Gln Gln Ala Phe Leu Gly Ile Asp Tyr Gly
1      5      10      15
Lys Lys Arg Ile Gly Leu Ala Phe Ala Ser Ser Pro Leu Leu Ile Pro
      20      25      30
Leu Pro Ile Gly Asn Val Glu Ala Arg Ser Ser Leu Thr Thr Ala
      35      40      45
Gln Ala Leu Val Ser Ile Ile Lys Glu Arg Ala Val Thr Thr Val Val
      50      55      60
Phe Gly Glu Ser Ile Thr Tyr Ala Lys Ser Leu Cys Phe Lys Arg Ala
65      70      75      80
Ile Arg Asn Ser Arg Thr Ser Arg Thr His Pro Arg Asn Asp Cys Tyr
      85      90      95
Arg Ser His Ser Leu Gly
      100
  
```

(2) INFORMATIONS POUR LA SEQ ID NO: 268:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 539 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(268500..270116)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 268:

```

Met Ser Phe Lys Ser Ile Phe Leu Thr Gly Gly Val Val Ser Ser Leu
1      5      10      15
Gly Lys Gly Leu Thr Ala Ala Ser Leu Ala Leu Leu Leu Glu Arg Gln
      20      25      30
Asp Leu Lys Val Ala Met Leu Lys Leu Asp Pro Tyr Leu Asn Val Asp
      35      40      45
Pro Gly Thr Met Asn Pro Tyr Glu His Gly Glu Val Tyr Val Thr Asp
      50      55      60
Asp Gly Val Glu Thr Asp Leu Asp Leu Gly His Tyr His Arg Phe Ser
65      70      75      80
Ser Val Gln Leu Ser Lys Tyr Ser Ile Ala Thr Ser Gly Gln Ile Tyr
      85      90      95
Thr Lys Val Leu Thr Lys Glu Arg Asn Gly Glu Phe Leu Gly Ser Thr
      100      105      110
Val Gln Val Ile Pro His Val Thr Asn Glu Ile Ile Asn Val Ile Gln
      115      120      125
Ser Cys Ala Asp His His Lys Pro Asp Ile Leu Ile Val Glu Ile Gly
      130      135      140
  
```

Gly	Thr	Ile	Gly	Asp	Ile	Glu	Ser	Leu	Pro	Phe	Leu	Glu	Ala	Val	Arg	145	150	155	160
Gln	Phe	Arg	Cys	Glu	His	Pro	Gln	Asp	Cys	Leu	Ser	Ile	His	Met	Thr	165	170	175	
Tyr	Val	Pro	Tyr	Leu	Arg	Ala	Ala	Lys	Glu	Ile	Lys	Thr	Lys	Pro	Thr	180	185	190	
Gln	His	Ser	Val	Gln	Asn	Leu	Arg	Ser	Ile	Gly	Ile	Ser	Pro	Asp	Val	195	200	205	
Ile	Leu	Cys	Arg	Ser	Glu	Ala	Pro	Leu	Ser	Thr	Glu	Val	Lys	Arg	Lys	210	215	220	
Ile	Ser	Leu	Phe	Cys	Asn	Val	Pro	Glu	His	Ala	Val	Phe	Asn	Ala	Ile	225	230	235	240
Asp	Leu	Glu	Arg	Ser	Ile	Tyr	Glu	Met	Pro	Leu	Leu	Leu	Ala	Lys	Glu	245	250	255	
Asn	Ile	Ser	Asp	Phe	Leu	Leu	Asn	Lys	Leu	Gly	Phe	Ser	Pro	Lys	Pro	260	265	270	
Leu	Asp	Leu	Ser	Asp	Trp	Gln	Asp	Leu	Val	Glu	Ala	Leu	Cys	Asp	Lys	275	280	285	
Glu	Arg	Gln	His	Val	Arg	Ile	Gly	Leu	Val	Gly	Lys	Tyr	Leu	Glu	His	290	295	300	
Lys	Asp	Ala	Tyr	Lys	Ser	Val	Phe	Glu	Ala	Leu	Phe	His	Ala	Ser	Val	305	310	315	320
Pro	Ala	Asn	Cys	Ser	Leu	Glu	Leu	Val	Pro	Ile	Ala	Pro	Glu	Ser	Glu	325	330	335	
Asp	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Cys	Asp	Gly	Cys	Leu	Ile	Pro	Gly	340	345	350	
Gly	Phe	Gly	Thr	Arg	Ser	Trp	Glu	Gly	Lys	Ile	Ser	Ala	Ala	Arg	Tyr	355	360	365	
Cys	Arg	Glu	Gln	Asn	Ile	Pro	Cys	Phe	Gly	Ile	Cys	Leu	Gly	Met	Gln	370	375	380	
Ala	Leu	Val	Val	Glu	Tyr	Ala	Arg	Asn	Val	Leu	Asp	Lys	Pro	Leu	Ala	385	390	395	400
Asn	Ser	Met	Glu	Met	Asn	Pro	Glu	Thr	Pro	Asp	Pro	Val	Val	Cys	Met	405	410	415	
Met	Glu	Gly	Gln	Asp	Ser	Val	Val	Lys	Gly	Gly	Thr	Met	Arg	Leu	Gly	420	425	430	
Ala	Tyr	Pro	Cys	Arg	Ile	Ala	Pro	Gly	Ser	Leu	Ala	Ser	Ala	Ala	Tyr	435	440	445	
Lys	Thr	Asp	Leu	Val	Gln	Glu	Arg	His	Arg	His	Arg	Tyr	Glu	Val	Asn	450	455	460	
Pro	Ser	Tyr	Ile	Glu	Arg	Leu	Glu	Glu	His	Gly	Leu	Lys	Ile	Ala	Gly	465	470	475	480
Val	Cys	Pro	Leu	Gly	Glu	Leu	Cys	Glu	Ile	Val	Glu	Ile	Pro	Asn	His	485	490	495	
Arg	Trp	Met	Leu	Gly	Val	Gln	Phe	His	Pro	Glu	Phe	Leu	Ser	Lys	Leu	500	505	510	
Ala	Lys	Pro	His	Pro	Leu	Phe	Ile	Glu	Phe	Ile	Arg	Ala	Ala	Lys	Ala	515	520	525	
Tyr	Ser	Leu	Glu	Lys	Ala	Asn	His	Glu	His	Arg						530	535		

(2) INFORMATIONS POUR LA SEQ ID NO: 269:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 254 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(270095..270856)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 269:

```

Met Phe Ala Phe Leu Thr Ser Lys Lys Val Gly Ile Leu Pro Ser Arg
1      5      10      15
Trp Gly Ser Ser Arg Phe Pro Gly Lys Pro Leu Ala Lys Ile Leu Gly
20      25      30
Lys Thr Leu Val Gln Arg Ser Tyr Glu Asn Ala Leu Ser Ser Gln Ser
35      40      45
Leu Asp Cys Val Val Val Ala Thr Asp Asp Gln Arg Ile Phe Asp His
50      55      60
Val Val Glu Phe Gly Gly Leu Cys Val Met Thr Ser Thr Ser Cys Ala
65      70      75      80
Asn Gly Thr Glu Arg Val Glu Glu Val Val Ser Arg His Phe Pro Gln
85      90      95
Ala Glu Ile Val Val Asn Ile Gln Gly Asp Glu Pro Cys Leu Ser Pro
100     105     110
Thr Val Ile Asp Gly Leu Val Ser Thr Leu Glu Asn Asn Pro Ala Ala
115     120     125
Asp Met Val Thr Pro Val Thr Glu Thr Thr Asp Pro Glu Ala Ile Leu
130     135     140
Thr Asp His Lys Val Lys Cys Val Phe Asp Lys Asn Gly Lys Ala Leu
145     150     155     160
Tyr Phe Ser Arg Ser Ala Ile Pro His Asn Phe Lys His Pro Thr Pro
165     170     175
Ile Tyr Leu His Ile Gly Val Tyr Ala Phe Arg Lys Ala Phe Leu Ser
180     185     190
Glu Tyr Val Lys Ile Pro Pro Ser Ser Leu Ser Leu Ala Glu Asp Leu
195     200     205
Glu Gln Leu Arg Val Leu Glu Thr Gly Arg Ser Ile Tyr Val His Val
210     215     220
Val Gln Asn Ala Thr Gly Pro Ser Val Asp Tyr Pro Glu Asp Ile Thr
225     230     235     240
Lys Val Glu Gln Tyr Leu Leu Cys Leu Ser Lys Ala Ser Phe
245     250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 270:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 141 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 271191..271613

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 270:

```

Ser Asn Glu Lys Leu Leu Tyr Phe Ile Ile Ile Met Leu Ser Lys Phe
1      5      10      15
Cys Lys Leu Ser Leu Ser Ala Ile Leu Leu Ile Asn Thr Leu Ala Pro
20      25      30

```

Ser	Glu	Ala	Phe	Ser	Glu	Glu	Gly	Thr	Ser	Gly	Phe	Leu	Gly	Arg	Met
		35					40					45			
Lys	Ser	Trp	Ile	Leu	Lys	Asp	Lys	Thr	Ile	Leu	Ser	Thr	Thr	Glu	Glu
	50					55					60				
Ser	Gln	Thr	Ser	Ala	Ile	Glu	Lys	Val	Ser	Asp	Leu	Leu	Ser	Trp	Lys
65					70					75					80
Arg	Tyr	Asp	Tyr	Thr	Gln	Glu	Ser	Gly	Phe	Ala	Ile	Gln	Phe	Pro	Glu
				85					90					95	
Ser	Pro	Glu	His	Ser	Glu	Gln	Val	Ile	Glu	Val	Pro	Gln	Ser	Asp	Leu
			100					105					110		
Ala	Ile	Arg	Tyr	Asp	Thr	Tyr	Val	Ala	Glu	Thr	Pro	Ser	Asp	Ser	Thr
		115					120					125			
Val	Tyr	Val	Val	Ser	Val	Leu	Gly	Ile	Ser	Arg	Glu	Asn			
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 271:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 238 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 272219..272932

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 271:

Phe	Leu	Phe	Arg	Ser	Cys	Phe	Pro	Met	Leu	Asp	Val	Lys	Ser	Leu	Tyr
1				5					10					15	
Tyr	Ser	His	Ala	Ser	His	Ser	Val	Phe	Glu	Asp	Ala	Ser	Ala	Gly	Phe
			20					25					30		
Ala	Ser	Gly	Gln	Ile	Ser	Met	Val	Leu	Gly	Ala	Ser	Gly	Ser	Gly	Lys
		35					40					45			
Thr	Thr	Leu	Phe	Arg	Ile	Ile	Val	Gly	Leu	Leu	Ser	Cys	Ser	Leu	Gly
	50					55					60				
Glu	Ile	Leu	Trp	Lys	Gly	Gln	Pro	Ile	Gln	Gln	Glu	Gln	Ile	Ala	Tyr
65					70					75					80
Met	Gln	Gln	Lys	Glu	Ala	Leu	Leu	Pro	Trp	Arg	Thr	Val	Arg	Lys	Asn
			85						90					95	
Ile	Leu	Leu	Leu	Thr	Glu	Leu	Gly	Ser	Arg	Lys	Gln	Lys	Thr	Thr	Ile
			100					105					110		
Glu	Glu	Glu	Cys	Phe	Tyr	Asn	Val	Val	His	Ser	Phe	Gly	Leu	Ser	Ser
		115					120					125			
Leu	Leu	Asp	Arg	Phe	Pro	Asp	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg
	130					135					140				
Val	Val	Phe	Ala	Met	Gln	Ser	Leu	Ser	Pro	Lys	Pro	Ile	Leu	Leu	Leu
145					150					155					160
Asp	Glu	Pro	Phe	Thr	Ser	Leu	Asp	Pro	Ile	Thr	Lys	Xaa	Ile	Leu	Tyr
			165						170					175	
Gln	Asp	Val	Lys	Arg	Leu	Ala	Lys	Glu	Gly	Lys	Thr	Ile	Ile	Leu	
		180						185				190			
Ala	Ser	His	Asp	Val	Gln	Asp	Cys	Leu	Gly	Val	Gly	Glu	Ala	Phe	Phe
		195					200					205			
Ala	Ile	Lys	Asn	Gln	Lys	Leu	His	Ser	Ile	Ala	Leu	Asn	Lys	Glu	Gln
	210					215					220				
Gly	Ile	Ala	Gly	Leu	Leu	Gln	Gln	Met	Lys	Asp	His	Leu	Val		

225

230

235

(2) INFORMATIONS POUR LA SEQ ID NO: 272:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 235 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 272884..273588

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 272:

Arg	Thr	Arg	Asn	Arg	Trp	Val	Ile	Ala	Ala	Asn	Glu	Gly	Pro	Pro	Ser
1			5					10						15	
Leu	Thr	Ile	Pro	Pro	Leu	Lys	Leu	Val	Gln	Ala	Ala	Arg	Pro	Leu	Tyr
			20					25					30		
Asp	Gln	Gln	Leu	His	Lys	Leu	Ser	Arg	Glu	Glu	Lys	Leu	Ser	Leu	Gln
			35			40						45			
Gly	Glu	Ile	Arg	Thr	His	Glu	Val	Arg	Ser	Val	Pro	Leu	Val	Phe	Phe
			50			55				60					
Ala	Met	Leu	Ala	Ala	Val	Gly	Ala	Phe	Leu	Ala	Leu	Cys	Ile	Gly	Gly
					70			75						80	
65	Val	Leu	Cys	Cys	Ile	Asp	Asn	Val	Val	Phe	Leu	Ser	Glu	Ile	Phe
					85			90					95		
Pro	Phe	Ile	Leu	Pro	Gly	Ile	Leu	Ser	Leu	Leu	Pro	Ile	Ala	Leu	Leu
			100					105				110			
Leu	Arg	Leu	Ala	Trp	Lys	Glu	Gln	Lys	Leu	Ala	Ala	Gln	Lys	Gln	Gln
			115				120					125			
Arg	Ile	Ala	Ala	Ser	Cys	Tyr	Phe	Glu	Ser	Leu	Ala	Leu	Cys	Arg	Thr
			130			135				140					
Tyr	Lys	Ser	Gly	Ala	Pro	Ser	Val	Lys	Gly	Leu	Val	Asn	Phe	Ile	Gln
			145			150			155					160	
Ser	Glu	Ile	Leu	Pro	Ser	Gly	Phe	Ser	Lys	Arg	Phe	Lys	Phe	Ala	Val
			165					170					175		
Leu	Thr	Gln	Ala	Lys	Pro	Ser	Leu	Leu	Thr	Lys	Lys	Ile	Gln	Leu	Thr
			180					185				190			
Lys	Thr	Pro	Phe	Asp	Glu	Thr	Ile	Glu	Thr	Ala	Phe	Ser	His	Ile	Arg
			195				200					205			
Glu	Gly	Leu	Tyr	Leu	Ser	Glu	Ser	Glu	Gln	Arg	Asp	His	Asp	Lys	Lys
			210			215					220				
Leu	Xaa	Xaa	Glu	Ala	Asn	Thr	Ser	Pro	Lys	Gly					
					230					235					
225															

(2) INFORMATIONS POUR LA SEQ ID NO: 273:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 407 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(273596..274816)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 273:

Ser	Trp	Cys	Met	Glu	Lys	Asp	Phe	Leu	Glu	Asn	Val	Tyr	Arg	His	Phe
1			5						10					15	
Arg	Tyr	Arg	Phe	Phe	Lys	Leu	Ser	Ile	Leu	Pro	Ala	Leu	Leu	Gly	Leu
			20					25					30		
Trp	Leu	Phe	Phe	Thr	Pro	Asn	Ile	Leu	Asn	Tyr	Leu	Asp	Ser	Ser	Val
		35				40						45			
Ile	Leu	Ser	Asp	Lys	Ile	Cys	Gly	Val	Leu	Leu	Ile	Leu	Ser	Ala	
	50					55					60				
Leu	Ser	Phe	Tyr	Asn	Pro	Val	Ile	Leu	Gln	Leu	Gly	Ile	Phe	Ile	Gly
65				70						75					80
Leu	Trp	Val	Ser	Phe	Phe	Ser	Cys	Ser	Ser	Asp	Leu	Leu	Pro	Leu	Val
				85					90					95	
Phe	Ala	His	Asp	Ser	Leu	Leu	Gly	Phe	Ala	Thr	Leu	Ala	Ile	Ile	Phe
			100					105					110		
Leu	Ile	Pro	Asn	Arg	Pro	Glu	Asp	Leu	Glu	Val	Gly	Pro	Thr	Ile	Pro
		115					120					125			
Glu	Thr	Cys	His	Tyr	Asn	Pro	Ser	Ser	Gly	Gly	Lys	Arg	Ala	Ala	Val
	130					135					140				
Leu	Ile	Phe	Ala	Phe	Val	Gly	Trp	Leu	Gln	Ser	Arg	Tyr	Leu	Thr	Ser
145					150					155					160
Ala	Ala	Leu	Asn	Ile	Ala	Asp	Ala	Asp	Thr	Ser	Cys	Ser	Leu	Phe	Phe
				165					170					175	
Ser	Ser	Thr	Leu	Met	Val	Ile	Tyr	Ser	Met	Leu	Ile	Val	Leu	Ser	Leu
			180					185					190		
Thr	Gly	Gly	Glu	Arg	Arg	Trp	His	Thr	Gln	Pro	Lys	Val	Val	Phe	Ile
		195					200					205			
Thr	Ala	Ile	Leu	Leu	Phe	Ile	Ala	Ile	Gly	Leu	Thr	Leu	Ala	Ala	Ile
	210					215					220				
Leu	Leu	Ser	Gln	Leu	Phe	Leu	Thr	Asn	Tyr	Glu	Gly	Val	Cys	Leu	Thr
225					230					235					240
Val	Ala	Pro	Val	Phe	Ser	Leu	Ala	Phe	Phe	Tyr	Asp	Glu	Ile	Arg	Ala
				245					250					255	
Thr	Trp	Asn	Tyr	Leu	Ser	Gln	Asn	Tyr	Ser	Asn	Arg	Lys	Gln	Leu	Ala
		260						265					270		
Ile	Thr	Ala	Phe	Tyr	Gly	Ser	Glu	Tyr	Tyr	Lys	Glu	Ser	Leu	Phe	Trp
		275					280					285			
Glu	Glu	Arg	Ser	Val	Leu	Pro	Phe	Ser	Gln	Ala	Cys	Lys	Gln	Ala	Phe
	290					295					300				
Ala	Gly	Leu	Ser	Phe	Pro	Leu	Asn	Leu	Ile	Phe	Ala	Cys	Ile	Phe	Ser
305					310					315					320
Ile	Phe	Phe	Val	Gln	Leu	Asn	Val	Asn	Leu	Ser	Ile	Pro	Asp	Thr	Cys
				325					330					335	
Arg	Phe	Phe	Val	Asn	Ser	Ala	Cys	Trp	Phe	Ile	Leu	Val	Leu	Ser	Ile
			340					345					350		
Phe	Ser	Phe	Ala	Glu	Ser	Leu	Arg	His	Leu	Arg	Trp	Leu	Ser	Leu	Leu
		355					360					365			
Phe	Ala	Ala	Gly	Ile	Ile	Leu	Ser	Pro	Val	Ile	Phe	His	Leu	Pro	Leu
	370					375					380				
Glu	Ala	Ser	Thr	Leu	Leu	Ser	Ile	Ile	Val	Ser	Gly	Ile	Ala	Phe	Ile
385					390					395					400
Ile	Leu	Ser	Met	Gly	Arg	Leu									
				405											

(2) INFORMATIONS POUR LA SEQ ID NO: 274:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 274821..275666

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 274:

```

Leu Ser Phe Leu Thr His Lys Lys Ser Glu Arg Lys Glu Lys Val Phe
1      5      10      15
Phe Asn Lys Glu Ala Ser Phe Ile Ser Ala Arg Lys Arg Phe Arg Phe
20      25      30
Phe Tyr Phe Cys Leu Ile Ser Ile Leu Asn Gly Arg Met Asp Thr Arg
35      40      45
Thr Pro Leu Arg Lys Lys Ile Leu Ile Ile Ser Thr Ala Leu Gly Phe
50      55      60
Val Leu Cys Val Gly Leu Met Ile His Thr Lys Arg Ser Ile Met Pro
65      70      75      80
Pro Lys Thr His Ile Pro Thr Thr Ala Lys Tyr Phe Pro Thr Ile Gly
85      90      95
Asp Pro Tyr Ala Pro Ile Asn Ile Thr Val Phe Glu Glu Pro Ser Cys
100      105      110
Ser Ala Cys Glu Glu Phe Ser Ser Glu Val Phe Pro Leu Ile Lys Lys
115      120      125
His Phe Val Asp Thr Gly Glu Ala Ser Leu Thr Leu Val Pro Val Cys
130      135      140
Phe Ile Arg Gly Ser Met Pro Ala Ala Gln Ala Leu Leu Cys Val Tyr
145      150      155      160
His His Asp Pro Lys Arg Pro Asp Pro Glu Ala Tyr Met Glu Tyr Phe
165      170      175
His Arg Ile Leu Thr Tyr Lys Lys Thr Lys Gly Ser His Trp Ala Thr
180      185      190
Pro Glu Val Leu Ala Lys Leu Ala Glu Lys Ile Pro Thr His Ser Gly
195      200      205
Arg Glu Ile Asn Pro Lys Gly Leu Ile Gln Cys Ile Asn Ser Gln Arg
210      215      220
Phe Thr Glu Gln Leu Lys Lys Asn Asn Ile Tyr Gly Ser Gln Ile Met
225      230      235      240
Gly Gly Gln Leu Ala Thr Pro Thr Ala Val Val Gly Asp Tyr Leu Ile
245      250      255
Glu Asp Pro Thr Phe Asp Glu Ile Glu Arg Val Ile Thr Gln Leu Arg
260      265      270
His Leu Gln Ala Ile Glu Glu Glu Val Arg
275      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 275:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 529 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(276103..277689)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 275:

Met	His	His	Arg	Lys	Phe	Leu	Ala	Val	Ser	Ile	Ala	Phe	Val	Ser	Leu	1	5	10	15
Ala	Phe	Gly	Leu	Thr	Ser	Cys	Tyr	His	Gln	Lys	Glu	Glu	Pro	Lys	Asp	20	25	30	
Val	Leu	Arg	Ile	Ala	Ile	Cys	His	Asp	Pro	Met	Ser	Leu	Asp	Pro	Arg	35	40	45	
Gln	Val	Phe	Leu	Ser	Lys	Asp	Val	Ser	Ile	Val	Lys	Ala	Leu	Tyr	Glu	50	55	60	
Gly	Leu	Val	Arg	Glu	Lys	Glu	Ala	Ala	Phe	Gln	Leu	Ala	Leu	Ala	Glu	65	70	75	80
Arg	Tyr	His	Gln	Ser	Asp	Asp	Gly	Cys	Val	Tyr	Thr	Phe	Phe	Leu	Lys	85	90	95	
Asn	Thr	Phe	Trp	Ser	Asn	Gly	Asp	Val	Val	Thr	Ala	Tyr	Asp	Phe	Glu	100	105	110	
Glu	Ser	Ile	Lys	Gln	Ile	Tyr	Phe	Arg	Glu	Ile	Asp	Asn	Pro	Ser	Leu	115	120	125	
Arg	Ser	Leu	Ala	Leu	Ile	Lys	Asn	Ser	His	Ala	Val	Leu	Thr	Gly	Ala	130	135	140	
Leu	Pro	Val	Glu	Asp	Leu	Gly	Val	Arg	Ala	Leu	Asn	Ala	Lys	Ser	Leu	145	150	155	160
Glu	Ile	Val	Leu	Glu	Asn	Pro	Phe	Pro	Tyr	Phe	Leu	Glu	Ile	Leu	Ala	165	170	175	
His	Pro	Val	Phe	Tyr	Pro	Val	His	Thr	Ser	Leu	Arg	Glu	Tyr	Tyr	Lys	180	185	190	
Asp	Lys	Arg	Asn	Lys	Arg	Val	Phe	Pro	Met	Ile	Ser	Asn	Gly	Pro	Phe	195	200	205	
Ala	Ile	Gln	Cys	Tyr	Glu	Pro	Gln	Arg	Tyr	Leu	Leu	Ile	Asn	Lys	Asn	210	215	220	
Pro	Leu	Tyr	His	Ala	Lys	His	Asp	Val	Leu	Leu	Asn	Ser	Val	Cys	Leu	225	230	235	240
Gln	Ile	Val	Pro	Asp	Ile	His	Thr	Ala	Met	Gln	Leu	Phe	Gln	Lys	Asn	245	250	255	
His	Ile	Asp	Leu	Val	Gly	Leu	Pro	Trp	Ser	Ser	Ser	Phe	Ser	Leu	Glu	260	265	270	
Glu	Gln	Arg	Asn	Leu	Pro	Arg	Glu	Lys	Leu	Phe	Asp	Tyr	Pro	Val	Leu	275	280	285	
Ser	Cys	Ser	Val	Leu	Phe	Cys	Asn	Ile	His	Gln	Thr	Pro	Leu	Asn	Asn	290	295	300	
Pro	Ser	Leu	Arg	Thr	Ala	Leu	Ser	Leu	Ala	Ile	Asn	Arg	Glu	Thr	Leu	305	310	315	320
Leu	Lys	Leu	Ala	Gly	Lys	Gly	Cys	Ser	Ala	Thr	Ser	Phe	Val	His	Pro	325	330	335	
Gln	Leu	Ser	Gln	Ile	Pro	Ala	Thr	Thr	Leu	Ser	Gln	Asp	Glu	Arg	Ile	340	345	350	
Ala	Leu	Ala	Lys	Gly	Tyr	Leu	Thr	Glu	Ala	Leu	Lys	Thr	Leu	Ser	Gln	355	360	365	
Glu	Asp	Leu	Glu	Lys	Ile	Thr	Leu	Ile	Tyr	Pro	Ile	Glu	Ser	Val	Cys	370	375	380	
Leu	Arg	Ala	Val	Val	Gln	Glu	Ile	Arg	Gln	Gln	Leu	Phe	Asp	Val	Leu	385	390	395	400
Gly	Phe	Lys	Ile	Ser	Thr	Leu	Gly	Leu	Glu	Tyr	His	Cys	Phe	Leu	Asp	405	410	415	
Lys	Arg	Ser	Arg	Gly	Glu	Phe	Ser	Leu	Ala	Thr	Gly	Asn	Trp	Ile	Ala				

Asp Tyr His Gln Ala Ser Ala Phe Leu Ser Val Leu Gly Asn Gly Thr
 420 425 430
 435 440 445
 Arg Tyr Lys Asp Phe Gln Leu Ile Asn Trp Gln Asn Gln Lys Tyr Thr
 450 455 460
 Asn Ile Val Ala Gln Leu Leu Ile Gln Glu Ser Ser Asp Leu Gln Leu
 465 470 475 480
 Met Ala Glu Gln Leu Leu Lys Glu Ser Pro Leu Ile Pro Leu Tyr
 485 490 495
 His Leu Asp Tyr Val Tyr Ala Lys Gln Pro Arg Val Ser Asp Leu Gln
 500 505 510
 Thr Ser Ser Leu Gly Glu Ile Asp Leu Lys Arg Val Ser Leu Ala Glu
 515 520 525
 Gly

(2) INFORMATIONS POUR LA SEQ ID NO: 276:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 183 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 278268..278816

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 276:

Ile Ile Thr Thr Leu Phe Val Lys Thr Ser Met Phe Phe Leu Ala Lys
 1 5 10 15
 Arg Leu Val Gln Leu Asn Lys Asn Pro Phe Leu Leu Lys Lys Phe Ser
 20 25 30
 Glu Thr Thr Val Leu Phe Ile Phe Glu Arg Gln Leu Lys Met Trp Glu
 35 40 45
 Gly Tyr Ser Ile Asp Glu Asn Asn Tyr Ile Ser Asp Tyr Asn Met Glu
 50 55 60
 Phe Gly Arg Pro Leu Leu Gln Lys Leu Ala Asn Pro Val Cys Lys Ala
 65 70 75 80
 Leu Leu Gln Lys Gln Leu Glu Ala Glu Gln Ala Met Thr Leu Ser Asn
 85 90 95
 Gln Val Thr Val Gly Asp Ile Val Leu Met Arg Ser Pro Ile Phe Glu
 100 105 110
 Lys Ser Val Leu Leu Glu Ala Leu Ile Asn Glu Ile Ile Tyr Gln Glu
 115 120 125
 Ser Leu Phe Leu Phe Lys Lys Pro Glu Asn Cys Ser Met Ser Glu Asp
 130 135 140
 Glu Phe Arg Ala Arg Cys Thr Arg Asn Leu Val Glu Asp Leu Phe Asp
 145 150 155 160
 Gly Leu Met Asn Leu Trp Val Gln Ile Lys Leu Ile Lys Gly Tyr Asp
 165 170 175
 Ser Met Gln Asp Tyr Gln Glu
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 277:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 253 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(279013..279771)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 277:

```

Met Ser Lys Leu Thr Gln Val Phe Lys Gln Thr Lys Pro Cys Ile Gly
1          5          10          15
Tyr Leu Thr Ala Gly Asp Gly Gly Thr Ser Tyr Thr Ile Glu Ala Ala
          20          25          30
Lys Ala Leu Ile Gln Gly Gly Val Asp Ile Leu Glu Leu Gly Phe Pro
          35          40          45
Phe Ser Asp Pro Val Ala Asp Asn Pro Glu Ile Gln Val Ser His Asp
          50          55          60
Arg Ala Leu Ala Glu Asn Leu Thr Ser Glu Thr Leu Leu Glu Ile Val
65          70          75          80
Glu Gly Ile Arg Ala Phe Asn Gln Glu Val Pro Leu Ile Leu Tyr Ser
          85          90          95
Tyr Tyr Asn Pro Leu Leu Gln Arg Asp Leu Asp Tyr Leu Arg Arg Leu
          100          105          110
Lys Asp Ala Gly Ile Asn Gly Val Cys Val Ile Asp Leu Pro Ala Pro
          115          120          125
Leu Ser His Gly Glu Lys Ser Pro Phe Phe Glu Asp Leu Leu Ala Val
          130          135          140
Gly Leu Asp Pro Ile Leu Leu Ile Ser Ala Gly Thr Thr Pro Glu Arg
145          150          155          160
Met Ser Leu Ile Gln Glu Tyr Ala Arg Gly Phe Leu Tyr Tyr Ile Pro
          165          170          175
Tyr Glu Ala Thr Arg Asp Ser Glu Val Gly Ile Lys Glu Glu Phe Arg
          180          185          190
Lys Val Arg Glu His Phe Asp Leu Pro Ile Val Asp Arg Arg Asp Ile
          195          200          205
Cys Asp Lys Lys Glu Ala Ala His Val Leu Asn Tyr Ser Asp Gly Phe
          210          215          220
Ile Val Lys Thr Ala Phe Val His Gln Thr Thr Met Asp Ser Ser Val
225          230          235          240
Glu Thr Leu Thr Ala Leu Ala Gln Thr Val Ile Pro Gly
          245          250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 278:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(279767..280777)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 278:

Leu Lys Leu Arg Ile Leu Leu Gly Ala Ile Asp Gly Pro Arg Val Phe
 1 5 10 15
 Leu Lys Arg Glu Asp Leu Leu His Thr Gly Ala His Lys Leu Asn Asn
 20 25 30
 Ala Leu Gly Gln Cys Leu Leu Ala Lys Tyr Leu Gly Lys Thr Arg Val
 35 40 45
 Val Ala Glu Thr Gly Ala Gly Gln His Gly Val Ala Thr Ala Thr Ala
 50 55 60
 Cys Ala Tyr Leu Gly Leu Asp Cys Val Val Tyr Met Gly Ala Lys Asp
 65 70 75 80
 Val Glu Arg Gln Lys Pro Asn Val Glu Lys Met Arg Phe Leu Gly Ala
 85 90 95
 Glu Val Val Ser Val Thr Lys Gly Ser Cys Gly Leu Lys Asp Ala Val
 100 105 110
 Asn Gln Ala Leu Gln Asp Trp Ala Thr Thr His Ser Phe Thr His Tyr
 115 120 125
 Cys Leu Gly Ser Ala Leu Gly Pro Leu Pro Tyr Pro Asp Ile Val Arg
 130 135 140
 Phe Phe Gln Ser Val Ile Ser Ala Glu Val Lys Glu Gln Ile His Ala
 145 150 155 160
 Val Ala Gly Arg Asp Pro Asp Ile Leu Ile Ala Cys Ile Gly Gly Gly
 165 170 175
 Ser Asn Ala Ile Gly Phe Phe His His Phe Ile Pro Asn Pro Lys Val
 180 185 190
 Gln Leu Ile Gly Val Glu Gly Gly Gly Leu Gly Ile Ser Ser Gly Lys
 195 200 205
 His Ala Ala Arg Phe Ala Thr Gly Arg Pro Gly Val Phe His Gly Phe
 210 215 220
 Tyr Ser Tyr Leu Leu Gln Asp Asp Asp Gly Gln Val Leu Gln Thr His
 225 230 235 240
 Ser Ile Ser Ala Gly Leu Asp Tyr Pro Ser Val Gly Pro Asp His Ala
 245 250 255
 Glu Met His Glu Ser Gly Arg Ala Phe Tyr Thr Leu Ala Thr Asp Glu
 260 265 270
 Glu Ala Leu Arg Ala Phe Phe Leu Leu Thr Arg Asn Glu Gly Ile Ile
 275 280 285
 Pro Ala Leu Glu Ser Ser His Ala Leu Ala His Leu Val Ser Ile Ala
 290 295 300
 Pro Ser Leu Pro Lys Glu Gln Ile Val Ile Val Asn Leu Ser Gly Arg
 305 310 315 320
 Gly Asp Lys Asp Leu Pro Gln Ile Ile Arg Arg Asn Arg Gly Ile Tyr
 325 330 335
 Glu

(2) INFORMATIONS POUR LA SEQ ID NO: 279:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 103 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(281295..281603)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 279:

Tyr	Tyr	Ser	Ile	Thr	Lys	Arg	Cys	Asp	Met	Lys	Asn	Gln	Glu	Glu	Ser
1				5					10					15	
Gly	Trp	Gln	Ala	Phe	Leu	Thr	Leu	Cys	Ser	Lys	Met	Gln	Lys	Glu	Lys
			20					25					30		
Phe	Leu	Gln	Asp	Leu	Phe	Ser	Leu	Phe	Leu	Ser	Phe	Gly	Glu	Arg	Lys
		35					40					45			
Asp	Val	Ala	Ser	Arg	Tyr	His	Ile	Ile	Arg	Ala	Leu	Leu	Glu	Gly	Glu
	50					55					60				
Leu	Thr	Gln	Arg	Glu	Ile	Ala	Glu	Lys	Tyr	Gly	Val	Ser	Ile	Ala	Gln
65					70					75					80
Ile	Thr	Arg	Gly	Ser	Asn	Ala	Leu	Lys	Gly	Ser	Asp	Pro	Gln	Phe	Lys
				85					90					95	
Glu	Phe	Leu	Gln	Lys	Glu	Ile									
															100

(2) INFORMATIONS POUR LA SEQ ID NO: 280:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 106 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(281787..282104)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 280:

Leu	Pro	Ser	Glu	Ala	Cys	Met	Ser	Leu	Asp	Thr	Ala	Gly	Lys	Pro	His
1				5					10					15	
Trp	Lys	Ile	Pro	Glu	Gly	Phe	Leu	Gln	Phe	Ala	Phe	Ala	Tyr	Tyr	Arg
			20					25					30		
Ser	Trp	Val	Glu	His	Trp	Val	Lys	Lys	Ser	Leu	Arg	Arg	Gly	Ser	Leu
		35					40					45			
Ile	Gln	Leu	Pro	Ala	Arg	Ser	Ile	Gln	Val	Ser	Leu	Ile	Thr	Thr	Gln
	50					55					60				
Thr	Gly	Tyr	Phe	Ala	Arg	Gln	Asn	Arg	Arg	Gly	Gly	Phe	Gln	Val	Phe
65					70					75					80
Tyr	Ser	Ile	Tyr	Gly	Leu	Glu	Gly	Lys	Val	Gln	Pro	His	Gln	Ala	Pro
				85					90					95	
Gly	Asp	Met	Leu	Cys	Asp	Ile	Thr	Glu	Asp						
															100
															105

(2) INFORMATIONS POUR LA SEQ ID NO: 281:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 514 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(282794..284335)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 281:

```

Ser Glu Gly Leu Glu Met Phe Val Ser Phe Asp Lys Ser Arg Cys Arg
1      5      10      15
Ala Asp Val Pro Asp Phe Phe Glu Arg Thr Gly Asn Phe Leu Leu His
20      25      30
Cys Val Ala Arg Gly Ile Asn Val Leu Tyr Arg Val Lys Gln Ile Pro
35      40      45
Asn Tyr Pro Ser Cys Tyr Phe Ser His Lys Glu Ile Ser Cys Cys Arg
50      55      60
Arg Ile Ala Asn Ile Val Ile Cys Ile Leu Thr Gly Pro Leu Met Leu
65      70      75      80
Leu Ala Thr Val Leu Gly Leu Leu Ala Tyr Arg Phe Ser Ser Thr Tyr
85      90      95
Gln Thr Ser Leu Gln Glu Arg Phe Arg Tyr Lys Tyr Glu Gln Lys Gln
100     105     110
Ala Leu Asp Glu Tyr Arg Asp Arg Glu Glu Lys Val Ile Thr Leu Gln
115     120     125
Lys Phe Cys Arg Gly Phe Leu Val Arg Asn His Leu Leu Asn Gln Glu
130     135     140
Thr Leu Thr Thr Cys Lys Gln Trp Gly Gln Lys Leu Leu Glu Gly Glu
145     150     155     160
Lys Phe Pro Arg Val Pro Glu Gly Arg Ser Leu Val Tyr Ile Ser Lys
165     170     175
Gln Phe Pro Ser Leu Val Glu Asn Phe Leu Phe Glu Glu Lys Leu Pro
180     185     190
Val Ser Arg Ile Ser Val Asp Ser Met Cys Leu Tyr Lys Glu Asn Pro
195     200     205
Gln Ala Phe Asp Glu Ala Ile Lys Glu Leu Leu Phe Leu Phe Lys Glu
210     215     220
Val His Phe Arg Asp Phe Val Val Glu Thr Glu Ser Pro Thr Asp Asp
225     230     235     240
Phe Pro Leu Ala Val Lys Val His Asn Tyr Trp Val Cys Pro Arg Tyr
245     250     255
Asp Asn Leu Pro Leu Phe Ile Gln Glu Gly Lys Asp Gly Ser Pro Glu
260     265     270
Gly Arg Ile Gly Leu Val Asp Leu Glu Thr Phe Ser Trp Ser Pro His
275     280     285
Pro Cys Pro Val Glu Glu Leu Ala Val Met Phe Pro Met Ser Lys Glu
290     295     300
Leu Leu Met Thr Glu Ala Lys Lys Leu Gln Ile Pro Phe Ser Thr Lys
305     310     315     320
Glu Val Glu Arg Ser Val Glu Lys Gly Leu Ala Phe Phe Glu His Met
325     330     335
Leu Gly His Pro Asp Phe Cys Ser Gln Lys Ser Val Thr Pro Leu Arg
340     345     350
Asn Cys Ala Pro Tyr Leu His Leu Glu Val Trp Arg Phe Ser Leu Lys
355     360     365
Ile Phe Asp Ile Leu Lys Ala Ala Ile Arg Leu Asn Gly Ala Leu Asn
370     375     380
Val Leu Leu Ser Pro Asp Ile Arg Glu Arg Leu Ser Ala Ile Ser Asp
385     390     395     400
Lys Gln Trp Leu Ala Ile Ser Ser Gln Val Thr Ser Ser Leu Leu Glu
405     410     415
Gln Val Ser Thr Asn Ile Tyr Gln Ser His Thr Glu Glu Ala Lys Arg
420     425     430
Val Asn Ser Ser Gly Thr Phe Ile Met Cys Arg Ser Pro Ile Phe Arg
435     440     445

```

Lys Ser Ile Phe Ile Lys Asn Leu Pro Glu Leu Leu Asn Lys Lys Leu
 450 455 460
 Gln Leu Leu Pro Glu Glu Lys Glu Ile Ser Glu Ala Leu Ala Ser Leu
 465 470 475 480
 Cys Leu Arg Ala Val Met Glu Glu Leu Val Ala Thr Gly Asn Ile Tyr
 485 490 495
 Ser Tyr Asp Ser Met Asp Asp Phe Phe Glu Gly Gln Tyr Cys Arg Ile
 500 505 510
 Arg Tyr

(2) INFORMATIONS POUR LA SEQ ID NO: 282:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 112 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 284460..284795

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 282:

Lys Ile His Lys Lys Ile Lys Lys Cys Leu Thr Thr Thr Leu Leu Pro
 1 5 10 15
 Asn Leu Phe Ser Leu Phe Thr Asn Arg Asn Arg Glu Thr Leu Met Ile
 20 25 30
 Val Thr Phe Asp Lys Tyr Leu Ala Pro Glu Leu Gly Pro Asp Pro Leu
 35 40 45
 Glu Arg Leu Gly Asn Val Leu Leu Tyr Pro Ile Ile Arg Gly Phe Gly
 50 55 60
 Ser Leu Val Ser Val Lys Thr Leu Gly Glu Lys Arg Phe Leu Cys Phe
 65 70 75 80
 Ser Asp Lys Val Val Ser Leu Cys Val Asn Ala Phe Phe Val Trp Tyr
 85 90 95
 Ala Ile Phe Ser Gln His Leu Leu Arg Val Cys Ser Leu Cys Glu Gly
 100 105 110

(2) INFORMATIONS POUR LA SEQ ID NO: 283:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 286 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 284817..285674

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 283:

Arg Pro Ile Lys Leu His Glu Leu Phe Leu Ile Val Leu Leu Lys Arg
 1 5 10 15
 Glu Thr Arg Leu Arg Ser Leu Ser Lys Asn Asn Ala Pro Pro Leu Ser

```

                20                25                30
Leu Tyr Lys Asn Ile Tyr Val Ala Arg Lys Pro Leu Val Asp Arg Asp
                35                40                45
His Phe Pro Lys Tyr Arg Thr Ile Cys Asp Ala Ile Met Glu Gly Asn
                50                55                60
Leu Glu Asn Ile Arg Phe Ser Asp Lys Thr Gly Glu Ser Val Tyr Ser
65                70                75                80
Ser Lys Glu Leu Pro Ser Val Leu Phe Lys Arg Ile Gly Gln Lys Asn
                85                90                95
Ala Lys Gln Arg Val Leu Asn Asn Ile Ala Leu Asn Ala Tyr Leu Ala
                100                105                110
Lys Thr Gly Val Asp Gly Leu Gln Val Leu Ser Ala Ser Thr Tyr Lys
                115                120                125
Asp Phe Leu Ile Glu Asp Lys Pro Phe Gly Lys Gly Ala Leu Asp Thr
130                135                140
Leu Ile Ala Tyr Arg Leu Asn Pro Ser Leu Phe Asp Arg Ala Val Lys
145                150                155                160
Ser Leu Cys Lys Leu Phe Ser Phe Tyr His Cys Pro Asp Leu Phe Val
                165                170                175
Lys Ser Gly Asp Leu Leu Lys Asp Ser Pro His Ser Lys Leu Leu Leu
                180                185                190
Gly Phe Lys Glu Asn Asn Glu Ser Leu Ala Ala Glu Ser Ala Thr Leu
                195                200                205
Gln Pro Ile Leu Tyr Leu Thr Gly Ile Gln Cys Ile Leu Glu Glu Pro
210                215                220
Thr Pro Asp Leu Glu Ala Lys Leu Ser Ser Leu Phe Pro Tyr His Lys
225                230                235                240
Thr Leu Ile Gln Gln Glu Leu Ser Lys Leu Arg Val Ser Lys Pro Lys
                245                250                255
Val Glu Ala Ser Lys Glu Pro Thr Pro Pro Ser Thr Tyr Asp Glu Arg
                260                265                270
Leu Lys Ser Ser Pro Pro Thr Glu Met Glu Asn Phe Tyr Asp
275                280                285

```

(2) INFORMATIONS POUR LA SEQ ID NO: 284:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 167 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 285637..286137

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 284:

```

Lys Ala Leu Pro Leu Gln Lys Trp Lys Ile Phe Met Thr Glu Gln Pro
1                5                10                15
His Arg Leu Ser Glu Glu Ala Arg Ser Ile Ala Asn Glu Ala Lys Glu
                20                25                30
Arg Leu Leu Lys Leu Asn Asp Lys Pro Glu Leu Ser Arg Pro Tyr Leu
35                40                45
Val Lys Gly Phe Leu Ser Lys Ile Ser Arg Gly Ile Ser Asp Lys Glu
50                55                60
Ala Ala Ser Lys Phe Ser Lys Ala Ile Val Thr Ser Leu Leu Gly Tyr
65                70                75                80

```



```

Leu Trp Asn His Ile Leu Gln Asn Lys Glu Arg Ile Leu Ser Ala Asp
      85                      90                      95
Ala Arg Asp Leu Glu Ala His Ser Ala Leu Leu Asp Thr Lys Glu Ile
      100                    105                    110
Leu Ala Leu Cys Lys Tyr Phe Ala Ile Asn Arg Cys Thr Trp Leu Ser
      115                    120                    125
Ser Ser Ser Thr Gln Glu Glu Glu Asn Leu Ile Cys Gln Asp Ile Ala
      130                    135                    140
Lys Glu Met Phe Ser Ser Leu Tyr Met Leu Leu Trp Asn Asn Ser Gly
145                      150                      155                      160
Ser Glu Asp Met Ile Phe Gln
      165

```

(2) INFORMATIONS POUR LA SEQ ID NO: 285:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 286357..286677

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 285:

```

Ser Lys Thr Phe Arg Arg Arg Lys Lys Ser Phe Phe Phe Ser Met Ser
1      5                      10                      15
Val Asn Arg Asn His Asn Asn Phe Pro Pro Tyr Gly Glu Asn Glu Thr
      20                    25                    30
Pro Pro Pro Glu Ser Gln Pro Thr Asp Gly Pro Glu Asp Pro Ser Met
      35                    40                    45
Gln Gly Ala Tyr Tyr Ile Ala Pro Glu Asp Leu Pro Gln His Gln Leu
      50                    55                    60
Ala Ala Ala Val Glu Gly Leu His Ile Gly Ser Thr Leu Asn Pro Thr
65      70                    75                    80
Ala Pro Glu Phe Thr Pro Gly Ala Val Ser His His Phe Glu Thr Phe
      85                      90                      95
Thr Pro Ser Phe Pro Pro Ala Pro Gln Gln Pro
      100                    105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 286:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 349 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 286852..287898

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 286:

```

Pro Gln Ala Thr Ala Arg Asp Arg Gly Asp Leu Glu Lys Glu Ala Asn

```

```

1          5          10          15
Asn Thr Asn Ser Phe Ala Thr Gln Ala Ile Glu Thr Thr Pro Ser Asn
20          25          30
Ile Ser Pro Cys Phe Asn Leu His Gly Glu Ala Ile Gln Leu Phe Ser
35          40          45
Thr Glu Ser Gly Pro Ser Pro Leu Arg Ala Ile Leu Gln Ala Ile Lys
50          55          60
Gln Ala Lys Tyr His Ile Tyr Ile Gln Ile Tyr Arg Phe Thr Ser Glu
65          70          75          80
Glu Ile Ala Ala Ala Leu Leu Glu Arg Ala Asn Asn Gly Val Arg Ile
85          90          95
His Tyr Asn Ile Asn Thr Ser Ala Ala Gln Lys Pro Leu Phe Asp Ile
100          105          110
Leu Thr Cys Lys Phe Lys Ala Thr Asn Gln Ala Arg Leu His Cys Lys
115          120          125
Asn Ile Val Val Asp Gly Ser Leu Val Ile Thr Gly Ser Ala Asn Phe
130          135          140
Ser Asp Ala Ala Phe Ser Arg Asp Ile Asn Leu Val Ala Ile Ile Arg
145          150          155          160
Asn Pro Ser Leu Gly Gln Leu Val Val Ser Gln Gln Ser Gly Trp Ile
165          170          175
Thr Gly Gly Ser Gln Gln Ile Glu Tyr Cys Ser Leu Tyr Cys His Asn
180          185          190
His Gln Gly Val Asp Glu Val Val Lys Ala Val Gln Ser Ala Val Lys
195          200          205
Thr Ile Arg Val Ala Met Leu Val Leu Ser His Glu Val Leu His
210          215          220
Ala Leu His Gln Ala Ala Gln Arg Gly Val Glu Val Thr Val Leu Val
225          230          235          240
Asn Pro His Asn Lys Ala Val Leu Phe Tyr Ala Leu Gln Asp Leu Asn
245          250          255
Ser Lys Val Lys Leu Arg Asp Val Val Val Glu Glu Asn Ala Leu Leu
260          265          270
His Cys Lys Val Gly Leu Ile Asp Thr Asn Leu Leu Ile Thr Gly Ser
275          280          285
Ala Asn Trp Thr Val Arg Gly Leu Gln Tyr Asn Ile Glu Asp Leu Ile
290          295          300
Phe Ile His Gln Pro Thr Pro Ser Gln Leu Ser Ala Phe Phe Asn Leu
305          310          315          320
Trp Glu Gln Ala Met Ser Leu Ser Arg Glu Val Thr Ala Lys Lys Ile
325          330          335
Lys Lys Ser Ala Arg Ala Gln His Lys Tyr Asp Asp Glu
340          345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 287:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 367 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 288127..289227

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 287:

```

Ser Leu Ile Leu Glu Asp Ala Val Ala Leu Asp Pro Pro Pro Pro Pro
1      5      10      15
Pro His Thr Ser Gln Asn Thr Pro Ser Pro Lys Asp Ser Ser Leu Val
20      25      30
Ala Arg Thr Asp Lys Ala Ala Thr Asp Ile Phe Asn Ser Ala Lys His
35      40      45
Lys Ala Ile Glu Thr Thr Lys Arg Ser Asp Gln Gln Ser Arg Ser Leu
50      55      60
Pro Ile Leu His Leu Leu Ala Ala Asp Pro Glu Pro Ile Val Phe His
65      70      75      80
Ser Thr His Gln Thr Asn His Asn Asp Pro Gln Arg Met Leu Cys Asp
85      90      95
Ala Ile Leu Gln Ala Asn Arg Ile Ile Thr Met Arg Ile Phe Asn Ile
100     105     110
Gly Ser Pro Glu Ile Ile Arg Ala Leu Ile Arg Ala Val Arg Arg Asn
115     120     125
Ile Pro Val Ile Val Ser Ala Trp Asn Phe Pro Asn Leu Ser Asn Trp
130     135     140
Asp Arg Glu Ser Lys Leu Tyr Val Glu Leu Arg Gly Asn Pro Gln Ile
145     150     155     160
Cys Leu His Lys Lys Thr Thr Leu Ile Asp Asn Gln Leu Thr Ile Ile
165     170     175
Gly Thr Ala Asn Tyr Thr Lys Ser Ser Phe Phe Lys Asp Ile Asn Leu
180     185     190
Thr Ala Leu Ile Gln Asn Pro Ala Leu Tyr Ser Leu Ile Leu Ser Gly
195     200     205
Thr Arg Gly Ser Val Ser Ile Gly Ser Gln Thr Ile Ser Tyr Tyr Pro
210     215     220
Leu Pro Phe Pro Gln Ser Asn Thr Lys Thr Leu Pro Ile Ile Gln Glu
225     230     235     240
Ile Gln Lys Ala Gln Arg Thr Ile Lys Ile Ala Met Asn Ile Phe Ser
245     250     255
His Pro Glu Ile Phe Leu Ala Leu Glu Gln Ala Arg Leu Arg Gly Val
260     265     270
Thr Ile Thr Ile Val Ile Asn Lys Glu Ser Ala His Thr Leu Asp
275     280     285
Ile Leu His Arg Ile Ser Ala Leu Leu Leu Leu Lys Ser Val Thr Thr
290     295     300
Val Asp Ser Leu His Ala Lys Ile Cys Leu Ile Asp Asp Gln Thr Leu
305     310     315     320
Ile Phe Gly Ser Pro Asn Trp Thr Tyr His Gly Met His Lys Asn Leu
325     330     335
Glu Asp Leu Leu Ile Val Thr Pro Leu Thr Pro Lys Gln Ile His Ser
340     345     350
Ile Gln Glu Ile Trp Ala Phe Leu Leu Lys Asn Ser Ser Pro Val
355     360     365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 288:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 312 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 289744..290679

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 288:

```

Met Leu Ala Gly Ser Lys Arg Lys His Lys Thr Pro Glu Asp Thr Ser
1      5      10      15
Ser Ser Ser Ser Lys Arg Ala Arg Ser Ser Ser Ser Gln Val Val Pro
20      25      30
Arg Leu Leu Gln His His Glu Leu Ile Gln Leu Tyr Ser Ala His Gln
35      40      45
Gln Arg Asn Asn Glu Pro Val Lys Met Ile Cys Glu Thr Ile Leu Gln
50      55      60
Ala Lys Arg Ser Val Leu Leu Lys Val Phe Asn Ile Gly Ser Pro Arg
65      70      75      80
Ile Leu Ala Ala Leu Ala Glu Ala Ser Asn Arg Ala Pro Val Ser Val
85      90      95
His Tyr Gln Met Gly Pro Phe Ser Lys His Cys Thr Glu Gly Asn Val
100     105     110
Gln Phe Arg Pro Arg Arg Gly Cys Ser Leu Leu His Arg Lys Thr Leu
115     120     125
Leu Ile Asp Asn Asn Ile Val Val Thr Gly Thr Ala Asn Tyr Thr Glu
130     135     140
Ala Ser Leu Glu Lys Asp Val Asn Leu Thr Ala Lys Ile Phe Ser Glu
145     150     155     160
His Leu Tyr Arg Trp Ala Phe Arg His Asp Arg Gly Glu Val Arg Val
165     170     175
Gly Ser Gln Gln Val Ser Tyr Tyr Ser Leu Ser Gln Ile Arg Arg Asp
180     185     190
Leu Cys Val Lys Ala Ile Leu Glu Ala Asn Gly Ile Val Leu Arg Glu
195     200     205
Arg Thr Cys Glu Gly Ile Leu His Thr Lys Val Cys Cys Ile Asp Ser
210     215     220
Ser Thr Leu Ile Ile Gly Ser Val Asn Trp Ser Arg Gly Gly Leu Thr
225     230     235     240
Leu Asn Leu Glu Glu Phe Leu Ile Ile Asn Pro Leu Thr Glu Thr Gln
245     250     255
Leu Glu Cys Tyr Asn Glu Leu Trp Ala Tyr Ile Glu Thr Asn Ser Arg
260     265     270
Leu Met Thr Lys Glu Leu Ile Gln Leu His Glu Lys Arg Lys Lys Ser
275     280     285
Ile Thr Asp Pro Lys Gln Thr Ser Ser Ser Thr Gln Asp Glu Glu Asn
290     295     300
Ala Ser Thr Ser Ala Glu Gln Gln
305      310

```

(2) INFORMATIONS POUR LA SEQ ID NO: 289:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 290828..291535

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 289:

```

Leu Phe Ser Ser Ala Ser Pro Arg Thr Phe Thr Ser Pro Phe Phe Cys
1      5      10      15
Arg Ile Ile Ser Tyr Ser Ser Val Arg Phe Lys Ser Leu Ser Ile Phe
      20      25      30
Thr Ala Phe Arg Gln Ser Ser Glu Ser Arg Asn Ser Pro Leu Arg Glu
      35      40      45
Thr Thr Gly Ser Ser Ser Arg His Arg Tyr His Arg His Gly Glu Thr
      50      55      60
Ser Ser Ser Ser Arg Ile Glu Thr Val Gly Ser Arg His Phe Ser Ser
65      70      75      80
Arg Arg Glu Ser Ser Arg Thr Gly Ser Arg Ser Ser Arg His Ser Glu
      85      90      95
Arg Ala Arg His His Glu Ser Arg Ser His Arg His Ser Ser Ser Ser
      100      105      110
Arg His His Val Thr Arg Ser Gln Ser Ser Ala Leu Pro Gln Leu Gln
      115      120      125
Glu Arg Pro Val Pro His Pro Leu Ala Glu Arg Glu Leu Ile Thr Phe
      130      135      140
His Ser Val His Gln Gln Gln Asn Asn Asn Pro Leu Arg Met Ile Cys
145      150      155      160
Asp Thr Ile Arg Gln Ala Gln Arg Gly Ile Phe Met Arg Ile Tyr Ala
      165      170      175
Ile Ser Ser Asp Asp Ile Ile Gln Ser Leu Ile Gln Thr Ser His His
      180      185      190
Val Pro Val Glu Val Lys Tyr His Cys Gly Glu Ser Leu Pro Val Ala
      195      200      205
Cys Gln Asn Ser Arg Val Val Leu Arg Pro Thr Asn Gly Arg Thr Leu
      210      215      220
Gln His Lys Lys Leu Cys Trp Leu Ile Ser Lys Gln
225      230      235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 290:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 209 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 291604..292230

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 290:

```

Glu Ser Ser Glu Leu His Asp Ala Val Phe Ser Glu Arg Pro Gln Leu
1      5      10      15
Val His Val Gly Pro Gln Leu Leu Asn Tyr Ile Pro Ile Gln Arg Leu
      20      25      30
Ile Pro Asn Ala Ala Ser Lys Met Ile Leu Asn Ala Ile Asn Gln Ala
      35      40      45
Thr Asp Ser Ile Phe Val Leu Met Tyr Ile Phe Leu Ser Pro Glu Phe
      50      55      60
Phe Leu Ala Leu Ala Gln Ala Met Arg Arg Gly Val Arg Val Lys Val
65      70      75      80
Ile Ile Asp Asn His Ser Lys Gln Asp Thr Cys Lys Leu Leu Ser Lys
      85      90      95
Leu Gly Ile Gln Leu Pro Leu Tyr Glu Arg Lys Thr Glu Gly Ile Leu

```

```

              100              105              110
His Thr Lys Ile Cys Cys Ile Asp Asn Lys Thr Pro Ile Phe Gly Ser
              115              120              125
Ala Asn Trp Ser Gly Ala Gly Met Ile Lys Asn Phe Glu Asp Leu Phe
              130              135              140
Ile Leu Arg Pro Ile Thr Glu Thr Gln Leu Gln Ala Phe Met Asp Val
145              150              155              160
Trp Ser Leu Leu Glu Thr Asn Ser Ser Tyr Leu Ser Pro Glu Ser Val
              165              170              175
Leu Thr Ala Pro Thr Pro Ser Ser Arg Pro Thr Gln Gln Asp Thr Asp
              180              185              190
Ser Asp Asp Glu Gln Pro Ser Thr Ser Gln Gln Ala Ile Arg Met Arg
              195              200              205
Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 291:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 241 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 292326..293048

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 291:

```

Arg Leu Ser Ser Ser Ser Val Ser Leu Leu Phe Phe Lys Ala Ser Ser
1              5              10              15
Phe His Tyr Arg Val Ser Ile Thr Val Gln Pro Gly Glu Phe Leu Met
              20              25              30
Thr Lys Pro Ser Xaa Leu Tyr Val Ile Gln Pro Phe Ser Val Phe Asn
              35              40              45
Pro Arg Leu Gly Arg Phe Ser Ile Asp Ser Asp Thr Tyr Ile Glu Glu
              50              55              60
Glu Asn Arg Leu Ala Ser Phe Ile Glu Ser Leu Pro Leu Glu Ile Phe
65              70              75              80
Asp Ile Pro Ser Phe Met Glu Thr Ala Ile Ser Asn Ser Pro Tyr Ile
              85              90              95
Leu Ser Trp Glu Thr Thr Lys Asp Gly Ala Leu Phe Thr Ile Leu Glu
              100              105              110
Pro Lys Leu Ser Ala Cys Ala Ala Thr Cys Leu Val Ala Pro Ser Ile
              115              120              125
Gln Met Lys Ser Asp Ala Glu Leu Leu Glu Glu Ile Lys Gln Ala Leu
              130              135              140
Leu Arg Ser Ser His Asp Gly Val Lys Tyr Arg Ile Thr Arg Glu Ser
145              150              155              160
Phe Ser Pro Glu Lys Lys Thr Pro Lys Val Ala Leu Val Asp Asn Asp
              165              170              175
Ile Glu Leu Ile Arg Asn Val Asp Phe Leu Gly Arg Ala Val Asp Ile
              180              185              190
Val Lys Leu Asp Pro Ile Asn Ile Leu Asn Thr Val Ser Glu Glu Asn
              195              200              205
Ile Leu Asp Tyr Ser Phe Thr Arg Glu Thr Ala Gln Leu Ser Ala Asp
210              215              220

```

Gly Arg Phe Gly Ile Pro Pro Gly Thr Lys Leu Phe Ser Lys Pro Ser
225 230 235 240
Phe

(2) INFORMATION POUR LA SEQ ID NO: 292:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 508 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 293330..294853

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 292:

Lys 1	Pro	Asn	Pro	His 5	Arg	Gly	Lys	Arg	Pro 10	Ser	Arg	Leu	Thr	Arg 15	Ile
His	Arg	Ile	Glu	Val	Gln	Leu	Pro	Asp 25	Ser	Ser	Arg	Ile	Pro 30	Tyr	Asp
Cys	Ser	Cys 35	Ile	Asn	Arg	Tyr	Gly 40	Ile	Phe	Pro	Arg	Phe 45	Asn	Pro	Asn
Gln	Asn 50	Lys	Leu	Asn	Val	Ile 55	Arg	Lys	Ile	Lys	Ser 60	Gly	Phe	Gln	Arg
Ser 65	Leu	Asp	Asp	Tyr	His 70	Ile	Tyr	Gln	Ile	Glu 75	Arg	Lys	Xaa	Xaa	Phe 80
Ser	Phe	Ser	Pro	Lys 85	His	Arg	Ser	Leu	Ser 90	Ser	Thr	Ser	His	Ser 95	Glu
Asp	Ser	Asp	Leu 100	Asp	Leu	Ser	Glu	Ala 105	Ala	Ala	Phe	Ser	Gly 110	Ser	Leu
Thr	Cys	Glu 115	Phe	Val	Lys	Lys	Ser 120	Thr	Gln	His	Ala	Lys 125	Asn	Thr	Val
Thr	Cys 130	Ser	Thr	Ala	Ala	His 135	Ser	Leu	Tyr	Thr	Leu 140	Lys	Glu	Asp	Asp
Ser 145	Ser	Asn	Pro	Ser	Glu 150	Lys	Arg	Leu	Glu	Asn 155	Cys	Phe	Arg	Asn	Trp 160
Ile	Asp	Asn	Lys	Leu 165	Ser	Ala	Asn	Ser	Pro 170	Asp	Ser	Trp	Ser	Ala	Phe 175
Ile	Gln	Lys	Phe 180	Gly	Thr	His	Tyr 185	Ile	Ala	Ser	Ala	Thr 190	Phe	Gly	Gly
Ile	Gly 195	Phe	Gln	Val	Leu	Lys 200	Leu	Ser	Phe	Glu	Gln 205	Val	Glu	Asp	Leu
His 210	Ser	Lys	Lys	Ile	Ser 215	Leu	Glu	Thr	Ala	Ala 220	Ala	Asn	Ser	Leu	Leu
Lys 225	Gly	Ser	Val	Ser	Ser 230	Ser	Thr	Glu	Ser	Gly 235	Tyr	Ser	Ser	Tyr	Ser 240
Ser	Thr	Ser	Ser	Ser 245	His	Thr	Val	Phe	Leu 250	Gly	Gly	Thr	Val	Leu	Pro
Ser	Val	His	Asp 260	Glu	Arg	Leu	Asp	Phe 265	Lys	Asp	Trp	Ser	Glu 270	Ser	Val
His	Leu 275	Glu	Pro	Val	Pro	Ile	Gln 280	Val	Ser	Leu	Gln 285	Pro	Ile	Thr	Asn
Leu	Leu 290	Val	Pro	Leu	His	Phe 295	Pro	Asn	Ile	Gly 300	Ala	Glu	Leu	Ser	
Asn	Lys	Arg	Glu	Ser	Leu	Gln	Gln	Ala	Ile	Arg	Val	Tyr	Leu	Lys	Glu

```

305          310          315          320
His Lys Val Asp Glu Arg Gly Glu Arg Thr Thr Phe Thr Ser Gly Ile
          325          330          335
Asp Asn Pro Ser Ser Trp Phe Thr Leu Glu Ala Ala His Ser Pro Leu
          340          345          350
Val Val Ser Thr Pro Tyr Val Ala Ser Trp Ser Thr Leu Pro Tyr Leu
          355          360          365
Phe Pro Thr Leu Arg Glu Arg Ser Ser Ala Thr Pro Ile Val Phe Tyr
          370          375          380
Phe Cys Val Asp Asn Asn Glu His Ala Ser Gln Lys Ile Leu Asn Gln
385          390          395          400
Ser Tyr Cys Phe Leu Gly Ser Leu Pro Ile Arg Gln Lys Ile Phe Gly
          405          410          415
Ser Glu Phe Ala Ser Phe Pro Tyr Leu Ser Phe Tyr Gly Asn Ala Lys
          420          425          430
Glu Ala Tyr Phe Asp Asn Thr Tyr Tyr Pro Thr Arg Cys Gly Trp Ile
          435          440          445
Val Glu Lys Leu Asn Thr Thr Gln Asp Gln Phe Leu Arg Asp Gly Asp
          450          455          460
Glu Val Arg Leu Lys His Val Ser Ser Gly Lys Tyr Leu Ala Thr Thr
465          470          475          480
Pro Leu Lys Asp Thr His Gly Thr Leu Thr Arg Thr Thr Asn Cys Glu
          485          490          495
Asp Ala Ile Phe Ile Ile Lys Lys Ser Ser Gly Tyr
          500          505

```

(2) INFORMATIONS POUR LA SEQ ID NO: 293:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 225 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(295010..295684)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 293:

```

Met Val Ile Leu Val Glu Ala Lys His Ile Ser Lys Val Ile Gln Gln
1          5          10          15
Gln Asp Val Cys Ile Pro Ile Leu Lys Asp Val Ser Phe Gln Leu His
          20          25          30
Ala Gly Glu Val Val Ala Ile Thr Gly Ala Ser Gly Ser Gly Lys Ser
          35          40          45
Ser Leu Leu His Leu Leu Gly Thr Leu Asp Gln Pro Ser Ser Gly Gln
          50          55          60
Ile Leu Phe Phe Gly Lys Gln Val Arg Arg Glu Glu Leu Pro Ile Phe
65          70          75          80
Arg Asn Cys Arg Ile Gly Phe Ile Phe Gln Asn Phe Tyr Leu Leu Glu
          85          90          95
Asp Asp Ser Val Ile Asn Asn Val Leu Met Pro Ala Gln Ile Ala Arg
          100          105          110
Lys Asp Thr Gly Gln Lys Ser Lys Ala Arg Glu Arg Ala Leu Ala Leu
          115          120          125
Leu Glu Ser Val Gly Leu Val Asp Arg Arg Asp Glu Lys Gly Ser Leu
          130          135          140

```



```

Leu Ser Gly Gly Glu Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Met
145                      150                      155                      160
Asn Asp Pro Glu Ile Val Leu Ala Asp Glu Pro Ser Gly Asn Leu Asp
                      165                      170                      175
His Arg Thr Ala Asp Thr Ile His Glu Leu Leu Leu Ala Leu Ala Glu
                      180                      185                      190
Lys His Arg Gly Val Leu Ile Val Thr His Asp Arg Glu Leu Ala Glu
                      195                      200                      205
Lys Cys His Arg Glu Glu Ile Leu Arg Asp Gly Thr Leu Met Gln Arg
210                      215                      220
Gln
225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 294:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 215 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(295692..296336)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 294:

```

Gly Ile Gly Cys Ile His Pro Leu Gly Ile Arg Arg Leu Gly Met His
1                      5                      10                      15
Asn Gly Trp Gln Val Phe Leu Pro Ser Val Gln Asp Ile Pro Val Met
                      20                      25                      30
Lys Gln Ser Ile Gln Lys Ile Phe Lys Glu Ser Glu Val Ser Ser Tyr
                      35                      40                      45
Trp Glu Ile Ser Ser Leu Tyr Asp Tyr Glu Phe Phe Lys Pro Ile Leu
50                      55                      60
Asp Gln Leu Gln Ser Asp Gln Val Leu Phe Ser Ile Val Ser Phe Ile
65                      70                      75                      80
Val Leu Ile Val Ala Cys Ser Asn Ile Val Thr Met Ser Ile Leu Leu
                      85                      90                      95
Val Asn Asn Lys Lys Lys Glu Ile Gly Ile Leu Lys Ala Met Gly Val
100                      105                      110
Ser Ser Ser Arg Leu Gln Leu Val Phe Gly Leu Cys Gly Ala Cys Ser
115                      120                      125
Gly Leu Val Gly Ala Leu Leu Gly Ser Ile Leu Ala Ala Leu Thr Leu
130                      135                      140
Lys Asn Leu Gly Val Leu Thr His Trp Leu Ser Lys Leu Gln Gly Arg
145                      150                      155                      160
Glu Ala Phe Asn Pro Ser Phe Phe Gly Glu Gln Leu Pro Gln Asp Phe
                      165                      170                      175
His Leu Pro Thr Val Ile Cys Leu Ser Leu Gly Ala Leu Val Leu Ala
180                      185                      190
Ala Ile Ser Gly Ala Ile Pro Ala Gln His Val Ala Arg Met Gln Val
195                      200                      205
Ser Asp Ile Leu Lys Ser Glu
210                      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 295:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 332 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(296243..297238)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 295:

```

Val Gly Phe Tyr Leu Ala Ser Lys Ile Pro Lys Gly Val Met Lys Leu
1          5          10          15
Glu Leu Leu Leu Ala Phe Lys Tyr Leu Ile Pro Lys Arg Lys Arg Leu
20          25          30
Ser Ser Ser Ile Val Ser Ala Phe Ser Ile Gly Ile Val Ala Leu Val
35          40          45
Val Trp Leu Ser Val Val Phe Met Ser Val Ile His Gly Leu Gln Gln
50          55          60
Arg Trp Val Gly Asp Leu Ala Ser Leu His Ser Ser Ile Arg Ile Glu
65          70          75          80
Pro Ser Asp Lys Tyr Tyr Glu Ser Tyr Tyr Tyr Gln Ile Asp Ser His
85          90          95
Ala Glu Ala Ser Gln Tyr Ile Tyr Lys Thr Ile Gly Glu Lys Leu Leu
100          105          110
Cys Glu Gln Thr Asp Pro Tyr Asp Pro Asp Val Asp Phe Leu Leu Pro
115          120          125
Glu Ala Phe Pro Asp Pro Glu Phe Ser Asp Asn Gly Glu Met Ile Asp
130          135          140
Pro Val Arg Thr Ala Asn Glu Arg Met Leu Ser Leu Phe Ser Ser Arg
145          150          155          160
Lys Gly Ser Phe Val Glu Phe Glu Glu Gly Met Gly His Val His Met
165          170          175
Asp Arg Ala Phe Arg Gly His Lys Gly Glu Pro Arg Ala Leu Ser Gln
180          185          190
Tyr Ile Ala Tyr Ser Ser Asp Ile Leu Tyr Gln Gln Arg Val Leu Pro
195          200          205
Phe Glu Glu Thr Asp Tyr Ser Thr Glu Val Leu Asn Arg Phe Asn Ala
210          215          220
Ser Ser Glu Gly Trp Leu Ala Asp Phe Leu Val Leu Gln Glu Lys Phe
225          230          235          240
Arg Gly Met Ser Val Ile Leu Pro Val Val Tyr Arg Asp Gln Gly Tyr
245          250          255
Arg Val Gly Asp Thr Ala Ser Leu Ser Val Phe Ser Val Lys Lys Glu
260          265          270
Gly Glu Val Arg Phe Pro Leu Arg Val Ile Gly Phe Tyr Asn Pro Gly
275          280          285
Val Ser Pro Phe Gly Gly Lys Thr Ile Phe Ile Asp Lys Glu Leu Ala
290          295          300
Ala Ser Ile Arg Ser Glu Ser Glu Gly Leu Val Cys Ile Met Ala Gly
305          310          315          320
Arg Tyr Phe Phe Leu Val Phe Lys Ile Ser Leu Ser
325          330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 296:

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 297791..298735

Met 1	Lys	Lys	Phe	Ala 5	Thr	Phe	Leu	Cys	Val 10	Leu	Leu	Ser	Gly	Ser 15	Gly
Phe	Ala	Ala	Pro 20	Val	Glu	Ala	Pro	Gly 25	Phe	Pro	Ser	Ile	Pro 30	Glu	Thr
Tyr	Ile	Thr 35	Ile	Asn	Asp	Lys	Glu 40	Leu	Gly	Leu	Gln	Glu 45	His	Cys	Arg
Gly	Val 50	Asn	Val	Leu	Ser	Cys 55	Gly	Tyr	Asn	Leu 60	Val	Gly	Met	Phe	His
Thr 65	Pro	Thr	Thr	Pro	Met 70	Pro	Leu	Gly	Gly	Tyr 75	Pro	Thr	Val	Ile	Phe 80
Phe	His	Gly	Phe	Arg 85	Gly	Asn	Cys	Thr	Gly 90	Lys	Asp	Gly	Val 95	Tyr	Arg
Asp	Leu	Ala	Arg 100	Leu	Leu	Thr	Ala	Asn 105	Gly	Ile	Ala	Val	Ala 110	Arg	Phe
Asp	Met	Ala 115	Gly	Cys	Gly	Asn	Ser 120	Glu	Gly	Ile	Cys	Asp 125	Gln	Ile	Pro
Ala	Arg 130	Thr	Tyr	Leu	Arg	Asn 135	Gly	Glu	Asp	Ile 140	Leu	Ala	Thr	Val	Ala
Lys 145	Tyr	Pro	Glu	Val	Asn 150	Pro	His	Arg	Ile 155	Gly	Ile	Ala	Gly	Val	Ser 160
Leu	Gly	Cys	His 165	Thr	Thr	Ile	His	Leu	Ala 170	Ser	Thr	Tyr	Arg 175	Pro	Arg
Asp	Tyr	Thr 180	Val	Gln	Ala	Ile	Ser	Val 185	Trp	Ala	Pro	Ile 190	Ala	Asp	Gly
Val	Ile 195	Leu	Leu	Lys	Glu	Ile	Cys 200	Ala	Thr	Ile	Gly	Leu 205	Thr	Met	Thr
Gln	Phe 210	Ser	Asp	Met	Gly	Glu	Val 215	Gly	Lys	Ala 220	Phe	Gly	Phe	Lys	Gln
Leu 225	Pro	Leu	Lys	Leu	Cys 230	Arg	Asp	Asp	Ile	Asp 235	Phe	Phe	Leu	Gly	Ile 240
Gln	Asp	His	Ile 245	Leu	Leu	Ser	Leu	Pro	Arg 250	Arg	Arg	Ile	Pro 255	Val	Leu
His	Gln	Gln 260	Gly	Leu	Glu	Asp	Arg	Val 265	Val	Ser	Thr	Ala 270	His	Gln	Arg
Leu	Phe 275	Leu	Gly	Ala	Ala	Pro	Ala 280	Gln	Met	Leu	Ser	Lys 285	Ser	Tyr	Pro
Glu	Thr 290	Pro	His	Glu	Ile	Ala 295	Leu	Ser	Pro	Tyr 300	Arg	Gln	Glu	Val	Leu
Gln 305	Glu	Ile	Leu	Thr	His 310	Phe	Gln	Ser	Xaa	Leu 315					

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 298905..300458

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 297:

```

Glu Lys Ser Thr Phe Leu Leu Val Arg Ile Thr Met Ile Asp Val Leu
1      5      10      15
Ile Met Gly Ala Asn Pro Ser Gly Leu Ile Leu Ala Ser Ile Leu Gln
20     25     30
Gln His Arg Ala Arg Ile Lys Val Ile Asp Ser Arg Asp Ser Ile Thr
35     40     45
Ala Ser Leu Pro Leu Pro Leu His Ser Leu Pro Val Val Leu Ser Ser
50     55     60
Ser Ser Leu Glu Leu Leu Asp Asn Ile Asn Leu Leu Gly Asp Leu Leu
65     70     75     80
Asp Lys Gly Arg Lys Ile Phe Gly Ala Arg Tyr His Trp Lys Gln Arg
85     90     95
Thr Val Leu Phe Lys Phe Asn Gln Ser Ser Ala Ser Arg Cys Pro Phe
100    105    110
Ser Leu Leu Ile Ser Tyr Asn Glu Leu Val Thr His Leu Leu Glu Glu
115    120    125
Phe Glu Arg Leu Gly Gly Val Val Asn Trp Ala Thr Arg Pro Val Thr
130    135    140
Gln Val Glu Gln Asn Leu Phe Ile Glu Ser Thr Lys Ser Ser Ser Gln
145    150    155    160
Val Tyr Glu Gly Arg Glu Ile Phe Thr Pro Lys Trp Ile Ile Ala Cys
165    170    175
Glu Met Asp Ala Asp Pro Asp Leu Lys Asp Leu Leu Lys Thr Gln Ile
180    185    190
Lys Thr Lys Lys Ile His Lys Glu Ala Leu Phe Val Asp Cys Glu Glu
195    200    205
Gly Glu Pro Phe Glu Glu Ser His Ile His Leu Leu Pro Val Thr Lys
210    215    220
Ser Phe Val Asn Phe Val Phe Tyr Asn Pro Tyr Arg Gly Ser Arg Gln
225    230    235    240
Leu Tyr Leu Ala Asn Thr Ser Gly Ser Leu Ser Ser Lys Phe Lys Asn
245    250    255
Lys Leu Leu Tyr Thr Tyr Ser Leu Ala Leu Ala Glu Asp Pro Leu Ser
260    265    270
Ile Ser Ser Ser Leu Leu Gln Tyr Pro Phe Cys His Asp Arg Tyr Ile
275    280    285
Phe Leu Gly Ser Ile Ala Asn Asn Leu Ser Phe Ser Tyr Leu Ser Gly
290    295    300
Val Asn Ser Asn Ile His Asp Ala Phe Asn Leu Gly Trp Lys Leu Leu
305    310    315    320
Pro Val Ile Lys Lys Ala Ala Ser Ser Gln Leu Ile Leu Ser Lys Glu
325    330    335
Leu Lys Thr Ser His Val Leu Pro His Phe Asn Glu Val His Gln Lys
340    345    350
Arg Ala Thr Lys Leu Leu Phe Ser Asn Met Tyr Thr Pro Ala Leu Met
355    360    365
Tyr Tyr Tyr Leu Lys Gly Cys Lys Gln Leu Asp Ala Ala Glu Gly Glu
370    375    380
Leu Tyr Tyr Pro Ser His Arg Ala Ser Lys Tyr Glu Ala Ser Asp Ile
385    390    395    400

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Ile Lys Val Ser Pro Asn Asp Lys Glu Ile Gln Gly Pro Arg Pro Gly
      405      410      415
Ser Arg Ala Leu Asp Ile Arg Leu Asp Thr Gly Asn Tyr Leu Leu Asp
      420      425      430
Ser Leu Lys Asn Ala Lys His Leu Leu Val Phe Phe Lys Glu Arg Pro
      435      440      445
Asp Leu Val His Ala Leu Leu Glu Glu Tyr Gly Glu Trp Val Asp Val
      450      455      460
Ile Val Thr Glu Asp Pro Lys Val His Lys Leu Tyr His Ala Asn Pro
      465      470      475      480
Glu Ser Leu Phe Ile Ile Arg Pro Asp Arg Tyr Ile Gly Tyr Arg Thr
      485      490      495
His Thr Phe Lys Leu His Glu Leu Ile Ser Tyr Leu Leu Arg Ile Phe
      500      505      510
Ala Ala Glu Asn Ala Asn
      515

```

(2) INFORMATIONS POUR LA SEQ ID NO: 298:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 542 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(300527..302152)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 298:

```

Gly Cys Leu Phe Ser Glu Glu Leu Val Ser Asp Gly Arg Lys Leu Pro
1      5      10      15
Tyr Pro Asp Leu Gly Asp Gln Asn Ile Lys His Leu Glu Lys Ile Arg
      20      25      30
Asp Val Tyr Gly Leu Asp Gly Val Ala Glu Leu Arg Val Ala Glu Ala
      35      40      45
Ala Leu Leu Gly Val Gln Lys Lys Leu Pro Glu Glu Gln Lys Gln Glu Ser
      50      55      60
Leu Lys Ser Ala Val Lys Ala Leu Arg Ala Asp Ala Lys Val Leu Asn
      65      70      75      80
Lys Lys Phe Lys Lys Leu Pro Glu Ser Tyr Gln Pro Gln His Ser Glu
      85      90      95
Val Thr Gly Val Gln Gly Val Thr Glu Gln Glu Ser Arg Asp Asp Val
      100      105      110
Leu Val Ala Gln Asp Met Ala Ala Ile Glu Glu Leu Gln Asp Gln Tyr
      115      120      125
His Ala Ala Cys Leu Gln Phe Glu Ser Val Ser Met Arg Phe Leu Ala
      130      135      140
Glu Gln Arg Lys Ala Lys Phe Leu Glu Lys Leu Leu Ile Gln Lys Arg
      145      150      155      160
Arg Asp Val Ser His Leu Ser His Gln Glu Ala His Tyr Thr Gln Val
      165      170      175
Val Ser His Leu Lys Glu Arg Ile Ser Met Arg Lys Gly Ala Ser Thr
      180      185      190
Gln His Ala Ser Lys Glu Glu Ile Ser Thr Lys Met Arg Glu Leu Leu
      195      200      205
Ser Leu Asp Asp Gln Leu Leu Lys Ala His Thr Ala Gln Asp Val Asn

```

210	215	220
Trp Asp Asn Ser Ile Asn Gly Gln Leu Gln Gln Gln Phe Lys Lys Leu		
225	230	235
Ser Glu Glu Gly Ser Leu Gln Lys Val Lys Ala Leu Leu Glu Leu Asn		
	245	250
Met Cys Leu Gly Asn Ala Gly Gln Thr Leu Tyr His Ser Arg Leu Lys		
	260	265
Arg Glu Val Phe Glu Ala Ser Cys Ser Asn Thr Ser Gln Gln Leu Leu		
	275	280
Gln Tyr Gly Glu Asp Leu Phe Ala Ser Tyr Asp Gly Ser Asp Arg Ser		
	290	295
Ala Leu Leu Arg Phe Val Leu Gly Ser Gly Tyr Glu Met Ile Ser Glu		
305	310	315
Ala Ser Ser Glu Leu Lys Ser Leu Arg Lys Arg Trp Lys Arg Ser Ala		
	325	330
Ser Gln Ala Ala Ile Ala Pro Glu Asp Tyr Glu Lys Val Cys Arg Val		
	340	345
Leu Glu Arg Phe Leu Lys Ala Arg Asp Ser Leu Arg Pro Lys Leu Gly		
	355	360
Leu Pro Leu Gly Lys Ser Ser Asp Ala Thr Val Gly Leu Gln His Gln		
	370	375
Ile Arg Asp Asn Gln Arg Val Lys Ala Arg Val Thr Ala Cys Tyr Gln		
385	390	395
Glu Ser Cys Arg Asn Val Leu Gln His Leu Glu Asp Trp Val Arg Lys		
	405	410
Thr Arg Gln Glu Ser Ala Glu Cys Gln Lys Val Glu Thr Lys Ile Arg		
	420	425
Glu Phe Cys Gln Lys Ala Gly Ser Lys Glu Asn Leu Ala Glu Ser Thr		
	435	440
Glu Met Leu Phe Ser Ser Leu Glu Glu Asp Leu Asn Lys Ile Pro Leu		
	450	455
Asp Val Leu Arg Ala Ile Leu Arg Ser Leu Ser Ser Lys Val Leu His		
465	470	475
Ile Arg Asp Gln Lys Leu Glu Leu Glu Lys Leu Glu Glu Gln Phe Ala		
	485	490
Lys Thr Asn Ile Ile Val Lys Ala Lys Glu Ala Glu Phe Glu Lys Asn		
	500	505
Gly Glu Val Trp His Asn Gln Tyr Gln Met Leu Lys Ser Gln Met Glu		
	515	520
Lys Leu Glu Ser Gln Lys Arg Arg Leu Thr Asp Lys Lys Glu		
530	535	540

(2) INFORMATIONS POUR LA SEQ ID NO: 299:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 949 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(302071..304917)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 299:

Glu Tyr Gly Ile Ile Leu Pro Ser Lys Ile Val Phe Gln Glu Ser Met
1 5 10 15

Ala	Asn	Pro	Ser	Thr	Pro	Pro	Ser	Asn	His	Ser	Gly	Leu	Ser	Leu	Gln
		20						25					30		
Gly	Arg	Leu	Arg	Ala	Ser	Ser	Gln	Gln	Cys	Thr	Gln	Ala	Gly	Gln	Gly
		35					40				45				
Asp	Pro	Gln	Pro	Leu	Ser	Pro	Glu	Ser	Arg	Gly	Leu	Thr	Ser	Asn	Phe
	50					55					60				
Ser	Thr	Arg	Arg	Asp	Leu	Ile	Asp	Val	Val	Glu	Glu	Ser	Ile	Glu	Thr
65				70						75				80	
Ala	Lys	Gly	Ser	Glu	Leu	Lys	Lys	Leu	Arg	Ile	Tyr	Glu	Ile	Ala	Leu
			85						90					95	
Lys	Ile	Leu	Thr	Ile	Ile	Gly	Ala	Ala	Ile	Leu	Phe	Ala	Val	Pro	Leu
			100					105						110	
Cys	Met	Leu	Gly	Val	Pro	Leu	Trp	Ile	Pro	Ile	Val	Thr	Cys	Ile	
	115					120					125				
Gly	Val	Gly	Ile	Ala	Phe	Ser	Ile	Ala	Lys	Gly	Cys	Leu	Gln	Lys	Arg
	130					135					140				
Cys	Gln	Gln	Ile	Arg	Glu	Glu	Tyr	Arg	Ala	Leu	His	Leu	Tyr	His	Arg
145				150						155					160
Tyr	Leu	Leu	Ser	Asn	Lys	Asp	Ser	Ile	Asp	Gly	Thr	Leu	Leu	Ser	Arg
			165						170					175	
Phe	Asp	Ile	Arg	Phe	Arg	Lys	Ala	Glu	Gly	Lys	Leu	His	Gly	Leu	Asp
		180						185					190		
Leu	Asp	Lys	Arg	Glu	Ala	Asn	His	Pro	Leu	Glu	Ala	Asp	Lys	Arg	Tyr
	195					200						205			
Asp	Phe	Ala	Gly	Leu	Ala	His	Gln	Arg	Tyr	Gln	Val	Asp	Ala	Ala	Leu
	210					215					220				
Gly	Ile	Ser	Ser	Ser	Gln	Asp	Ala	Phe	Trp	Arg	Gly	Val	Ala	Gln	Gln
225					230					235					240
Val	Lys	Ser	Val	Lys	Asp	Asp	Val	Val	Leu	Gly	Asp	Lys	Ala	Ser	Thr
			245						250					255	
Asp	Leu	Tyr	Pro	Ile	Ala	Gln	Gln	Ala	Leu	Gln	Ala	Ala	Gly	Val	Gly
		260						265					270		
Phe	Ser	Gly	Ala	Ala	Gly	Lys	Glu	Ser	Leu	Leu	Asp	Leu	Ala	Lys	Ser
	275						280					285			
Leu	Ser	Ser	Leu	Phe	Ala	Trp	Gly	Ser	Gln	Val	Gly	Lys	Asp	Ser	His
	290					295					300				
Glu	Ala	Leu	Gln	Arg	Tyr	Gln	Met	Arg	Phe	Leu	Ser	Ser	Pro	Ile	Leu
305					310					315					320
Ala	Thr	Trp	Cys	Gly	Ala	Gly	Phe	Ser	Thr	Ser	Ala	Gln	Asp	Phe	Val
			325						330					335	
Leu	Lys	Gly	Lys	Asn	Val	Leu	Asp	Ile	Ala	Ser	Glu	Asn	His	Thr	Lys
		340						345					350		
Met	Gln	Asn	Ala	Ile	Lys	Cys	Val	Gln	Leu	Val	Ser	Val	Leu	Gly	Lys
	355						360					365			
Met	Arg	Asn	Trp	Lys	Glu	Lys	Ile	Asp	Thr	Leu	Ile	Gln	Asn	Lys	Asn
	370					375					380				
Leu	Asp	Gln	Asp	Ser	Leu	Arg	Lys	Leu	Tyr	Gln	Asp	Ile	Glu	Lys	Ala
385					390					395					400
Met	His	Lys	Val	Cys	Ile	Glu	Asp	Gly	Val	Ser	Ala	Ser	Ile	Gln	Ala
			405						410					415	
Arg	Val	Arg	Lys	Val	Thr	Gln	Lys	Tyr	Leu	Arg	Gln	Asp	Leu	Gln	Glu
			420					425					430		
Leu	Leu	Asn	Lys	Lys	Ala	Pro	Leu	Asn	Glu	Ser	Asp	Leu	Ser	Lys	Met
	435					440						445			
Gln	Lys	Gly	Ile	Ser	Ser	Cys	Ala	Asn	Leu	Val	Val	Thr	Leu	Leu	Glu
	450					455					460				
Ser	Gln	Leu	Gly	Ile	Ser	Glu	Gln	Thr	Ser	Ile	Lys	Glu	Val	Glu	Glu
465					470					475					480
Ser	Ile	Tyr	Arg	Asp	Leu	Ile	Asp	Thr	Ile	Leu	Gln	Met	Gly	Ser	Ala

485 490 495
 Ala Gly Gly Val Thr Pro Leu Val Asp Gly Val His Lys Ala Ile Arg
 500 505 510
 Glu Gly Lys Thr Leu Arg Ser Glu Leu Ser Arg Ala Met Ser Leu His
 515 520 525
 Pro Arg Gln Ser Phe Leu Gly Val Gln Ser Ala Val Glu Lys Leu Gln
 530 535 540
 Ala Phe Ile Arg Asp Pro Lys Trp Gly Ala Ser Ala Val His Thr Ser
 545 550 555 560
 Ala Glu Glu Thr Leu Ala Gln Lys Gln Lys Phe Val Ser Asp Leu Thr
 565 570 575
 Arg Ile Gln Thr Ser Leu Ala Asp Trp Arg Glu Arg Tyr Gly Leu Phe
 580 585 590
 Glu Glu Thr Lys Leu Asn His Ile Val Ser Thr Asp Phe Val Ser Arg
 595 600 605
 Thr Glu Ala Phe Leu Asp Thr Leu Lys Asn Val Ala Glu Ala Cys Ser
 610 615 620
 Leu Glu Gln Ala Val Ala Glu Leu Lys Asp Cys Glu Asp Ala Met Lys
 625 630 635 640
 Ala Asp Leu Thr His Val Glu Gln Lys Met Asn Pro Thr Glu Ile Glu
 645 650 655
 Ser Ala Arg Glu Glu Phe Lys Gln Leu Met Glu Glu Leu Ala Gly Ile
 660 665 670
 Gln Glu Gln Leu Glu Gln Ile Ala Arg Pro Ile Tyr Glu Glu Gly Val
 675 680 685
 Ser Gly Lys Arg Leu Leu Leu Asn Thr Val Phe Ser His Pro Glu Ala
 690 695 700
 Leu Arg Lys Lys Val Gln Ala Lys Glu Thr Leu Leu Glu Ala Leu Thr
 705 710 715 720
 Lys Gly Glu Gln Pro Ser Pro Thr Lys Lys Lys Thr Leu Lys Gln Leu
 725 730 735
 Ser Glu Gly Cys Glu Tyr Phe Ser Ser Leu Val Ser Lys Ile Asn Ala
 740 745 750
 Val Lys Thr Ile Leu Glu Gly Ser Arg Gly Lys Lys Ile Ala Ser Gln
 755 760 765
 Asp Ile Arg Gln Leu Ile Gly Leu Thr Asp Glu Leu Ala Leu Lys Leu
 770 775 780
 Ser Ser Phe Gln Gln Asp Ser Leu Glu Ser Leu Leu Tyr Gly Leu Glu
 785 790 795 800
 Gly Leu Ser Ile Pro Ala Ala Ser Ile Glu Gln Lys Lys Gly Ser Pro
 805 810 815
 Lys Ser Ser Ser Ile Ala Glu Lys Val Val Tyr Ala Ser His Gln Arg
 820 825 830
 Val Tyr Asn Gly Val Lys Ala Lys Val Asn Arg Thr Leu Glu Ala Phe
 835 840 845
 Ser Gln Leu Ile Lys Gly Leu Arg Gly Ser Leu Arg Asn Ala Met Ile
 850 855 860
 Thr Lys Ala Val Val Ala Ala Ile Leu Ser Val Ala Phe Ser Cys Leu
 865 870 875 880
 Ala Ile Ala Leu Phe Ser Val Gln Leu Thr Trp Leu Pro Ile Met Leu
 885 890 895
 Cys Val Leu Ala Leu Val Leu Glu Ala Ile Pro Ser Ala Leu Ser Ile
 900 905 910
 Trp Val Glu Lys Arg Asn Trp Lys Tyr Glu Val Ala Ser Leu Ala Lys
 915 920 925
 Ser Trp Phe Arg Met Glu Glu Ser Phe Leu Ile Gln Ile Trp Gly Ile
 930 935 940
 Lys Ile Ser Ser Ile
 945

(2) INFORMATIONS POUR LA SEQ ID NO: 300:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 395 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(304973..306157)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 300:

Arg	Arg	Cys	Gly	Ala	Val	Leu	Arg	Met	Ala	Ile	Asp	Gly	Val	Val	Ile
1				5					10					15	
Lys	Val	Asp	Asn	Ile	Ala	His	Gln	Asp	Arg	Leu	Gly	Leu	Thr	Ser	Lys
		20					25						30		
His	Tyr	Arg	Trp	Ala	Ile	Ala	Tyr	Lys	Tyr	Ala	Pro	Glu	Arg	Ala	Glu
	35						40					45			
Thr	Ile	Leu	Glu	Asp	Ile	Val	Phe	Gln	Val	Gly	Lys	Thr	Gly	Ile	Leu
	50					55					60				
Thr	Pro	Val	Ala	Glu	Leu	Ala	Pro	Val	Phe	Leu	Ser	Gly	Ser	Arg	Val
65					70					75					80
Ser	Arg	Ala	Ser	Leu	Tyr	Asn	Gln	Asp	Glu	Ile	Glu	Lys	Lys	Asp	Ile
			85					90						95	
Arg	Ile	Gly	Asp	Ser	Val	Tyr	Val	Glu	Lys	Gly	Gly	Glu	Val	Ile	Pro
		100						105					110		
Lys	Ile	Val	Gly	Ile	Asn	Leu	Ala	Lys	Arg	Ser	Leu	Glu	Ser	Glu	Pro
	115					120						125			
Trp	Lys	Met	Pro	Ser	Leu	Cys	Pro	Val	Cys	His	Glu	Pro	Val	Val	Lys
	130					135					140				
Glu	Lys	Val	Ser	Val	Arg	Cys	Ile	Asn	Pro	Leu	Cys	Ser	Gly	Gly	Met
145					150					155					160
Leu	Glu	Lys	Ile	Cys	Phe	Phe	Ala	Ser	Lys	Ser	Ala	Leu	Asn	Ile	Asp
			165						170					175	
His	Leu	Gly	Glu	Lys	Val	Val	Thr	Lys	Leu	Phe	Glu	Val	Gly	Leu	Ile
		180						185					190		
Ser	Ser	Cys	Ser	Asp	Ile	Phe	Ala	Leu	Thr	Glu	Glu	Asp	Leu	Lys	Gln
	195						200					205			
Val	Pro	Gly	Phe	Lys	Asp	Arg	Ser	Ile	Gln	Asn	Leu	Leu	Ala	Ser	Ile
	210					215					220				
Ala	Gly	Ala	Lys	Lys	Val	Ala	Leu	Asp	Arg	Leu	Leu	Thr	Ala	Leu	Ser
225					230					235					240
Ile	Pro	Phe	Val	Gly	Ser	Ser	Gly	Ala	Ile	Ala	Leu	Ala	Asp	His	Phe
			245					250						255	
Gly	Thr	Leu	Asp	Lys	Val	Ile	Glu	Ala	Ser	Leu	Asp	Glu	Leu	Met	Ser
		260						265					270		
Ile	Glu	Gly	Ile	Gly	Pro	Lys	Val	Ala	Ala	Ser	Ile	Val	Ala	Phe	Phe
	275						280					285			
Ser	Lys	His	Glu	Asn	Arg	Glu	Glu	Ile	Arg	Arg	Met	Gln	Glu	Leu	Gly
	290					295					300				
Val	Gln	Val	Leu	Ser	Lys	Gln	Ser	Asp	Lys	Glu	Ala	Pro	Leu	Gln	Gly
305					310					315					320
Lys	Val	Phe	Val	Leu	Thr	Gly	Thr	Leu	Gln	Gln	Met	Thr	Arg	Thr	Gln
			325					330						335	
Ala	Glu	Glu	Arg	Ile	Arg	Ser	Leu	Gly	Gly	Lys	Val	Ser	Ser	Ser	Val

```

                340                345                350
Ser Lys Ser Thr Tyr Ala Val Ile Ala Gly Ser Glu Ala Gly Gly Lys
                355                360                365
Leu Lys Lys Ala Gln Asp Leu Gly Leu Ser Ile Trp Asn Glu Ser Lys
                370                375                380
Leu Ser Arg Ile Leu Asp Ala Lys Ser Val Ser
385                390                395

```

(2) INFORMATIONS POUR LA SEQ ID NO: 301:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306111..306494)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 301:

```

Asp Ser Leu Lys Lys Ala Pro Glu Asp Leu Glu Val Arg Gly Glu Val
1      5      10      15
Phe Leu Ser Tyr Glu Ala Phe Glu Glu Leu Asn Ala Cys Gln Arg Glu
20     25     30
Gln Gly Lys Leu Glu Phe Ala Asn Pro Arg Asn Ala Ala Gly Gly Thr
35     40     45
Leu Lys Leu Leu Ser Ser Lys Glu Ala Ala Lys Arg Lys Leu Asp Leu
50     55     60
Ser Val Tyr Gly Leu Ile Thr Asp Gln Lys Lys Arg Ser His Phe Glu
65     70     75     80
Asn Leu Gln Leu Cys Ser Gln Trp Gly Phe Phe Val Ala Gly Met Pro
85     90     95
Lys Gln Cys Arg Ser Arg Gln Glu Val Val Glu Arg Ile Arg Glu Ile
100    105    110
Glu Glu Met Arg Arg Ser Ala Pro Asp Gly Tyr Arg Trp Ser Arg His
115    120    125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 302:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306436..306963)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 302:

```

Met Gly Ala Val Ser Arg Asp Asp Tyr Ile Ala Leu Cys Thr Glu Leu
1      5      10      15
Val Glu His Asp Arg Arg Tyr Tyr Ala Leu Asn Gln Pro Thr Ile Ser
20     25     30

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Asp Tyr Ser Tyr Asp Met Lys Met Arg Glu Leu Gln Glu Ile Glu Val
      35                      40                      45
Gln His Pro Glu Trp Lys Val Ser Trp Ser Pro Thr Met Tyr Leu Gly
      50                      55                      60
Asp Arg Pro Ser Gly Gln Phe Pro Val Val Pro His Ser Ser Pro Met
65                      70                      75                      80
Leu Ser Ile Ala Asn Val Tyr Ser Leu Gln Glu Leu Glu Glu Phe Phe
      85                      90                      95
Ser Arg Thr Glu Lys Leu Leu Gly Tyr Ser Pro Gly Tyr Ser Leu Glu
      100                     105                     110
Leu Lys Ile Asp Gly Ile Ala Val Ala Ile Arg Tyr Glu Lys Arg Leu
      115                     120                     125
Phe Ala Gln Ala Leu Ser Arg Gly Asn Gly Val Lys Gly Glu Asp Ile
      130                     135                     140
Thr Ala Asn Val Ser Thr Ile Arg Ser Leu Pro Met Arg Leu Pro Gln
145                     150                     155                     160
Glu Gly Ser Arg Gly Ser Arg Ser Ala Arg Arg Ser Val Ser Phe Ile
      165                     170                     175

```

(2) INFORMATIONS POUR LA SEQ ID NO: 303:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 599 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(306977..308773)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 303:

```

Ser Gln Asn Ser Asp Met Asp Leu Trp Ser Arg Asp Val Leu Ala Glu
1      5      10      15
His Arg Phe Ile Lys Lys Arg Tyr Ile Leu Lys Ile Leu Pro Ser Glu
      20      25      30
Leu Ser Ser Ser Glu Asn Phe Met Arg Val Phe Gln Glu Val Ile Val
      35      40      45
Gln Leu Ala Ala Ile Arg His Ala Ser Leu Val Ala Ile Glu Asn Val
      50      55      60
Ser Arg Glu Gly Asp Arg Tyr Phe Val Val Thr Glu Glu Asn Gly Gly
65      70      75      80
Thr Ile Ser Leu Ala Gln Tyr Leu Ser Gly Arg Lys Leu Ser Glu Glu
      85      90      95
Glu Val Val His Leu Ile Gln Gln Leu Cys Asp Ala Leu Glu Leu Val
      100     105     110
His Ser Ile Gly Leu Ala His Gly Gln Ile His Leu His Ser Val His
      115     120     125
Val Ser Phe Phe Asn Gly Ile Ala Asn Ile Tyr Leu Pro Glu Val Gly
      130     135     140
Phe Ala Ser Leu Leu Arg Glu Arg Met Phe Ser Thr Ile Met Gln Ser
145     150     155     160
Gly Ser Ala Arg Glu Ser Ile Thr Arg Ile Arg Asp Leu Leu Met Phe
      165     170     175
Glu Ala Pro Glu Glu Gln Glu Val Phe Gly Arg Glu Ala Asp Val Tyr
      180     185     190
Ser Val Gly Val Leu Ala Tyr Tyr Leu Leu Val Gly Ser Phe Pro Trp

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                195                200                205
Gly Ser Phe Pro Lys Pro Ser Leu Cys Met Pro Asp Ser Trp Tyr Asp
210                215                220
Trp Asp Gly Phe Ile Leu Ser Cys Leu Gln Gln Gln Arg Glu Ala Arg
225                230                235
Pro Lys Cys Leu Arg Glu Ala Leu Arg Arg Lys Thr Ser Gly Glu Gln
245                250                255
Leu Gln Val Thr Leu Asp Ser Cys Arg Glu Pro Leu Arg Glu Met Glu
260                265                270
Ile Glu Asp Thr Pro Thr Glu Leu Gly Pro Pro Ser Ala Leu Ile Arg
275                280                285
Glu Gly Glu Arg Leu Cys Glu Val Lys Glu Glu Gln His Ala Phe Val
290                295                300
Leu Val Glu Ala Lys Ser Ile Asp Glu Ala Met Val Thr Thr Val Asp
305                310                315
Ser Glu Glu Glu Leu Glu Ser Ser Glu Gly Tyr Ala Asn Pro Leu Gln
325                330                335
Ser Leu Leu Ala Arg Glu Pro Val Val Ser Arg Tyr Val Glu Val Glu
340                345                350
Arg Glu Glu Ile Lys Pro Gln Pro Leu Leu Thr Glu Met Ile Phe Ile
355                360                365
Glu Gly Gly Glu Phe Ser Arg Gly Ser Gly Asp Gly Gln Arg Asp Glu
370                375                380
Leu Pro Val His Asn Ile Thr Leu Pro Gly Phe Phe Leu Asp Ile His
385                390                395
Pro Val Thr Asn Glu Gln Phe Val Arg Phe Leu Glu Cys Val Gly Ser
405                410                415
Glu Gln Asp Glu His Tyr Asn Glu Leu Ile Arg Leu Lys Asp Ser Arg
420                425                430
Ile Gln Arg Arg Ser Gly Arg Leu Ile Ile Glu Pro Gly Tyr Ala Lys
435                440                445
His Pro Val Val Gly Val Thr Trp Tyr Gly Ala Ser Ser Tyr Ala Cys
450                455                460
Trp Ile Gly Lys Arg Leu Pro Ser Glu Ala Glu Trp Glu Val Ala Ala
465                470                475
Ser Gly Gly Lys Leu Gly Leu Arg Tyr Pro Thr Gly Glu Glu Ile Asp
485                490                495
Lys Ser Lys Ala Asn Phe Phe Ser Ser Asp Thr Thr Pro Val Met Ser
500                505                510
Tyr Pro Ser Ser Ile Leu Gly Leu Tyr Asp Met Ala Gly Asn Val Tyr
515                520                525
Glu Trp Cys Gln Asp Trp Tyr Ser Tyr Asp Phe Tyr Glu Ser Ser Ala
530                535                540
Leu Asp Pro Asp Ala Pro Leu Gly Pro Pro Gln Gly Val Tyr Arg Val
545                550                555
Leu Arg Gly Gly Cys Trp Lys Ser Leu Lys Asp Asp Leu Arg Cys Ala
565                570                575
His Arg His Arg Asn Asn Pro Gly Ala Ile Asn Ser Thr Tyr Gly Phe
580                585                590
Arg Cys Ala Lys Asp Val Lys
595

```

(2) INFORMATIONS POUR LA SEQ ID NO: 304:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 202 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(309276..309881)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 304:

```

Gly Gly Arg Leu Met Thr Thr Pro Asp Asn Asn Thr Ile Asp Val Ser
1      5      10      15
Phe Pro Thr Phe Val Arg Leu Asn Val Ala Thr Thr Asp Leu Ala Asp
      20      25      30
Gly Asn Lys Ser Asn Ala Val Thr Ile Thr Glu Thr Ala Thr Ala Asn
      35      40      45
Tyr Val Asn Val Thr Gln Asp Leu Thr Ser Ser Thr Ala Lys Leu Glu
50      55      60
Cys Thr Gln Asp Leu Ile Ala Gln Gly Lys Leu Ile Val Thr Asn Pro
65      70      75      80
Lys Ser Asp Ile Ser Phe Gly Gly Arg Val Asn Leu Ala Asp Asn Thr
      85      90      95
Ile Thr Tyr Asn Pro Tyr Asn Asn Gly Gly Glu Val Ala Phe Thr
      100      105      110
Asp Ile Asn Ser Arg Gln Gly Lys Gln Tyr Val Pro Tyr Gly Leu Tyr
      115      120      125
Lys Asn Gly Ala Pro Lys Ile Ser Met Arg Ser Ala Leu Ser Gly Gly
      130      135      140
His Val Gly Ser Gly Asp Thr Arg Gly Trp Gly Ala Glu Val Leu Trp
145      150      155      160
Asp Ala Tyr Thr Gln Gln Arg Glu Asp Leu Glu Asp Lys Ala Val Thr
      165      170      175
Phe Ser Pro Ala Asn Arg Gly Lys Leu Tyr Phe Glu Ala Ser Leu Arg
      180      185      190
Leu Pro Phe Cys Ser Val Ser Pro Ser Leu
      195      200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 305:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 283 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(309872..310720)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 305:

```

Glu Asp Asn Met Lys Lys Pro Val Phe Thr Gly Gly Ala Pro Ile Pro
1      5      10      15
Gly Ile Ser Thr Glu Glu Gly Thr Gly Val Lys Asp Gln Asn Leu Trp
      20      25      30
Met Arg Asn Ala Thr Leu Lys Val Glu Gly Asp Ala Thr Ile Asp Asp
      35      40      45
Thr Leu Thr Ser Arg Asp Leu Lys Val Thr Gly Pro Thr Ile His Thr
50      55      60
Asp Leu Asp Leu Ser Val Gly Gly Asp Val Lys Gly Gly Arg Thr Val

```

```

65          70          75          80
Leu Gly Glu Thr Val Leu Glu Gly Asp Phe Asn Ile Lys Cys Asn Gln
      85          90          95
Gly Gln Val Pro Gln Phe Thr Asn Leu Ser Asp Pro Leu Ser Ala Arg
      100          105          110
Asp Ala Ile Thr Phe Asp Tyr Tyr Arg Asp Arg Ser Thr Gln Ala Tyr
      115          120          125
Asn Cys Ala Thr His Arg Asn Gly Ala Leu Val Lys Gly Asn Arg Phe
      130          135          140
Ile Asp Leu Arg Met His Asn Ile Asp Asp Ser Glu Ser Tyr Thr Pro
      145          150          155          160
Met Tyr Gln Asn Arg Phe Tyr Trp Lys Asp Asn Asp Gln Lys Lys Leu
      165          170          175
Tyr Leu Lys Ser Pro Gly Ile Tyr Gln Val Ala Phe Gln Ile Phe Arg
      180          185          190
Ser Gly Gly Tyr His Ser Gly Asn Glu Asp Pro Thr Ile Phe Leu Arg
      195          200          205
Leu Tyr Thr Ser Ala Tyr Glu Tyr Thr Asn Leu Cys Thr Gly Asp Thr
      210          215          220
Arg Gly Phe Asn Pro Glu His Thr Thr Asn Thr Ser Leu Tyr Ser Ile
      225          230          235          240
Phe Ser Ile Pro Ser Ile Gly Asn Glu His Pro Phe Ile Gln Val Phe
      245          250          255
Thr Lys Ile His Val Asn Ile Ala Tyr Ser Met Ile Asn Val Ile Trp
      260          265          270
Phe Pro Phe Gly Ser Ser Tyr Lys Glu Ala Asp
      275          280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 306:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 285 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(310716..311570)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 306:

```

Met Ser Asp Ser Asp Lys Ile Ile Asn Asp Cys Arg Phe Asp Phe Asn
1          5          10          15
Thr Thr Val His Gly Asp Leu Leu Ala Ser Asn Leu Thr Thr Glu Gly
      20          25          30
Asp Val Thr Val Lys Ser Ile Ser Ala Lys Glu Ser Phe Ser Val Lys
      35          40          45
Arg Lys Val Asp Val Asn Glu Asn Asp Ile Ile Val Asn Gly Phe Thr
      50          55          60
Gly Ala Ala Gly Tyr Asp Leu Thr Thr Arg Gly Lys Ile Ser Ile Asn
      65          70          75          80
Leu Asn Gly Asn Arg Leu Ser Asn Val Lys Cys Pro Glu Lys Asp Ser
      85          90          95
Gln Pro Val Pro Ala Asn Tyr Ile Arg Thr Pro Glu Tyr Tyr Phe Cys
      100          105          110
Ser Leu Gln Asp Gly Ala Arg Ile Glu Trp Lys Arg Gly Gln Lys Leu
      115          120          125

```

```

Pro Leu Ile Gly Pro Ser Arg Leu Val Tyr Gln Ser Ser Arg Ile Asn
  130                      135                      140
Glu Phe Ile Arg Phe Val Ser Phe Glu Glu Asn Lys Thr Arg Thr Gln
145                      150                      155                      160
Val Lys Ile Asn Leu Ser Gly Thr Thr Gly Leu Gln Met Leu Ala Lys
                      165                      170                      175
Gly Val Tyr Ile Ile Asn Val Gly Val Gly Lys Arg Trp Gly Trp Asn
                      180                      185                      190
Asn Gly Tyr Gly Gly Asp Tyr Cys Leu Ala Val Pro Leu Gly Lys Glu
                      195                      200                      205
Tyr Ser Glu Ser Ser Thr Phe Ser Arg Gly Gly Tyr Tyr Ala Ser Thr
210                      215                      220
Ala Val Gly Thr Ala Ile His Ile Arg Lys Glu Ser Thr Asn Pro Asp
225                      230                      235                      240
Gly Pro Phe Ser Ser Ser Asp Thr Glu Leu Met Lys Thr Leu Leu Glu
                      245                      250                      255
Val Arg Tyr Lys Gly Gly Asp Tyr Val Asp Lys Ser Ala Leu Ser Thr
260                      265                      270
Leu Tyr Phe Gly Val Leu Val Tyr Pro Glu Ile Gly Gly
275                      280                      285

```

(2) INFORMATIONS POUR LA SEQ ID NO: 307:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(311972..312451)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 307:

```

Leu Ile Leu Arg Met Arg Arg Asp Arg Lys Glu Leu Met Leu Lys Lys
 1                      5                      10                      15
Pro Asn Arg Asn Asp Pro Cys Pro Cys Gly Ser Gly Lys Lys Tyr Lys
20                      25                      30
Gln Cys Cys Leu Lys Xaa Gln Ala Leu Thr Ala Arg His Thr Pro Glu
35                      40                      45
Gly Lys Phe Lys Phe Ser Ile Thr Ala Ser Pro Ala Ala Gly Ala Ser
50                      55                      60
Thr Glu Gly Phe Thr Lys Leu Phe Arg Gln Ser Val Asp Ser Tyr Thr
65                      70                      75                      80
Ser Glu Gln Lys Glu Gly Met Ser Arg Phe Leu Ile Thr Lys Asn Lys
85                      90                      95
Glu Pro Ile Gly Lys Arg Ala Ile Arg Lys Ala Lys Ala Lys Glu Glu
100                      105                      110
Arg Ile Ile Ser Glu Lys Leu Ser Gln His Glu Phe Gln Val Met Asp
115                      120                      125
Thr Glu Val Ser Gly Glu Asp Ile Gln Ser Ser Leu Asp Tyr Glu Gln
130                      135                      140
Phe Leu Pro Thr Glu Glu Asp Tyr Arg Val Gln Lys Glu Glu Asp Ser
145                      150                      155                      160

```

(2) INFORMATIONS POUR LA SEQ ID NO: 308:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 310 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 313435..314364

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 308:

```

Phe Tyr Arg Asn Thr Gln Lys Tyr Phe Met Tyr Val Arg Ser Ile Phe
1      5      10      15
Phe Ser Ile Ile Ala Phe Leu Thr Val Gly Cys Ser Phe Ser Pro Pro
20      25      30
Glu Ser Gly Leu Ile Ile Ala Ile His Asp Asp Pro Arg Ser Leu Ser
35      40      45
Pro Glu Lys Gly Glu Asn Ala Phe His Phe Ser Leu Ser Lys Ala Leu
50      55      60
Phe Ala Thr Leu Phe Arg Glu Glu Leu Ser Gly Leu Thr Pro Ala Leu
65      70      75      80
Val Ser Ser Tyr Gln Ile Ser Glu Asp Gly Arg Phe Tyr Arg Phe Cys
85      90      95
Ile Arg Lys Asp Ala Lys Trp Ser Asp Gly Ser Leu Leu Leu Ala Glu
100     105     110
Asp Val Ile Ala Ala Trp Glu His Thr Lys Gln Ala Gly Arg Tyr Ser
115     120     125
Leu Leu Phe Glu Lys Leu Ser Phe Arg Ala Ser Ser Ser Glu Ile
130     135     140
Leu Ile Glu Leu Lys Glu Pro Glu Pro Gln Leu Leu Ala Ile Leu Ala
145     150     155     160
Ser Pro Phe Phe Ala Val Tyr Arg Pro Glu Asn Pro Phe Leu Ser Ser
165     170     175
Gly Pro Phe Met Pro Lys Thr Tyr Val Gln Gly Gln Thr Leu Val Leu
180     185     190
Gln Lys Asn Pro Tyr Tyr Tyr Asp His Ala His Val Glu Leu His Ser
195     200     205
Ile Asp Phe Arg Ile Ile Pro Asn Ile Tyr Thr Ala Leu His Leu Leu
210     215     220
Arg Arg Gly Asp Val Asp Trp Val Gly Gln Pro Trp His Gln Gly Ile
225     230     235     240
Pro Phe Glu Leu Arg Thr Thr Ser Ala Leu Tyr Thr His Tyr Pro Val
245     250     255
Asp Gly Thr Phe Trp Leu Ile Leu Asn Pro Lys Asp Pro Val Leu Ser
260     265     270
Ser Leu Ser Asn Arg Gln Arg Leu Ile Ala Ala Ile Gln Lys Glu Lys
275     280     285
Leu Val Lys Gln Ala Leu Gly Thr Gln Tyr Arg Val Ala Glu Ser Leu
290     295     300
His Leu Gln Arg Glu Ser
305     310

```

(2) INFORMATIONS POUR LA SEQ ID NO: 309:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 314340..314738

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 309:

```

Lys Ser Pro Ser Pro Glu Gly Ile Ile Ala His Gln Glu Ala Ser Thr
1      5      10      15
Pro Phe Pro Gly Lys Ile Thr Leu Ile Tyr Pro Asn Asn Ile Thr Arg
20      25      30
Cys Gln Arg Leu Ala Glu Val Leu Gln Glu Gln Cys Arg Asp Ala Gly
35      40      45
Ile Gln Leu Thr Leu Glu Gly Leu Glu Tyr His Val Phe Val Gln Lys
50      55      60
Arg Ala Thr Gln Asp Phe Ser Val Ser Thr Ala Thr Ser Ile Ala Phe
65      70      75      80
His Pro Leu Ala Lys Ser Lys Phe Asp Gln Thr Ala Leu Asp Asn Phe
85      90      95
Thr Cys Leu Pro Leu Tyr His Ile Glu Tyr Asp Tyr Ile Leu Ser Arg
100      105      110
Pro Leu Asp Gln Ile Val His Tyr Pro Ser Gly Ser Val Asp Leu Thr
115      120      125
Tyr Ala His Phe His
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 310:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 262 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(314741..315526)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 310:

```

Thr Lys Pro Ile Phe Phe Ser Leu Ile Glu Gln Asp Glu Arg Leu Thr
1      5      10      15
Pro Leu Ser Tyr Glu Pro Gln Val Glu Ser Ser Leu Gln Val Val Arg
20      25      30
Ser Ile Glu Asn Ala Ser Gly Leu Gly Ser Asp Ala Gln Pro Leu Gln
35      40      45
Glu Leu Phe Arg Lys Leu Leu Leu Leu His Glu Gln Gly Pro Leu Ala
50      55      60
Tyr Ile Gly Leu Val Trp Asn Phe Ala Asn Arg Phe Gly Gly Gly Ile
65      70      75      80
Leu Glu Pro Lys Arg Leu Ser Arg Asp Gly Lys Asn Leu Leu Glu Leu
85      90      95
Leu His Ala Leu Ala Ile Pro Val Asp Leu Ser His Cys Ser Asp Pro
100      105      110
Leu Ala Asp Asp Ile Leu Asp Phe Thr Ala Asp Lys Met Pro Asp Met

```

```

                115                120                125
Phe Val Leu Ala Cys His Ser Asn Phe Arg Ala Val Gln Asp Ile Glu
130                135                140
Arg Asn Leu Leu Asp Val His Ala Lys Glu Ile Phe Ala Arg Asp Gly
145                150                155                160
Val Ile Gly Leu Asn Gly Val Asn Tyr Phe Val Gly Ala Ser Leu Glu
                165                170                175
Asp Ile Lys Lys His Ile Ala His Ala Gln Glu Leu Gly Ile Leu Asp
                180                185                190
Ser Leu Val Leu Gly Thr Asp Phe Phe Tyr Thr Glu Glu Glu Lys Phe
195                200                205
Phe Pro Asn Phe Ser Thr Ala Lys Asp His Pro Lys Leu His Ala Leu
210                215                220
Ile Lys Glu Ala Ile Pro Ile Asp Lys Ala Gln Ser Leu Leu Glu Glu
225                230                235                240
Arg Ala Gln Arg Phe Leu Asn Arg Val Val Ser Ala Gln Lys Lys Val
                245                250                255
Val Asn His Ile Ala Phe
                260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 311:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 281 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(315665..316507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 311:

```

Val Phe Ser Gln Gln Ile Glu Glu Ser Ile Lys Ala Gly Gln Val Phe
1      5      10      15
Ala Phe Pro Thr Asp Thr Val Tyr Gly Leu Gly Val Ser Phe His Ile
20     25     30
Leu Asp Ala Asp Gln Arg Leu Phe Ala Leu Lys His Arg Ser Ser Gln
35     40     45
Lys Ala Leu Ser Val Tyr Val Ser Ser Leu Glu Glu Leu Glu Ala Val
50     55     60
Ala Gln Gln Ser Leu Gly Ala Ser Ser Arg Lys Ile Ile Gln Lys Phe
65     70     75     80
Leu Pro Gly Pro Leu Thr Leu Ile Thr Lys His Asn Asn Pro Arg Phe
85     90     95
Pro Gln Lys Thr Leu Gly Phe Arg Ile Val Asn His Pro Ile Val Gln
100    105    110
Gln Ile Ile Gln Lys Val Gly Pro Phe Leu Ala Thr Ser Ala Asn Leu
115    120    125
Ser Gly Phe Pro Ser Ala Val Ser Ala Asp Glu Val Lys Gln Asp Phe
130    135    140
Pro Glu Glu Asp Ile Val Met Ile Ser Gly Glu Cys Ser Ile Gly Leu
145    150    155    160
Glu Ser Thr Val Ile Asp Pro Glu Glu Arg Ile Val Tyr Arg Glu Gly
165    170    175
Ala Ile Ser Ile Ala Glu Ile Glu Thr Val Leu Gly Ala Pro Cys Ala
180    185    190

```

```

Asn Leu Ser Lys Glu Leu Gly Phe Arg Glu Lys Ile Gly Ile His Val
    195                200                205
Val Lys Thr Pro Ala Asp Leu Cys Ser Phe Leu Leu Ser Arg Pro His
    210                215                220
Phe Lys Gly Val Ile Cys His Gln Pro His Pro His Thr Phe Tyr Ser
    225                230                235                240
Val Leu Arg Gln Ala Leu Arg Ser Pro Thr Gln Glu Ile Ile Phe Val
    245                250                255
Tyr Asp Leu Cys Asn Thr Glu Tyr Pro Ile Leu Ser Arg Phe Leu Gly
    260                265                270
Val Ser Tyr Asp Ser Gly Tyr Ala Leu
    275                280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 312:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 232 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(316529..317224)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 312:

```

Arg Lys Leu Ala Gly Ile Glu Phe Ile Glu Cys Pro Gly Asp Pro Glu
1      5      10      15
Ala Pro Val Ile Phe Cys His Gly Tyr Gly Ala Ser Ala Asp His
    20      25      30
Leu Thr Phe Phe Pro Thr Met Cys Val Cys Ala Asn Leu Arg Pro Thr
    35      40      45
Trp Val Phe Pro His Gly Ile Glu Gln Leu Pro Tyr Gln Leu Gly Gly
    50      55      60
Gly Arg Ala Trp Phe Pro Leu Asp Thr Val Leu Phe Glu Lys Leu Ile
    65      70      75      80
Ser Ser Gln Glu Ile Thr Pro Asp Thr Asp Arg Leu Tyr Gln Gln Leu
    85      90      95
Leu Asp Val Asp Phe Glu Lys Pro Lys Gln Ala Leu Glu Gly Leu Ile
    100     105     110
His Glu Leu Glu Arg Asp Arg Ser Glu Val Ile Ile Gly Gly Phe Ser
    115     120     125
Gln Gly Ala Met Met Thr Thr His Leu Met Leu Ser Ser Arg Leu Pro
    130     135     140
Tyr Arg Gly Ala Leu Ile Cys Ser Gly Ala Ala Val Pro Asn Gln Ser
    145     150     155     160
Trp Glu Glu Asn Ala Ser Leu Cys Gly Lys Thr Pro Tyr Ile Gln Ser
    165     170     175
His Gly Tyr Asp Asp Pro Ile Leu Pro Tyr Phe Leu Gly Glu Arg Leu
    180     185     190
Tyr Lys Val Leu Thr Ala Ser Leu Lys Gly Glu Met Val Ser Phe His
    195     200     205
Gly Gly His Glu Ile Pro Val Val Met Met Gln Lys Ile Gln Glu Ser
    210     215     220
Ile Ala Leu Trp Ser Gln Ser Thr
    225     230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 313:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 85 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(317338..317592)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 313:

Ser	Arg	Thr	Ala	Arg	Cys	Ile	Gln	Arg	Gly	Ala	Leu	Tyr	Ala	Leu	Val
1				5					10					15	
Leu	Glu	Lys	Met	Gln	Arg	Phe	Pro	Lys	Glu	Phe	Leu	Lys	Asp	Gly	Val
			20					25					30		
Ala	Lys	Ser	Val	Val	Ala	Ile	Gln	Ala	Gly	Glu	Ser	Leu	Asp	Thr	Gly
		35					40					45			
Glu	Leu	Ala	Trp	Glu	Glu	Met	Pro	Ser	Ile	Thr	Ala	Cys	Leu	Gly	Arg
	50				55					60					
Glu	Gly	Ile	Asp	Ala	Gln	Ala	Tyr	Ser	Phe	Leu	Ser	Val	Ser	Pro	Leu
65					70				75						80
Asp	Ala	Arg	Ile	Glu											
				85											

(2) INFORMATIONS POUR LA SEQ ID NO: 314:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 324 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(317499..318470)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 314:

Asn	Ser	Leu	Lys	Lys	Ile	Trp	Gly	Asn	Glu	Ile	Lys	Glu	Val	Lys	Leu
1				5				10						15	
Leu	Lys	Met	Val	Ser	Phe	Asp	Leu	Asn	Asp	Pro	Val	Arg	Asn	Thr	Asp
			20					25					30		
Asn	His	Tyr	Arg	Asn	Ile	Asn	Arg	Met	Leu	Asn	Ser	Ala	Thr	Cys	Ala
		35					40					45			
Ala	Gly	Gly	Ile	Gly	Leu	Leu	Thr	Pro	Val	Val	Cys	Ser	Pro	Met	Gly
	50				55						60				
Ala	Phe	Cys	Phe	Ala	Gln	Gly	Pro	Ser	Ser	Ala	Glu	Asp	Leu	Gly	His
65					70					75					80
Arg	Ile	Gln	His	Phe	Val	Ala	Cys	Leu	Gly	Pro	Ala	Ala	Gly	Phe	Tyr
			85						90					95	
Ser	Leu	Ser	Asn	Glu	Arg	Ile	Met	Phe	Glu	Glu	Ala	Ala	Val	Pro	Ser
			100					105					110		
Val	Leu	Glu	Ala	Val	Glu	Ala	Thr	Phe	Trp	Ile	Ser	Ala	Phe	Ala	Arg
							115						125		
								120							

```

Leu Arg Gly Asn Lys Pro Ser Thr Cys Asp Thr Val Met Met Ser Cys
130                      135                      140
Leu Ile Gly Cys Ile Ser Leu Val Cys Gly Ala Met Phe Val Ala Ile
145                      150                      155                      160
Val Ser Cys Ala Val Lys Ile Ser Arg Ile Val Arg Thr Met Thr Gln
165                      170                      175
Ala His Ala Leu Arg Glu Thr Ile Gln Arg Gln Leu Ala Ala Arg Ala
180                      185                      190
Thr Asp Met Arg Ser Ala Tyr Ser Lys Leu Lys Gly Ile Ile Ala Ile
195                      200                      205
Arg Ala Leu Asn Glu Val Glu Arg Gly His Arg Lys Leu Arg Asn Lys
210                      215                      220
Met Ile Thr Ala Phe Val Ala Asn Ala Leu Ile Thr Leu Ala Phe Cys
225                      230                      235                      240
Ala Leu Leu Ala Ser Ala Val Ile Ala Ala Phe Phe Leu Gly Ala Ala
245                      250                      255
Ser Ala Gly Leu Ala Ser Val Phe Phe Gly Cys Leu Trp Gly Gly Ile
260                      265                      270
Gly Ala Leu Ala Val Gly Val Leu Val Gly Ile Val Ser Gly Ile Cys
275                      280                      285
Gln Arg Asn Tyr Lys Val Glu Leu Arg Gly Val Phe Ser Glu Val Leu
290                      295                      300
Phe Met Arg Leu Phe Leu Arg Lys Cys Ser Asp Ser Leu Lys Asn Ser
305                      310                      315                      320
Leu Lys Met Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 315:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 317599..317874

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 315:

```

Leu Arg Trp Gln Ile Pro Glu Thr Met Pro Thr Lys Thr Pro Thr Ala
1                      5                      10                      15
Lys Ala Pro Met Pro Pro His Lys His Pro Lys Lys Thr Leu Ala Ser
20                      25                      30
Pro Ala Leu Ala Ala Pro Lys Lys Asn Ala Ala Ile Thr Ala Glu Ala
35                      40                      45
Asn Lys Ala Gln Lys Ala Ser Val Met Ser Ala Phe Ala Thr Lys Ala
50                      55                      60
Val Ile Ile Leu Phe Leu Asn Phe Arg Trp Pro Leu Ser Thr Ser Leu
65                      70                      75                      80
Arg Ala Leu Met Ala Ile Met Pro Leu Ser Leu Glu
85                      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 316:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 157 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(318477..318947)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 316:

```

Leu Gly Glu Thr Glu Ala Ser Ile Glu Ser Lys Glu Ile Cys Gly Gly
1          5          10          15
Arg Arg Ala Val Met Ala Cys Cys Ala Cys Val Tyr Gly Tyr Asp Glu
20          25          30
Ile Cys Cys Arg Glu Glu Thr Ala Glu Lys Val Val Ala Val Ala Val
35          40          45
Asp Cys Val Leu Phe His Ile Ala Ala Ala Ile Thr Thr Ala Val Ser
50          55          60
Ala Val Trp Leu Leu Ile Arg Leu Ile Ala Cys Ala Ile His Asn Tyr
65          70          75          80
Cys Ser Pro Ala Ser Glu Arg Val Asn Phe Phe Pro Ile Thr Glu Ser
85          90          95
Arg Ala Glu Trp Phe Ser Leu Ile Pro Val Leu Gly Pro Met Val Val
100          105          110
Ala Ala Val Val Tyr Phe Lys Ala Arg Glu Glu Gly Tyr Gly His Leu
115          120          125
Asp Ser Leu Val Cys Ala Met Gln Ser Pro Trp Met Leu Leu Asp Ser
130          135          140
Leu Arg Leu Asn Arg Ser Glu Leu Lys Ile Val Met Val
145          150          155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 317:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 267 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 319342..320142

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 317:

```

Met Ser Arg Lys Pro Ala Ser Asn Ser Ser Arg Asn Thr Lys Arg Ser
1          5          10          15
Ser Asp Thr Ser Trp Glu Val Ile Ala Gln Asp Tyr Asn Lys Ala Val
20          25          30
Asp Arg Asp Gly His Phe Tyr His Lys Glu Val Ile Leu Pro Asn Leu
35          40          45
Leu Ser Lys Leu His Ile Ser Arg Ser Ser Ser Leu Val Asp Val Gly
50          55          60
Cys Gly Gln Gly Ile Leu Glu Lys His Leu Pro Lys Tyr Leu Pro Tyr
65          70          75          80
Leu Gly Ile Asp Leu Ser Pro Ser Leu Leu Arg Phe Ala Lys Lys Ser
85          90          95

```

Ala	Ser	Ser	Lys	Ser	Arg	Arg	Phe	Leu	His	His	Asp	Met	Thr	Gln	Pro
			100					105					110		
Val	Pro	Ala	Asp	His	His	Glu	Gln	Phe	Ser	His	Xaa	Thr	Ala	Ile	Leu
		115					120					125			
Ser	Xaa	Gln	Xaa	Met	Glu	Ser	Pro	Glu	Gln	Ala	Ile	Ala	His	Thr	Ala
	130					135					140				
Asn	Leu	Leu	Ala	Pro	Gln	Gly	Arg	Leu	Phe	Ile	Val	Leu	Asn	His	Pro
145					150					155					160
Cys	Phe	Arg	Ile	Pro	Arg	Leu	Ser	Ser	Trp	Leu	Tyr	Asp	Glu	Pro	Lys
			165					170					175		
Lys	Leu	Leu	Ser	Arg	Lys	Ile	Asp	Arg	Tyr	Leu	Ser	Pro	Val	Ala	Val
			180					185					190		
Pro	Ile	Val	Val	His	Pro	Gly	Glu	Lys	His	Ser	Glu	Thr	Thr	Tyr	Ser
		195					200					205			
Phe	His	Phe	Pro	Leu	Ser	Tyr	Trp	Val	Gln	Ala	Leu	Ser	Asn	His	Asn
	210					215					220				
Leu	Leu	Ile	Asp	Ser	Met	Glu	Glu	Trp	Ile	Ser	Pro	Lys	Lys	Ser	Ser
225					230					235					240
Gly	Lys	Arg	Ala	Arg	Ala	Glu	Asn	Leu	Ser	Arg	Lys	Glu	Phe	Pro	Leu
			245					250						255	
Phe	Leu	Phe	Ile	Ser	Ala	Leu	Lys	Ile	Ser	Lys					
			260					265							

(2) INFORMATIONS POUR LA SEQ ID NO: 318:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 318 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 320544..321497

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 318:

Phe	Leu	Cys	Leu	Leu	Leu	Gly	Arg	Tyr	Ser	Asp	Ala	Thr	Ile	Phe	Arg
1			5					10					15		
Ser	Gly	Leu	Asn	Lys	Ile	Phe	Cys	Ser	Gly	Ile	Thr	Gln	Ala	Ser	Leu
		20					25					30			
Lys	Arg	Leu	Ile	Ser	Tyr	Leu	Val	Ile	Thr	Leu	Val	Ser	Pro	Met	Ile
	35					40					45				
Phe	Ile	Ile	Val	Cys	Gly	Ser	Trp	Ile	Tyr	Ile	Thr	Gln	Ile	Leu	Pro
50					55					60					
Ile	Asn	Tyr	Pro	Gln	Leu	Phe	Ser	Phe	Ser	His	Ser	Met	Ala	Phe	Ile
65				70					75					80	
Tyr	Ile	Val	Ser	Arg	Leu	Leu	Pro	Tyr	Ala	Leu	Leu	Tyr	Gly	Ile	Leu
			85					90				95			
Phe	Cys	Cys	Tyr	Ala	Phe	Leu	Ser	Arg	Val	Pro	Thr	Lys	Lys	Ser	Ala
		100					105					110			
Ala	Phe	Phe	Ala	Ala	Thr	Ile	Ala	Gly	Ser	Ala	Trp	Ile	Leu	Ser	Gln
	115					120					125				
Lys	Ile	Phe	Phe	Cys	Leu	Gln	Leu	His	Leu	Phe	Asn	Tyr	Ser	Phe	Thr
	130				135					140					
Tyr	Gly	Ala	Leu	Val	Ala	Leu	Pro	Ser	Phe	Leu	Leu	Leu	Tyr	Leu	
145				150					155					160	
Tyr	Ala	Ile	Ile	Tyr	Leu	Phe	Gly	Gly	Ala	Leu	Thr	Phe	Leu	Phe	Gln

Asn Lys Gly Phe Ser Ile Leu Ile Pro Lys Glu Glu Ile Phe Pro Ser
 165 170
 180 185 190
 Ser Tyr Phe Lys Phe Ile Leu Cys Val Tyr Val Leu Ser Leu Ile Thr
 195 200 205
 Glu His Phe Asp Asn Ala Leu Pro Pro Pro Ser Ala Asn Tyr Leu Ala
 210 215 220
 Asn Lys Ala Lys Ala Ser Ile Gly Glu Thr Ser Gln Cys Leu Asp Ile
 225 230 235 240
 Leu Glu Arg Glu Gly Met Ile Leu Lys Tyr Lys Glu Gly Tyr Lys Pro
 245 250 255
 Ser His Asn Ile Ala Asn Leu His Ile Asn Thr Ile Phe Asp Gln Leu
 260 265 270
 Thr Lys Ser Pro Ala Phe Ser Lys Ile Cys Ser Pro Ser Leu Ile Pro
 275 280 285
 Ile Gln Asp Ala Leu Thr His Ile Leu Thr Glu Ile Lys Lys Asn Ser
 290 295 300
 His Asn Leu Ser Leu Ser Glu Ile Ala Lys Lys Val Asn Ser
 305 310 315

(2) INFORMATIONS POUR LA SEQ ID NO: 319:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 151 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 321485..321937

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 319:

Lys Ser Glu Phe Met Lys Arg Ser Pro Trp Tyr Lys Ile Phe Gly Tyr
 1 5 10 15
 Tyr Leu Leu Val Gly Val Pro Leu Ala Leu Leu Ala Leu Pro Lys
 20 25 30
 Phe Leu Ser Ser Glu Ser Gly Lys Tyr Leu Phe Leu Ser Val Leu Asn
 35 40 45
 Lys Glu Thr Gly Leu Gln Cys Glu Ile Glu Gln Leu His Leu Ser Trp
 50 55 60
 Phe Gly Ser Gln Thr Ala Lys Lys Ile Arg Ile Arg Gly Ile Asp Ser
 65 70 75 80
 Glu Ser Glu Ile Phe Ala Ala Glu Lys Ile Ile Val Lys Gly Ser Leu
 85 90 95
 Pro Arg Leu Leu Tyr Arg Phe Pro Lys Ala Leu Thr Leu Thr Gly
 100 105 110
 Trp Ser Leu Gln Ile Asp Glu Ser Leu Ser Met Asn Ser Pro Ser Leu
 115 120 125
 Tyr His Leu Asp Pro Gly Val Leu Leu Ser Lys Ile Glu Arg Arg Leu
 130 135 140
 Ser Leu Gln Asn Leu Asp Pro
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 320:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 154 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 321901..322362

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 320:

Asn	Arg	Ala	Gln	Val	Ile	Thr	Ser	Glu	Leu	Gly	Ser	Ile	Thr	Met	Lys
1				5					10					15	
Thr	Ile	Asn	Gly	Ser	Thr	Leu	Ser	Val	Ser	Gly	Phe	Tyr	Val	Lys	Lys
		20					25						30		
Thr	Ala	Glu	Gln	Leu	Leu	Ile	Arg	Ala	Leu	Thr	Lys	Glu	Asn	Asp	Val
	35					40						45			
Pro	Gly	Ser	Val	Ala	Val	Glu	Gly	Ala	Leu	Ser	Pro	Asn	Phe	Val	Leu
	50				55						60				
Asn	Val	Glu	Leu	Ser	Ser	Val	Pro	Ala	Ser	Leu	Phe	Lys	Leu	Phe	Ile
65					70					75					80
Ala	Ser	Pro	Ser	Leu	Asp	Arg	Ile	Leu	Ser	Thr	Glu	Asn	Leu	Ile	Asn
			85						90					95	
Leu	Thr	Ala	Lys	Ala	His	Gln	Glu	Lys	Asp	Ser	Thr	Leu	Ile	Thr	Leu
		100						105					110		
Thr	Ala	Glu	Gly	Asn	Gln	Ile	Ser	Ala	Lys	Leu	Arg	Gly	Tyr	Val	Arg
		115				120						125			
Asp	Arg	Val	Phe	Leu	Ile	Thr	Gln	Gly	Gly	Ala	Ser	Phe	Cys	Ala	Leu
	130					135					140				
Thr	Ala	Tyr	Asn	Asn	Phe	Ser	Asn	Ser	Leu						
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 321:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 280 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 322301..323140

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 321:

Ser	His	Lys	Ala	Glu	Pro	Pro	Ser	Val	Leu	Leu	Gln	Pro	Thr	Ile	Thr
1				5					10					15	
Ser	Arg	Ile	Leu	Ser	Glu	Leu	Ser	Pro	Leu	Asp	Thr	Pro	Ile	Arg	Ser
		20					25						30		
Gln	Glu	Ala	Tyr	Leu	Phe	Ile	Ser	Glu	Ala	Lys	Leu	Pro	Leu	Ser	Ile
	35					40						45			
Ser	Lys	Trp	Ser	Ala	Ser	Asp	Phe	Ser	Leu	Gln	Ala	Asn	Leu	Pro	Gln
	50				55					60					
Ile	Ser	Val	Asp	Thr	Leu	Asp	Pro	Asn	Leu	Ser	Ile	Arg	Thr	Glu	Asn
65				70						75					80
Thr	Lys	Ile	Ser	Ile	Arg	Lys	Ser	Asp	His	Leu	Thr	Val	Met	Arg	Ser

(2) INFORMATION POUR LA SEQ ID NO: 322:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(i) CARACTERISTIQUES DE LA SÉRIE
(A) LONGUEUR: 590 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 323144..324913

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 322:

[illegible]

Leu	Thr	Glu	Lys	Ala	His	Gly	Ser	Leu	Gln	Trp	Glu	Ile	Ser	Pro	Glu
145					150					155					160
Arg	Tyr	Ser	Ser	Phe	Phe	Glu	Lys	Ala	Ser	Cys	Pro	Pro	Ser	Cys	Ile
				165						170					175
Leu	His	Arg	Pro	Thr	Thr	Phe	Arg	Leu	Asp	Leu	Ser	Lys	Ile	Ser	Cys
			180					185					190		
Leu	Asp	Lys	Lys	Thr	Gly	Tyr	Ser	Cys	Leu	Ser	Leu	Leu	Ser	Gln	Gly
		195					200					205			
Gly	Ile	Glu	Gly	Lys	Leu	Ser	Ser	Thr	Pro	Leu	Val	Phe	Tyr	Asp	His
	210					215					220				
Leu	Ser	Lys	Glu	Asn	Phe	Ile	Val	Asn	Asn	Ile	Gly	Gly	Ser	Val	Tyr
225				230						235					240
Ala	Gln	Asn	Val	Asn	Asp	Leu	Ile	Gln	Tyr	Gln	Leu	Asn	Gly	Asn	Cys
			245						250					255	
Leu	Ala	Pro	Asn	Gln	Asp	Asn	Lys	Thr	Pro	Val	Ser	Phe	Ile	Ile	Glu
			260					265					270		
Gly	Glu	Ala	Arg	Asn	Ile	Phe	Ser	Asp	Glu	Thr	Arg	Ala	Cys	Ser	Gln
		275					280					285			
Thr	Ala	Thr	Trp	Val	Asn	Ile	Pro	Thr	Ser	Phe	Ile	Thr	Gly	Ile	Phe
	290				295						300				
Pro	Ile	Ser	Pro	Gly	Val	Arg	Ser	Lys	Leu	Thr	Ser	Leu	Ala	Gly	Pro
305				310						315					320
Lys	Ile	His	Val	Ser	Ile	His	Asn	Asp	Phe	Ser	Arg	Gly	Glu	Gly	Pro
			325						330					335	
Val	Thr	Ile	Lys	Val	Asp	Ser	Glu	Asn	Leu	Thr	Ala	Tyr	Phe	Pro	Leu
			340					345					350		
Val	Leu	Thr	Glu	Gln	Ala	Ile	Leu	Leu	Glu	Asp	Asp	Leu	Thr	Ala	Ser
		355					360					365			
Leu	His	Ile	Asn	Glu	Glu	Ile	Asn	Lys	Ala	Phe	Leu	Arg	Glu	Phe	Asn
	370					375					380				
Pro	Leu	Ile	Ala	Glu	Gly	Ala	Tyr	Ser	Lys	His	Pro	Val	Ser	Leu	
385				390					395						400
Arg	Val	Asn	Lys	Gln	Asn	Phe	Tyr	Leu	Pro	Ile	Lys	Pro	Tyr	Ser	Phe
			405						410					415	
Glu	Asn	Phe	Arg	Ile	Gln	Ser	Ala	Ser	Leu	Asp	Phe	Gly	Lys	Ile	Glu
			420					425					430		
Ile	Ala	Asn	Thr	Gly	Thr	Met	Gln	Asp	Leu	Phe	Gln	Phe	Leu	Asp	Val
		435					440					445			
Glu	Ala	Glu	Gln	Gln	Arg	Val	Glu	Ser	Trp	Phe	Thr	Pro	Ile	Phe	Phe
		450					455				460				
Ser	Val	Gln	Lys	Gly	Gln	Ile	Ile	Cys	Lys	Arg	Phe	Asp	Ala	Leu	Ile
465				470					475						480
Asp	Gly	Arg	Ile	Arg	Leu	Ala	Leu	Trp	Gly	Lys	Thr	Asp	Ile	Val	Arg
			485						490					495	
Glu	Arg	Leu	Ala	Met	Thr	Leu	Gly	Ile	Asp	Pro	Glu	Leu	Ile	Lys	Lys
			500					505					510		
Leu	Phe	Arg	Asn	Thr	Met	Leu	Lys	Thr	Lys	Asn	Phe	Phe	Leu	Ile	Lys
		515					520					525			
Ile	Arg	Gly	Pro	Ile	Ser	Ser	Pro	Glu	Ile	Asp	Trp	Ser	Ser	Ala	Tyr
		530				535					540				
Ala	Arg	Ile	Ala	Leu	Leu	Lys	Ser	Tyr	Thr	Ile	Ala	Gly	Pro	Leu	Asn
545					550					555					560
Ser	Leu	Ala	Asp	Lys	Leu	Phe	Ser	Ser	Leu	Gly	Glu	Pro	Thr	Pro	Thr
			565						570					575	
Gln	Thr	Val	Ser	Pro	Leu	Pro	Trp	Glu	Val	Ser	Glu	Thr	Glu		
			580					585					590		

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 215 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(324977..325621)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 323:

Met	Thr	Val	Glu	Val	Lys	Asp	Leu	Thr	Val	Ala	Val	Lys	Gly	Lys	Glu	1	5	10	15
Ile	Leu	Ser	Asn	Val	Ser	Phe	Ser	Leu	Val	Pro	Gly	Arg	Ile	Thr	Leu	20	25	30	35
Phe	Ile	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Ile	Leu	Arg	Ser	Leu	40	45	50	55
Val	Gly	Leu	Thr	Pro	Ile	Ser	Ser	Gly	Ser	Ile	Ser	Val	Val	Gly	Asp	60	65	70	75
Pro	Pro	Gly	Phe	Val	Phe	Gln	Gln	Pro	Glu	Leu	Phe	Pro	His	Met	Thr	80	85	90	95
Val	Leu	Asp	Asn	Cys	Ala	His	Pro	Gln	Met	Ile	Val	Lys	Lys	Arg	Gly	100	105	110	115
Glu	Arg	Glu	Ala	Lys	Asp	Lys	Ala	Leu	Asp	Leu	Leu	Gly	Met	Leu	Glu	120	125	130	135
Leu	Arg	Glu	Tyr	Ala	Ser	Ser	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	Gln	140	145	150	155
Arg	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Leu	Asp	Met	Arg	Ala	160	165	170	175
Ile	Leu	Phe	Asp	Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Phe	Ser	Ala	Ser	180	185	190	195
Lys	Phe	Leu	Gln	Ile	Val	Leu	Ser	Leu	Lys	Glu	Gln	Gly	Met	Thr	Ile	200	205	210	215
Ala	Ile	Ser	Thr	His	Asp	Met	Leu	Phe	Ile	Asn	Gln	Cys	Leu	Asp	Arg				
Val	Tyr	Leu	Val	Asp	Lys	Gly	Gln	Ile	Ile	Asp	Ala	Tyr	Asp	Ser	Leu				
His	Asp	Asp	Pro	Gln	Gly	Lys													

(2) INFORMATIONS POUR LA SEQ ID NO: 324:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(325621..326268)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 324:

Gly	Ile	Val	Glu	His	Tyr	Leu	Leu	Thr	Ala	Lys	Leu	Leu	Leu	Arg	Gly	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Cys Gly Tyr Thr Leu Leu Ile Thr Ala Ile Ser Leu Val Cys Gly Phe
 20 25 30
 Val Leu Gly Trp Gly Ile Gly Thr Val Asn Ser Arg Tyr Phe Pro Cys
 35 40 45
 Arg Ile Ser Lys Phe Leu Gly Asn Phe Tyr Val Val Ala Val Arg Gly
 50 55 60
 Thr Pro Leu Phe Ile Gln Ile Leu Ile Val Tyr Phe Gly Leu Pro Ser
 65 70 75 80
 Leu Ile Lys Val Asn Leu Ser Pro Leu Val Ala Gly Leu Ile Ala Leu
 85 90 95
 Thr Leu Asn Ser Ala Ala Tyr Leu Ala Glu Asn Val Arg Ala Gly Ile
 100 105 110
 Asn Ala Leu Pro Val Gln Gln Trp Glu Ala Ala Lys Val Leu Gly Tyr
 115 120 125
 Thr Gly Pro Gln Ile Phe Leu His Ile Leu Tyr Pro Gln Val Phe Lys
 130 135 140
 Asn Ile Leu Pro Ser Leu Ala Asn Glu Phe Val Ser Leu Ile Lys Glu
 145 150 155 160
 Ser Ser Ile Leu Met Val Val Gly Val Pro Glu Leu Thr Lys Val Thr
 165 170 175
 Lys Asp Ile Val Ala Arg Glu Leu Asn Pro Met Glu Met Tyr Leu Ile
 180 185 190
 Cys Ala Gly Leu Tyr Leu Ile Met Thr Ser Ala Phe Ser Tyr Phe Ala
 195 200 205
 Arg Leu Ser Glu Lys Glu Ser Ala
 210 215

(2) INFORMATIONS POUR LA SEQ ID NO: 325:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 326469..327203

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 325:

Met Asp Arg Ser Pro Leu Phe Leu Ile Ile Met Gly Ala Pro Gly Ser
 1 5 10 15
 Gly Lys Gly Thr Gln Ser Lys Leu Leu Ala Ser Gln Leu Ser Leu Leu
 20 25 30
 His Ile Ser Ser Gly Asp Leu Leu Arg Gly Ala Val Ser Lys Asp Thr
 35 40 45
 Pro Leu Ser Gln Glu Ile Lys Ser Tyr Leu Asp Gln Gly Lys Leu Leu
 50 55 60
 Pro Asp Thr Leu Val Trp Lys Leu Val His Glu Lys Leu Asp Glu Phe
 65 70 75 80
 Gln Gln Asp Thr Leu Leu Arg Arg Leu Ser Phe Leu Ser Arg Ser Glu
 85 90 95
 Asn Ser Ala Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Lys
 100 105 110
 Leu Leu His Glu Phe Leu Ser Ser Tyr Phe Pro Asn Tyr Lys Val Ile
 115 120 125
 Leu Leu Asp Ile Ser Asp Glu Glu Val Leu Asn Arg Leu Thr Ser Arg

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      130              135              140
Tyr Ile Cys Pro Ala Cys Gln Gly Ile Tyr Asn Glu Gln Gln Gly Phe
145              150              155              160
Ser Ser Cys Pro Lys Cys Ser Val Glu Leu Ile Arg Arg Ser Asp Asp
      165              170              175
Thr Leu Glu Val Ile Leu Asp Arg Ile Gln Thr Tyr Lys Gln Glu Thr
      180              185              190
Gln Pro Val Leu Asp Tyr Tyr Thr Glu Lys Gln Lys Leu Ile Thr Ile
      195              200              205
Asp Ala Asn Ala Pro Thr Gln Gln Val Phe Gln Ser Ile Leu Asp Ser
      210              215              220
Leu Ser Ala Ser Leu Val Tyr Gln Glu Arg Asp Cys Cys Asn Cys Asp
225              230              235              240
Cys Asp Asp Glu Asp
      245

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(2) INFORMATIONS POUR LA SEQ ID NO: 326:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 290 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 327281..328150

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 326:

```

Cys Leu Tyr Arg Gly Ser Pro Met Pro His Gln Val Leu Leu Ser Pro
1      5      10      15
Val Cys Asp Leu Leu Ser Asn Ala Glu Gly Ile Glu Thr Gln Val Leu
      20      25      30
Phe Gly Glu Arg Ile Cys Asn His Asn His Arg His Tyr Ala Tyr Ser
      35      40      45
Gln Leu Val Phe Ser Ser Ile Trp Lys Pro Tyr Pro Gly Asp Ser Leu
      50      55      60
Gln Asn Ile Pro Leu Phe Ser Ser Gln Leu Gln Pro Pro Asn Ala Val
      65      70      75      80
Val Cys Ser Gln Glu Ala Phe Leu Asp Pro Trp His Ile Pro Leu Pro
      85      90      95
Phe Ala Ala Pro Leu His Ile Asp Asn Gln Asn Gln Val Ser Leu Ser
      100      105      110
Pro Ala Ser Ile Ala Leu Leu Asn Ser Asn Ser Arg Ser Asn Tyr Ala
      115      120      125
Lys Ala Phe Cys Ser Thr Lys Glu Ile Arg Phe Leu Asn Ser Ser Phe
      130      135      140
Ser Leu Arg Asp Leu Val Ser Phe Ala Glu Gln Leu Ile Asp Thr Pro
145      150      155      160
Tyr Val Trp Gly Gly Arg Cys Ile His Lys Gln Leu Pro Arg Asn Gly
      165      170      175
Val Asp Cys Ser Gly Tyr Ile Gln Leu Leu Tyr Gln Val Thr Gly Arg
      180      185      190
Asn Ile Pro Arg Asn Ala Arg Asp Gln Tyr Arg Asp Cys Ser Pro Val
      195      200      205
Lys Asp Phe Ser Ser Leu Pro Ile Gly Gly Leu Ile Phe Leu Lys Lys
210      215      220

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Ala Ser Thr Gly Gln Ile Asn His Val Met Met Lys Ile Ser Glu His
 225 230 235 240
 Glu Phe Ile His Ala Ala Glu Lys Ile Gly Lys Val Glu Lys Val Ile
 245 250 255
 Leu Gly Asn Arg Ala Phe Phe Lys Gly Asn Leu Phe Cys Ser Leu Gly
 260 265 270
 Glu Pro Pro Ile Glu Ala Val Phe Gly Val Pro Lys Asn Arg Lys Ala
 275 280 285
 Phe Phe
 290

(2) INFORMATIONS POUR LA SEQ ID NO: 327:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(328204..328605)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 327:

Phe Val Thr Lys Asn Met Ile Gln Glu Ser Val Ala Thr Gly Arg Arg
 1 5 10 15
 Lys Gln Ala Val Ser Ser Val Arg Leu Arg Ser Gly Asn Gly Lys Ile
 20 25 30
 Asp Val Asn Gly Lys Thr Leu Glu Gln Tyr Phe Pro Leu Glu Val Gln
 35 40 45
 Arg Ala Thr Ile Leu Ala Pro Leu Arg Met Leu Gly Asp Val Asn Ser
 50 55 60
 Phe Asp Leu Ile Ile Arg Val Ser Gly Gly Gly Val Gln Gly Gln Val
 65 70 75 80
 Ile Ala Thr Arg Leu Gly Leu Ala Arg Ala Val Leu Gln Glu Lys Glu
 85 90 95
 Asp Ile Lys Gln Glu Leu Lys Ala Gln Gly Phe Leu Thr Arg Asp Pro
 100 105 110
 Arg Lys Lys Glu Arg Lys Lys Tyr Gly Arg Lys Lys Ala Arg Lys Ser
 115 120 125
 Phe Gln Phe Ser Lys Arg
 130

(2) INFORMATIONS POUR LA SEQ ID NO: 328:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 104 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(328734..329045)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 328:

Lys Thr Thr Leu Ala Lys Ala Ser Asp Asp Arg Asn Lys Ala Trp Tyr
 1 5 10 15
 Val Val Asn Ala Glu Gly Lys Thr Leu Gly Arg Leu Ser Ser Glu Val
 20 25 30
 Ala Lys Ile Leu Arg Gly Lys His Lys Val Thr Phe Thr Pro His Val
 35 40 45
 Ala Met Gly Asp Gly Val Ile Val Ile Asn Ala Glu Lys Val Arg Leu
 50 55 60
 Thr Gly Ala Lys Arg Ala Gln Lys Val Tyr His Tyr Tyr Thr Gly Phe
 65 70 75 80
 Ile Ser Gly Met Arg Glu Val Pro Phe Glu Asn Met Ile Ala Arg Asn
 85 90 95
 Cys Leu Cys Tyr Arg Ala Cys Cys
 100

(2) INFORMATIONS POUR LA SEQ ID NO: 329:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 124 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(329292..329663)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 329:

Phe Asn Ala Glu Ser Met Gln Arg Ile Gln Val Ile Thr Phe Thr Pro
 1 5 10 15
 Ser Pro Gly Arg Leu Asp Tyr Tyr Leu Pro Pro Ala Gly Pro Ala Val
 20 25 30
 Arg Val Asp Gly Ala Cys Tyr Ser Gly Tyr Ala Ile Pro Tyr Tyr
 35 40 45
 Asp Ser Met Ile Ala Lys Val Ile Thr Lys Gly Lys Asn Arg Glu Glu
 50 55 60
 Ala Ile Ala Ile Met Lys Arg Ala Leu Lys Glu Phe His Ile Gly Gly
 65 70 75 80
 Val His Ser Thr Ile Pro Phe His Gln Phe Met Leu Asp Asn Pro Lys
 85 90 95
 Phe Leu Leu Ser Asp Tyr Asp Ile Asn Tyr Val Asp Gln Leu Leu Ala
 100 105 110
 Ser Gly Ser Thr Phe Leu Asn Leu Ala Asp Gly Ser
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 330:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 353 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(329608..330666)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 330:

Leu	Met	Lys	Glu	Val	Leu	Ile	Ala	Asn	Arg	Gly	Glu	Ile	Ala	Val	Arg	1	5	10	15
Ile	Ile	Arg	Ala	Cys	His	Asp	Leu	Gly	Leu	Ala	Thr	Val	Ala	Val	Tyr	20	25	30	
Ser	Met	Ala	Asp	Gln	Glu	Ala	Leu	His	Val	Leu	Leu	Ala	Asp	Glu	Ala	35	40	45	
Val	Cys	Ile	Gly	Glu	Ala	Gln	Ala	Ala	Lys	Ser	Tyr	Leu	Lys	Ile	Ala	50	55	60	
Asn	Ile	Leu	Ala	Ala	Cys	Glu	Ile	Thr	Gly	Ala	Asp	Ala	Val	His	Pro	65	70	75	80
Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	Asn	Phe	Ala	Ser	Ile	Cys	Glu	85	90	95	
Ser	Cys	Gly	Leu	Thr	Phe	Ile	Gly	Pro	Ser	Ala	Glu	Ser	Ile	Ala	Thr	100	105	110	
Met	Gly	Asp	Lys	Val	Ala	Ala	Lys	Gln	Leu	Ala	Lys	Lys	Ile	Lys	Cys	115	120	125	
Pro	Val	Ile	Pro	Gly	Ser	Glu	Gly	Val	Val	Lys	Asp	Glu	Val	Glu	Gly	130	135	140	
Ile	Arg	Ile	Ala	Glu	Lys	Ile	Gly	Phe	Pro	Ile	Val	Ile	Lys	Ala	Val	145	150	155	160
Ala	Gly	Gly	Gly	Gly	Arg	Gly	Ile	Arg	Ile	Val	Arg	Glu	Lys	Asp	Glu	165	170	175	
Phe	Tyr	Arg	Ala	Phe	Thr	Ala	Ala	Arg	Ala	Glu	Ala	Glu	Ala	Gly	Phe	180	185	190	
Asn	Asn	Pro	Asp	Val	Tyr	Ile	Glu	Lys	Phe	Ile	Glu	Asn	Pro	Arg	His	195	200	205	
Leu	Glu	Val	Gln	Val	Ile	Gly	Asp	Lys	His	Gly	Asn	Tyr	Val	Tyr	Leu	210	215	220	
Gly	Glu	Arg	Asp	Cys	Thr	Val	Gln	Arg	Arg	Arg	Gln	Lys	Leu	Ile	Glu	225	230	235	240
Glu	Thr	Pro	Ser	Pro	Ile	Leu	Thr	Pro	Glu	Met	Gln	Ala	Lys	Val	Gly	245	250	255	
Lys	Val	Ala	Val	Asp	Leu	Ala	Arg	Ser	Ala	Gly	Tyr	Phe	Ser	Val	Gly	260	265	270	
Thr	Val	Glu	Phe	Leu	Leu	Asp	Lys	Glu	Lys	Arg	Phe	Tyr	Phe	Met	Glu	275	280	285	
Met	Asn	Thr	Arg	Ile	Gln	Val	Glu	His	Thr	Ile	Thr	Glu	Glu	Val	Thr	290	295	300	
Gly	Ile	Asp	Leu	Leu	Lys	Ala	Gln	Ile	Ser	Val	Ala	Lys	Gly	Glu	Lys	305	310	315	320
Leu	Pro	Trp	Lys	Gln	Lys	Asn	Ile	Glu	Phe	Lys	Gly	His	Val	Ile	Gln	325	330	335	
Cys	Arg	Ile	Asn	Ala	Glu	Asp	Pro	Ser	Asn	Asn	Phe	Tyr	Ser	Phe	Pro	340	345	350	
Trp																			

(2) INFORMATIONS POUR LA SEQ ID NO: 331:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 164 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(330670..331161)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 331:

```

Met Asp Leu Lys Gln Ile Glu Lys Leu Met Ile Ala Met Gly Arg Asn
1          5          10          15
Lys Met Lys Arg Ile Val Ile Lys Arg Glu Gly Leu Glu Leu Glu Leu
20          25          30
Glu Arg Asp Thr Val Pro Ser Ile Gln Glu Pro Val Phe Tyr Asp Asn
35          40          45
Arg Leu Phe Ala Gly Phe Ser Gln Glu Arg Pro Ile Pro Thr Asp Gln
50          55          60
Asn Leu Gly Asn Pro Ile Val Lys Glu Ser Ile Glu Lys Lys Glu Ser
65          70          75          80
Glu Ala Pro Ala Gln Gly Asp Phe Ile Val Ser Pro Leu Val Gly Thr
85          90          95
Phe Tyr Gly Ser Pro Ser Pro Glu Ala Pro Ala Phe Ile Lys Pro Gly
100         105         110
Asp Thr Val Ser Glu Asp Thr Val Val Cys Ile Val Glu Ala Met Lys
115         120         125
Val Met Asn Glu Val Lys Ala Gly Met Ser Gly Arg Val Glu Glu Ile
130         135         140
Leu Ile Thr Asn Gly Asp Pro Val Gln Phe Gly Ser Lys Leu Phe Arg
145         150         155         160
Ile Val Lys Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 332:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 185 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(331177..331731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 332:

```

Met Val Leu Ser Ser Gln Leu Ser Val Gly Met Phe Ile Ser Thr Lys
1          5          10          15
Asp Gly Leu Tyr Lys Val Val Ser Val Ser Lys Val Ser Gly Asn Lys
20          25          30
Gly Asp Thr Phe Ile Lys Val Ser Leu Gln Ala Ala Gly Ser Asp Val
35          40          45
Ile Val Glu Arg Asn Phe Lys Ala Gly Gln Glu Val Lys Glu Ala Gln
50          55          60
Phe Glu Pro Arg Asn Leu Glu Tyr Leu Tyr Leu Glu Glu Asp Lys Tyr
65          70          75          80
Leu Phe Leu Asp Leu Gly Asn Tyr Asp Lys Ile Tyr Ile Pro Lys Glu
85          90          95
Ile Met Lys Asp Asn Ala Met Phe Leu Lys Ala Gly Val Thr Val Phe
100         105         110

```

Ala Leu Val His Glu Gly Thr Val Phe Ser Met Glu Leu Pro His Phe
 115 120 125
 Leu Glu Leu Met Val Ala Lys Thr Asp Phe Pro Gly Asp Ser Leu Ser
 130 135 140
 Leu Ser Gly Gly Ala Lys Lys Ala Leu Leu Glu Thr Gly Val Glu Val
 145 150 155 160
 Leu Val Pro Pro Phe Val Glu Ile Gly Asp Val Ile Lys Val Asp Thr
 165 170 175
 Arg Thr Cys Glu Tyr Ile Gln Arg Val
 180 185

(2) INFORMATIONS POUR LA SEQ ID NO: 333:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 228 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(331721..332404)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 333:

Met Lys Lys Gln Gly Val Leu Val Ala Pro Ser Ile Met Gly Ala Asp
 1 5 10 15
 Leu Ala Cys Ile Gly Arg Glu Ala Arg Asn Ile Glu Glu Ser Gly Ala
 20 25 30
 Asp Leu Ile His Ile Asp Val Met Asp Gly His Phe Val Pro Asn Ile
 35 40 45
 Thr Phe Gly Pro Gly Val Val Ala Ala Ile Asn Arg Ser Thr Glu Leu
 50 55 60
 Phe Leu Glu Val His Ala Met Ile Tyr Thr Pro Phe Glu Phe Val Glu
 65 70 75 80
 Ala Phe Val Lys Ala Gly Ala Asp Arg Ile Val His Phe Glu Ala
 85 90 95
 Ala Glu Asn Ile Lys Glu Ile Ile Ser Tyr Ile Gln Lys Cys Gly Val
 100 105 110
 Gln Ala Gly Val Ala Phe Ser Pro Glu Thr Ser Ile Glu Phe Val Thr
 115 120 125
 Ser Phe Ile Pro Leu Cys Asp Val Ile Leu Leu Met Ser Val His Pro
 130 135 140
 Gly Phe Cys Gly Gln Lys Phe Ile Pro Asp Thr Ile Glu Arg Ile Gln
 145 150 155 160
 Phe Val Lys Gln Ala Ile Gln Val Leu Gly Arg Glu Gly Ser Cys Leu
 165 170 175
 Ile Glu Val Asp Gly Gly Ile Asp Lys Glu Ser Ala Arg Ala Cys Arg
 180 185 190
 Glu Ala Gly Ala Asp Ile Leu Val Ala Ala Ser Tyr Phe Phe Glu Lys
 195 200 205
 Asp Ser Ile Asn Met Lys Glu Lys Val Leu Leu Leu Gln Gly Glu Glu
 210 215 220
 His Gly Ala Lys
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 334:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 81 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 332779..333021

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 334:

Ser	Pro	Arg	Ile	Trp	Phe	Gln	Arg	Thr	Leu	Asn	Glu	Lys	Val	Pro	Met
1				5					10					15	
Thr	Thr	Pro	Thr	Leu	Ile	Val	Thr	Pro	Pro	Ser	Pro	Pro	Ala	Pro	Ser
			20					25					30		
Tyr	Ser	Ala	Asn	Arg	Val	Pro	Gln	Pro	Ser	Leu	Met	Asp	Lys	Ile	Lys
		35					40					45			
Lys	Ile	Ala	Ala	Ile	Ala	Ser	Leu	Ile	Leu	Ile	Gly	Thr	Ile	Gly	Phe
	50					55				60					
Leu	Ala	Leu	Leu	Gly	His	Leu	Val	Gly	Phe	Leu	Ile	Ala	Pro	Gln	Ile
65					70					75					80
His															

(2) INFORMATIONS POUR LA SEQ ID NO: 335:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 195 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 333005..333589

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 335:

Ser	Leu	His	Lys	Phe	Thr	Asn	Val	Leu	Leu	Ala	Leu	Phe	Ile	Thr	Ser
1				5					10					15	
Leu	Ala	Gly	Asn	Ala	Leu	Tyr	Leu	Gln	Lys	Thr	Ala	Asn	Leu	His	Leu
			20					25					30		
Tyr	Gln	Asp	Leu	Gln	Arg	Glu	Val	Gly	Ser	Leu	Lys	Glu	Ile	Asn	Phe
		35					40					45			
Met	Leu	Ser	Val	Leu	Gln	Lys	Glu	Phe	Leu	His	Leu	Ser	Lys	Glu	Phe
	50					55					60				
Ala	Thr	Thr	Ser	Lys	Asp	Leu	Ser	Ala	Val	Ser	Gln	Asp	Phe	Tyr	Ser
65					70					75					80
Cys	Leu	Gln	Xaa	Xaa	Arg	Asp	Asn	Tyr	Lys	Gly	Phe	Glu	Ser	Leu	Leu
			85						90					95	
Asp	Glu	Tyr	Lys	Asn	Ser	Thr	Glu	Glu	Met	Arg	Lys	Leu	Phe	Ser	Gln
			100					105					110		
Glu	Ile	Ile	Ala	Asp	Leu	Lys	Gly	Ser	Val	Ala	Ser	Leu	Arg	Glu	Glu
		115					120					125			
Ile	Arg	Phe	Leu	Thr	Pro	Leu	Ala	Glu	Glu	Val	Arg	Arg	Leu	Ala	His
			130				135					140			

```

Asn Gln Glu Ser Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg
145                      150                      155                      160
Asp Ser Leu Arg Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr
                      165                      170                      175
Leu Thr Ser Ala Lys Leu His Tyr Asn Glu Lys Arg Ala Gln Ile Cys
                      180                      185                      190
Val Pro Arg
                      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 336:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 184 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(333806..334357)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 336:

```

Gln Glu Thr Lys Phe Asp Lys Gly Ile Gly Gly Tyr Met Ile Cys Cys
1      5      10      15
Asp Lys Val Leu Ser Ser Val Gln Ser Met Pro Val Ile Asp Lys Cys
      20      25      30
Ser Val Thr Lys Cys Leu Gln Thr Ala Lys Gln Ala Val Val Leu Ala
      35      40      45
Leu Ser Leu Phe Ala Val Phe Ala Ser Gly Ser Leu Ser Ile Leu Ser
      50      55      60
Ala Ala Val Leu Phe Ser Gly Thr Ala Ala Val Leu Pro Tyr Leu Leu
65      70      75      80
Ile Leu Thr Thr Ala Leu Leu Gly Cys Val Tyr Ala Val Ile Val Leu
      85      90      95
Leu Arg Ser Leu Ser Ala Val Val Gln Ser Cys Lys Lys Arg Ser Pro
      100     105     110
Glu Glu Ile Glu Gly Ala Ala Arg Pro Ser Asp Gln Gln Glu Ser Gly
      115     120     125
Gly Arg Leu Ser Xaa Glu Ser Ala Ser Pro Gln Ala Ser Pro Thr Ser
      130     135     140
Ser Thr Leu Arg Leu Glu Ser Ala Phe Arg Ser Ile Gly Asp Ser Val
145      150      155      160
Ser Gly Ala Phe Asp Asp Ile Asn Lys Asp Asn Ser Arg Ser Arg Phe
      165      170      175
Thr Leu Leu Leu Arg Asp Asp Met
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 337:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 91 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 334089..334361

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 337:

Thr	His	Pro	Arg	Arg	Ala	Val	Val	Asn	Ile	Ser	Arg	Tyr	Gly	Arg	Thr
1				5					10					15	
Ala	Ala	Val	Pro	Leu	Asn	Ser	Thr	Ala	Ala	Asp	Asn	Met	Asp	Lys	Leu
			20					25					30		
Pro	Glu	Ala	Asn	Thr	Ala	Asn	Lys	Asp	Asn	Ala	Arg	Thr	Thr	Ala	Cys
		35					40					45			
Leu	Ala	Val	Cys	Lys	His	Phe	Val	Thr	Glu	His	Leu	Ser	Ile	Thr	Gly
	50					55					60				
Ile	Asp	Cys	Thr	Leu	Asp	Lys	Thr	Leu	Ser	Gln	Gln	Ile	Met	Tyr	Pro
65					70					75					80
Pro	Ile	Pro	Leu	Ser	Asn	Phe	Val	Ser	Cys	His					
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 338:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(334729..335142)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 338:

Glu	Phe	Leu	Gly	Gly	Ser	Met	Glu	Cys	Val	Lys	Gln	Leu	Cys	Arg	Asn
1				5					10					15	
His	Leu	Arg	Leu	Asp	Asn	Leu	Thr	Asp	Pro	Val	Arg	Ser	Val	Leu	Thr
			20					25					30		
Lys	Gly	Thr	Thr	Ala	Glu	Lys	Val	Gln	Leu	Ala	Ala	Cys	Cys	Leu	Gly
		35					40					45			
Val	Val	Cys	Ser	Ile	Ile	Cys	Leu	Ala	Leu	Gly	Ile	Ala	Ala	Ala	Ala
	50					55					60				
Val	Gly	Val	Ser	Cys	Gly	Gly	Phe	Ala	Leu	Gly	Leu	Gly	Ile	Ile	Ala
65					70					75					80
Ile	Leu	Leu	Gly	Ile	Val	Leu	Phe	Ala	Thr	Ser	Ala	Leu	Asp	Val	Leu
				85					90				95		
Glu	Asn	His	Gly	Leu	Val	Gly	Cys	Pro	Phe	Lys	Leu	Pro	Cys	Lys	Ser
			100					105					110		
Ser	Pro	Ala	Asn	Glu	Pro	Ala	Val	Gln	Phe	Phe	Lys	Gly	Lys	Asn	Gly
		115					120					125			
Ser	Ala	Asp	Gln	Val	Ile	Leu	Val	Thr	Gln						
			130				135								

(2) INFORMATIONS POUR LA SEQ ID NO: 339:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 335195..335602

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 339:

Leu	Ala	Pro	Phe	Leu	Leu	Thr	Glu	Phe	Ser	Ser	Leu	Ser	Leu	Leu	Leu
1				5					10					15	
Ala	Phe	Ala	Leu	Ala	Leu	Glu	Ile	Phe	Cys	Ser	Thr	Ser	Ala	Val	Leu
			20					25					30		
Gln	His	Lys	Leu	Phe	His	Ile	Lys	Val	Cys	Asp	Arg	Cys	Asn	Arg	Ser
		35					40					45			
Leu	Val	Thr	Ala	Ser	Val	Val	Ser	Thr	Pro	Pro	Thr	Lys	Ala	Pro	Pro
	50					55					60				
Lys	Arg	Lys	Ala	Pro	Thr	Pro	Lys	Asn	Lys	Asp	Ala	Ala	Thr	Thr	Glu
65					70					75					80
Thr	Gly	Leu	Gln	Ser	Thr	Pro	Glu	Asn	Asn	Lys	Pro	Ala	Thr	Thr	Arg
				85					90					95	
Arg	Ala	Met	Ala	Asn	Ile	Val	Ala	Thr	Ala	Ala	Ala	Asn	Leu	Phe	
			100				105					110			
Ala	Val	Gly	Asn	Glu	Leu	Leu	Arg	Ser	Lys	His	Leu	Ser	Lys	Arg	Ala
		115					120					125			
Ile	Leu	Ser	Thr	Thr	Leu	Ser	Cys								
	130					135									

(2) INFORMATIONS POUR LA SEQ ID NO: 340:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(335194..335673)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 340:

Val	Arg	Asn	Glu	Ile	Trp	Leu	Lys	Ser	Val	Glu	Val	Arg	Phe	Met	Thr
1				5					10					15	
Lys	Val	Tyr	Ala	His	Ser	Ile	Gln	Gln	Glu	Arg	Val	Val	Asp	Arg	Ile
			20					25					30		
Ala	Leu	Leu	Glu	Arg	Cys	Leu	Asp	Leu	Ser	Asn	Ser	Leu	Pro	Thr	Ala
		35					40					45			
Lys	Arg	Leu	Ala	Ala	Val	Ala	Val	Ala	Thr	Ile	Leu	Ala	Ile	Ala	Leu
	50					55					60				
Leu	Val	Val	Ala	Gly	Leu	Leu	Phe	Ser	Gly	Val	Leu	Cys	Ser	Pro	Val
65					70					75					80
Ser	Val	Val	Ala	Ala	Ser	Leu	Phe	Phe	Gly	Val	Gly	Ala	Phe	Leu	Leu
			85						90					95	
Gly	Gly	Ala	Leu	Val	Gly	Gly	Val	Leu	Thr	Thr	Glu	Ala	Val	Thr	Arg
			100					105					110		
Glu	Arg	Leu	His	Arg	Ser	Gln	Thr	Leu	Met	Trp	Asn	Asn	Leu	Cys	Cys
		115					120					125			
Lys	Thr	Ala	Glu	Val	Glu	Gln	Lys	Ile	Ser	Arg	Ala	Ser	Ala	Asn	Ala

130 135 140
 Lys Ser Asn Asp Lys Leu Glu Asn Ser Val Ser Lys Lys Gly Ala Ser
 145 150 155 160

(2) INFORMATION POUR LA SEQ ID NO: 341:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(335903..336334)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 341:

Lys 1	Ala	Ala	Gly	Glu 5	Ala	Leu	Leu	Lys	Lys 10	Ser	Ala	Glu	Lys	Thr 15	Arg
Arg	Gly	Ser	Ser 20	Ile	Tyr	Asp	Tyr	Phe 25	Gln	Gly	Tyr	Ile	Ser 30	Pro	Glu
Ile	Leu	Gly 35	Val	Leu	Phe	Ala	Asp 40	Ser	Gly	Val	Thr	Tyr 45	Gln	Glu	Thr
Leu	Glu 50	Tyr	Arg	Lys	Lys	Leu 55	Val	Met	Leu	Ser	Lys 60	Lys	Tyr	Pro	Lys
Ser 65	Gly	Ser	Leu	Arg	Leu	Arg 70	Leu	Ala	Thr	Thr 75	Ala	Leu	Glu	Leu	Gly 80
Leu	Val	Lys	Glu	Gly 85	Val	Gln	Leu	Leu	Glu 90	Glu	Ser	Val	Lys	Asp 95	Ala
Pro	Glu	Asp	Leu 100	Ser	Leu	Arg	Leu	Gln 105	Phe	Cys	Lys	Ile	Leu 110	Cys	Asn
Arg	His	Asp 115	Tyr	Val	Arg	Ala	Lys 120	Tyr	His	Phe	Asp	Gln 125	Ala	Gln	Val
Phe	Ser 130	Leu	Lys	Arg	Gly	Cys 135	Phe	Pro	Lys	Lys	Leu 140	Pro	Ile	Leu	Ser

(2) INFORMATION POUR LA SEQ ID NO: 342:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 347 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(336338..337378)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 342:

Leu	Cys	Leu	Lys	Leu	Lys	Gln	Ile	Gln	Leu	Cys	Arg	Thr	Phe	Val	Cys
1				5					10					15	
Leu	Arg	His	Trp	Met	Cys	Phe	Ile	Gly	Ile	Gly	Ser	Leu	Leu	Leu	Pro
			20					25					30		
Thr	Ala	Leu	Arg	Ala	Thr	Glu	Arg	Met	Arg	Lys	Glu	Pro	Ile	Pro	Leu
		35					40					45			


```

Leu Asp Lys Gln Gln Ser Phe Trp Asn Val Asp Pro Tyr Cys Leu Glu
 50          55          60
Ser Ile Cys Ala Cys Phe Val Ala His Arg Asp Pro Leu Ser Ala Lys
65          70          75          80
Arg Leu Met Tyr Leu Phe Pro Gln Leu Ser Glu Glu Asp Val Ser Val
          85          90          95
Phe Ala Arg Cys Ile Leu Ser Ser Lys Arg Pro Glu Tyr Leu Phe Ser
          100          105          110
Lys Ser Glu Glu Glu Leu Phe Ala Lys Leu Ile Leu Pro Arg Val Ser
          115          120          125
Leu Gly Val His Arg Asp Asp Asp Leu Ala Arg Val Leu Val Leu Ala
          130          135          140
Glu Pro Ser Ala Glu Glu Gln Lys Ala Arg Tyr Tyr Ser Leu Tyr Leu
145          150          155          160
Asp Val Leu Ala Leu Arg Ala Tyr Val Glu Arg Glu Arg Leu Ala Ser
          165          170          175
Ala Ala His Gly Asp Pro Glu Arg Ile Asp Leu Ala Thr Ile Glu Ala
          180          185          190
Ile Asn Thr Ile Leu Phe Gln Glu Glu Arg Trp Arg Tyr Pro Ser Lys
          195          200          205
Gln Glu Met Phe Glu Ser Arg Phe Ser Glu Leu Ala Ala Val Thr Asp
          210          215          220
Ser Lys Phe Gly Val Cys Leu Gly Thr Val Val Leu Tyr Gln Ala Val
225          230          235          240
Ala Gln Arg Leu Asp Leu Ser Leu Asp Pro Val Thr Pro Pro Gly His
          245          250          255
Ile Tyr Leu Arg Tyr Lys Asp Lys Val Asn Ile Glu Thr Thr Ser Gly
          260          265          270
Gly Arg His Leu Pro Thr Glu Arg Tyr Cys Glu Cys Ile Lys Glu Ser
          275          280          285
Gln Leu Lys Val Arg Ser Gln Met Glu Leu Ile Gly Leu Thr Phe Met
          290          295          300
Asn Arg Gly Ala Phe Phe Leu Gln Lys Gly Glu Phe Leu Gln Ala Ser
305          310          315          320
Leu Ala Tyr Glu Gln Ala Gln Ser Tyr Leu Ser Asp Glu Gln Ile Ser
          325          330          335
Asp Leu Leu Gly Ile Thr Tyr Val Leu Leu Gly
          340          345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 343:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 867 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(337347..339947)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 343:

```

Met Glu Lys Phe Ser Asp Ala Val Ser Glu Ala Leu Glu Lys Ala Phe
 1          5          10          15
Glu Leu Ala Lys Asn Ser Lys His Ser Tyr Val Thr Glu Asn His Leu
          20          25          30
Leu Lys Ser Leu Leu Gln Asn Pro Gly Ser Leu Phe Cys Leu Val Ile

```

35 40 45
 Lys Asp Val His Gly Asn Leu Gly Leu Leu Thr Ser Ala Val Asp Asp
 50 55 60
 Ala Leu Arg Arg Glu Pro Thr Val Val Glu Gly Thr Ala Val Ala Ser
 65 70 75 80
 Pro Ser Pro Ser Leu His Gln Leu Leu Leu Asn Ala His Gln Glu Ala
 85 90 95
 Arg Ser Met Gly Asp Glu Tyr Leu Ser Gly Asp His Leu Leu Leu Ala
 100 105 110
 Phe Trp Arg Ser Thr Lys Glu Pro Phe Ala Ser Trp Arg Lys Thr Val
 115 120 125
 Lys Thr Thr Ser Glu Ala Leu Lys Glu Leu Ile Thr Lys Leu Arg Gln
 130 135 140
 Gly Ser Arg Met Asp Ser Pro Ser Ala Glu Glu Asn Leu Lys Gly Leu
 145 150 155 160
 Glu Lys Tyr Cys Lys Asn Leu Thr Val Leu Ala Arg Glu Gly Lys Leu
 165 170 175
 Asp Pro Val Ile Gly Arg Asp Glu Glu Ile Arg Arg Thr Ile Gln Val
 180 185 190
 Leu Ser Arg Arg Thr Lys Asn Asn Pro Met Leu Ile Gly Glu Pro Gly
 195 200 205
 Val Gly Lys Thr Ala Ile Ala Glu Gly Leu Ala Leu Arg Ile Val Gln
 210 215 220
 Gly Asp Val Pro Glu Ser Leu Lys Glu Lys His Leu Tyr Val Leu Asp
 225 230 235 240
 Met Gly Ala Leu Ile Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu
 245 250 255
 Arg Leu Lys Ser Val Leu Lys Ser Val Glu Ala Ser Glu Gly Glu Cys
 260 265 270
 Ile Leu Phe Ile Asp Glu Val His Thr Leu Val Gly Ala Gly Ala Thr
 275 280 285
 Asp Gly Ala Met Asp Ala Ala Asn Leu Leu Lys Pro Ala Leu Ala Arg
 290 295 300
 Gly Thr Leu His Cys Ile Gly Ala Thr Thr Leu Asn Glu Tyr Gln Lys
 305 310 315 320
 Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Ile Phe
 325 330 335
 Val Thr Glu Pro Ser Leu Glu Asp Ala Val Phe Ile Leu Arg Gly Leu
 340 345 350
 Arg Glu Lys Tyr Glu Ile Phe His Gly Val Arg Ile Thr Glu Gly Ala
 355 360 365
 Leu Asn Ala Ala Val Val Leu Ser Tyr Arg Tyr Ile Thr Asp Arg Phe
 370 375 380
 Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu Ala Ala Ser Leu Ile
 385 390 395 400
 Arg Met Gln Ile Gly Ser Leu Pro Leu Pro Ile Asp Glu Lys Glu Arg
 405 410 415
 Glu Leu Ser Ala Leu Ile Val Lys Gln Glu Ala Ile Lys Arg Glu Gln
 420 425 430
 Ala Pro Ala Tyr Gln Glu Glu Ala Glu Asp Met Xaa Xaa Ala Ile Asp
 435 440 445
 Arg Val Lys Glu Glu Leu Ala Ala Leu Arg Leu Arg Trp Asp Glu Glu
 450 455 460
 Lys Gly Leu Ile Ala Gly Leu Lys Glu Lys Lys Asn Ala Leu Glu Asn
 465 470 475 480
 Leu Lys Phe Ala Glu Glu Glu Ala Glu Arg Thr Ala Asp Tyr Asn Arg
 485 490 495
 Val Ala Glu Leu Arg Tyr Ser Leu Ile Pro Ser Leu Glu Glu Ile
 500 505 510

His Leu Ala Glu Glu Ala Leu Asn Gln Arg Asp Gly Arg Leu Leu Gln
 515 520 525
 Glu Glu Val Asp Glu Arg Leu Ile Ala Gln Val Val Ala Asn Trp Thr
 530 535 540
 Gly Ile Pro Val Gln Lys Met Leu Glu Gly Glu Ser Glu Lys Leu Leu
 545 550 555 560
 Val Leu Glu Glu Ser Leu Glu Glu Arg Val Val Gly Gln Pro Phe Ala
 565 570 575
 Ile Ala Ala Val Ser Asp Ser Ile Arg Ala Ala Arg Val Gly Leu Ser
 580 585 590
 Asp Pro Gln Arg Pro Leu Gly Val Phe Leu Phe Leu Gly Pro Thr Gly
 595 600 605
 Val Gly Lys Thr Glu Leu Ala Lys Ala Leu Ala Glu Leu Leu Phe Asn
 610 615 620
 Lys Glu Glu Ala Met Ile Arg Phe Asp Met Thr Glu Tyr Met Glu Lys
 625 630 635 640
 His Ser Val Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr
 645 650 655
 Glu Glu Gly Gly Ser Leu Ser Glu Ala Leu Arg Arg Arg Pro Tyr Ser
 660 665 670
 Val Val Leu Phe Asp Glu Ile Glu Lys Ala Asp Lys Glu Val Phe Asn
 675 680 685
 Ile Leu Leu Gln Ile Phe Asp Asp Gly Ile Leu Thr Asp Ser Lys Lys
 690 695 700
 Arg Lys Val Asn Cys Lys Asn Ala Leu Phe Ile Met Thr Ser Asn Ile
 705 710 715 720
 Gly Ser Gln Glu Leu Ala Asp Tyr Cys Thr Lys Lys Gly Thr Ile Val
 725 730 735
 Asp Lys Glu Ala Val Leu Ser Val Val Ala Pro Ala Leu Lys Asn Tyr
 740 745 750
 Phe Ser Pro Glu Phe Ile Asn Arg Ile Asp Asp Ile Leu Pro Phe Val
 755 760 765
 Pro Leu Thr Thr Glu Asp Ile Val Lys Ile Val Gly Ile Gln Met Asn
 770 775 780
 Arg Val Ala Leu Arg Leu Leu Glu Arg Lys Ile Ser Leu Thr Trp Asp
 785 790 795 800
 Asp Ser Leu Val Leu Phe Leu Ser Glu Gln Gly Tyr Asp Ser Ala Phe
 805 810 815
 Gly Ala Arg Pro Leu Lys Arg Leu Ile Gln Gln Lys Val Val Thr Met
 820 825 830
 Leu Ser Lys Ala Leu Leu Lys Gly Asp Ile Lys Pro Gly Met Ala Val
 835 840 845
 Glu Leu Thr Met Ala Lys Asp Val Val Val Phe Lys Ile Lys Thr Asn
 850 855 860
 Pro Ala Val
 865

(2) INFORMATIONS POUR LA SEQ ID NO: 344:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 447 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 340507..341847

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 344:

```

Ala His Leu Thr His Asp Glu Asp Ile Ala Asn Gln Glu Thr Ala Ala
1      5      10      15
Asp Leu Lys Ser Ile Thr Phe Leu Leu Thr Ser Phe Val Glu Glu Ile
20      25      30
Ser Trp Ile Gln Pro Ala Leu Ile Ala Leu Pro Gln Gln Val Ala Asn
35      40      45
Met Leu Leu Ala Ser Pro Glu Leu Gln Glu Tyr His Phe Tyr Leu Lys
50      55      60
Lys Leu Phe Arg Leu Ala Pro His Thr Gly Thr Ser Arg Glu Glu Lys
65      70      75      80
Ile Leu Ala Ser Ser Phe Pro Ala Leu Glu Val Ala Tyr Lys Thr Phe
85      90      95
Cys Ser Leu Thr Asp Ser Glu Ile Pro Phe Gly Glu Ala Val Asp Ser
100     105     110
Glu Gly Lys Ser His Pro Leu Ser His Ala Leu Ala Ser Leu Tyr Met
115     120     125
Gln Ser Thr Asp Arg Glu Leu Arg Lys Asn Thr Tyr Gln Lys Gln Cys
130     135     140
Gln Arg His His Gly Tyr Arg Leu Ser Leu Ala Asn Leu Leu Asn Gly
145     150     155     160
Lys Ile Gln Ala His Leu Phe Asn Ala Lys Ala Arg Asp Tyr Asp Ser
165     170     175
Cys Leu Glu Ala Ala Leu Phe Gln Asn Asp Ile Ser Thr Ser Val Val
180     185     190
Thr Thr Leu Ile Asp Thr Val Lys Gln His Thr His Leu Ile Thr Lys
195     200     205
Tyr Phe Gln Leu Lys Gln Lys Ala Leu Gly Leu Ser Asp Phe His Phe
210     215     220
Tyr Asp Val Tyr Ala Pro Leu Val Ala Ser Glu Ala Ser Arg His Tyr
225     230     235     240
Ser Tyr Gln Glu Ala Val Thr Leu Ile Cys Asp Ser Leu Ser Pro Leu
245     250     255
Gly Asn Asp Tyr Val Glu Thr Leu Arg Lys Gly Leu Thr Ser Asp Gly
260     265     270
Trp Val Asp Lys Tyr Glu Asn Thr Asn Lys Arg Ser Gly Ala Tyr Ser
275     280     285
Ser Gly Cys Tyr Asn Ser Lys Pro Tyr Ile Leu Leu Asn Tyr Thr Gly
290     295     300
Thr Leu Tyr Asp Val Ser Val Val Ala His Glu Gly Gly His Ser Met
305     310     315     320
His Ser Phe Leu Ser His Lys His Gln Ser Tyr His Glu Ala Gln Tyr
325     330     335
Pro Ile Phe Leu Ala Glu Ile Ala Ser Thr Leu Asn Glu Thr Leu Leu
340     345     350
Met Glu Phe Leu Leu Lys Gln Ala Pro Ser Lys Glu Glu Lys Ile Ala
355     360     365
Ile Leu Ser Arg Ser Leu Asp Thr Val Phe Ala Thr Leu Phe Arg Gln
370     375     380
Thr Leu Phe Ala Ala Phe Glu Leu Glu Met His Ser Ala Ala Glu Gln
385     390     395     400
Gly Leu Pro Leu Thr Glu Glu Phe Phe Ser Gln Ser Tyr Glu Lys Leu
405     410     415
Gln Arg Leu Phe Tyr Gly Asp Cys Ile Thr Phe Asp Glu His Ser Cys
420     425     430
Ile Glu Ser Ala Arg Ile Pro His Phe Tyr Tyr Asn Phe Tyr Val
435     440     445

```

(2) INFORMATIONS POUR LA SEQ ID NO: 345:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 80 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 341783..342022

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 345:

Leu	Leu	Met	Asn	Ile	Ala	Val	Ser	Asn	Arg	Leu	Ala	Phe	Leu	Ile	Ser
1				5					10					15	
Thr	Thr	Thr	Ser	Met	Phe	Asn	Gln	Tyr	Ala	Thr	Gly	Ile	Ile	Ala	Ser
			20					25					30		
Leu	Cys	Phe	Ser	Glu	Arg	Ile	Leu	Ser	Gly	Glu	Glu	Gly	Ala	Gln	Glu
		35					40					45			
Ala	Tyr	Leu	Thr	Phe	Leu	Arg	Ser	Gly	Gly	Ser	Asp	Phe	Pro	Ile	Glu
	50					55					60				
Ile	Leu	Lys	Lys	Ser	Gly	Leu	Asp	Met	Thr	Ser	Ile	Ser	Ser	Tyr	Ala
65					70				75						80

(2) INFORMATIONS POUR LA SEQ ID NO: 346:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 74 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 342249..342470

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 346:

Met	Ser	Asp	Gln	Ala	Thr	Thr	Leu	Lys	Ile	Lys	Pro	Leu	Gly	Asp	Arg
1				5					10					15	
Ile	Leu	Val	Lys	Arg	Glu	Glu	Glu	Ala	Ser	Thr	Ala	Arg	Gly	Gly	Ile
			20					25					30		
Ile	Leu	Pro	Asp	Thr	Ala	Lys	Lys	Lys	Gln	Asp	Arg	Ala	Glu	Val	Val
		35					40					45			
Ala	Leu	Gly	Thr	Gly	Lys	Lys	Asp	Asp	Lys	Gly	Gln	Gln	Leu	Pro	Phe
	50					55					60				
Glu	Val	Gln	Val	Gly	Asp	Ile	Val	Leu	Ile						
65					70										

(2) INFORMATIONS POUR LA SEQ ID NO: 347:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 258 acides aminés
 (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 342597..343370

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 347:

```

Met Val Ala Lys Asn Ile Lys Tyr Asn Glu Glu Ala Arg Lys Lys Ile
1          5          10          15
Gln Lys Gly Val Lys Thr Leu Ala Glu Ala Val Lys Val Thr Leu Gly
          20          25          30
Pro Lys Gly Arg His Val Val Ile Asp Lys Ser Phe Gly Ser Pro Gln
          35          40          45
Val Thr Lys Asp Gly Val Thr Val Ala Lys Glu Val Glu Leu Ala Asp
          50          55          60
Lys His Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65          70          75          80
Thr Ala Asp Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
          85          90          95
Glu Ala Ile Tyr Thr Glu Gly Leu Arg Asn Val Thr Ala Gly Ala Asn
          100          105          110
Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Lys Val Val Val
          115          120          125
Asp Gln Val Lys Lys Ile Ser Lys Pro Val Gln His His Lys Glu Ile
          130          135          140
Ala Gln Val Ala Thr Ile Ser Ala Asn Asn Asp Ala Glu Ile Gly Asn
145          150          155          160
Leu Ile Ala Lys Ala Met Glu Lys Val Gly Lys Asn Gly Ser Ile Thr
          165          170          175
Val Glu Glu Ala Lys Gly Phe Glu Thr Val Leu Asp Val Val Glu Gly
          180          185          190
Met Asn Phe Asn Arg Gly Tyr Leu Ser Ser Tyr Phe Ala Thr Asn Pro
          195          200          205
Glu Thr Gln Glu Cys Val Leu Glu Asp Ala Leu Val Leu Ile Tyr Asp
          210          215          220
Lys Lys Ile Ser Gly Ile Lys Asp Phe Leu Pro Val Leu Gln Gln Val
225          230          235          240
Ala Glu Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly
          245          250          255
Glu Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 348:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 224 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 343361..344032

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 348:

```

Arg Arg Thr Leu Ala Thr Leu Val Val Asn Arg Ile Arg Gly Gly Phe
1      5      10      15
Arg Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala
20      25      30
Met Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Gln Leu Ile Ser Glu
35      40      45
Glu Leu Gly Met Lys Leu Glu Asn Ala Asn Leu Ala Met Leu Gly Lys
50      55      60
Ala Lys Lys Val Ile Val Ser Lys Glu Asp Thr Thr Ile Val Glu Gly
65      70      75      80
Met Gly Glu Lys Glu Ala Leu Glu Ala Arg Cys Glu Ser Ile Lys Lys
85      90      95
Gln Ile Glu Asp Ser Ser Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu
100     105     110
Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Arg Val Gly Ala
115     120     125
Ala Thr Glu Ile Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala
130     135     140
Gln His Ala Thr Ile Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly
145     150     155     160
Gly Thr Ala Leu Ile Arg Cys Ile Pro Thr Leu Glu Ala Phe Leu Pro
165     170     175
Met Leu Thr Asn Glu Asp Glu Gln Ile Gly Ala Arg Ile Val Leu Lys
180     185     190
Ala Leu Ser Ala Pro Leu Lys Gln Ile Ala Ala Asn Ala Gly Lys Glu
195     200     205
Gly Ala Ile Ile Phe Gln Gln Val Met Ser Phe Cys Glu Arg Arg Ile
210     215     220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 349:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 90 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 343956..344225

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 349:

```

Asn Lys Leu Leu Gln Thr Gln Glu Lys Lys Val Leu Ser Ser Ser Asn
1      5      10      15
Lys Leu Cys Pro Ser Ala Asn Glu Gly Tyr Asp Ala Leu Arg Asp Ala
20      25      30
Tyr Thr Asp Met Leu Glu Ala Gly Ile Leu Asp Pro Ala Lys Val Thr
35      40      45
Arg Ser Ala Leu Glu Ser Ala Ala Ser Val Ala Gly Leu Leu Leu Thr
50      55      60
Thr Glu Ala Leu Ile Ala Glu Ile Pro Glu Glu Lys Pro Ala Ala Ala
65      70      75      80
Pro Ala Met Pro Gly Ala Gly Met Asp Tyr
85      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 350:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 262 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 344357..345142

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 350:

```

Met Phe Lys Leu Ile Lys Ser Ala Phe Leu Ile Ala Cys Cys Ile Val
1      5      10      15
Gly Tyr Phe Trp Ile Lys Lys Glu Ser Ile Val Glu Gln Trp Leu Ser
20      25      30
Gln Gln Leu His Ala Gln Val Thr Val Gly Asn Ile Ser Pro Gly Leu
35      40      45
Ser Lys Thr Lys Ile Arg His Leu Cys Ile His Asn Pro Leu Ser Ser
50      55      60
Asp Lys Tyr Pro Tyr Ala Val Glu Ile Glu Tyr Val Ser Leu Lys Tyr
65      70      75      80
Ser Ile Val Thr Met Ile Leu Ser Lys Lys Ile Asp Ile Ser Asp Val
85      90      95
Ile Leu Gln Gly Thr Ser Leu Thr Val Phe Pro Cys Glu Gly Ser Ser
100     105     110
Lys Thr Asn Trp Ser Phe Phe Trp Asp Ser Phe Ile Asn His Ser Asn
115     120     125
Glu Leu Thr Lys Phe His Ser Ser Gln Phe Glu Ser Ser Val Asp Thr
130     135     140
Ile Pro Val Phe Ile Lys Arg Cys Leu Cys Thr Asn Thr Arg Val Ser
145     150     155     160
Gly Ile Lys Asn Asn Tyr Lys Glu Ile Pro Thr Thr Pro Val Pro Ser
165     170     175
Leu Glu Phe Arg Gly Ser Leu Ser Cys Ser Pro Leu Pro Thr Leu Gly
180     185     190
Glu Thr Ala Arg Ala Leu Leu Tyr Leu Ile Val Glu Glu Ser Phe Tyr
195     200     205
His Ala Asn Val Ser Gly Asp Ile Ala Arg Pro Leu Ser Lys Gln Ala
210     215     220
Arg Ala Tyr Phe Asn Ser Ser Leu Ser Asp Tyr Ser Tyr Leu Lys Lys
225     230     235     240
Arg Gly Ala Phe Pro Ser Asn Leu Thr Asn Glu Leu Glu Gly Phe Met
245     250     255
Lys Glu Leu Leu Phe Arg
260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 351:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 251 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(345161..345913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 351:

```

Met Asn Val Ser Asp Leu Leu Asn Ile Leu Asn Glu Leu Leu His Pro
1      5      10      15
Glu Tyr Phe Ser Asp Tyr Gly Pro Asn Gly Leu Gln Val Gly Asn Thr
      20      25      30
Gln Thr Ala Ile Arg Lys Val Ala Val Ala Val Thr Ala Asp Leu Ala
      35      40      45
Thr Ile Glu Lys Ala Ile Ala Cys Glu Ala Asn Val Leu Leu Val His
      50      55      60
His Gly Ile Phe Trp Lys Gly Met Pro Tyr Pro Ile Thr Gly Ile Leu
65      70      75      80
Tyr Gln Arg Met Gln Arg Leu Met Glu Gly Asn Ile Gln Leu Ile Ala
      85      90      95
Tyr His Leu Pro Leu Asp Ala His Thr Thr Ile Gly Asn Asn Trp Lys
      100     105     110
Val Ala Arg Asp Leu Gly Trp Glu Gln Leu Glu Ser Phe Gly Ser Ser
      115     120     125
Gln Pro Ser Leu Gly Val Lys Gly Val Phe Pro Glu Met Glu Val His
      130     135     140
Asp Phe Ile Ser Gln Leu Ser Ala Tyr Tyr Gln Thr Pro Val Leu Ala
145     150     155     160
Lys Ala Leu Gly Gly Lys Lys Arg Val Ser Ser Ala Ala Leu Ile Ser
      165     170     175
Gly Gly Ala Tyr Arg Glu Ile Ser Glu Ala Lys Asn Gln Gln Val Asp
      180     185     190
Cys Phe Ile Thr Gly Asn Phe Asp Glu Pro Ala Trp Ser Leu Ala His
      195     200     205
Glu Leu Ala Ile His Phe Leu Ala Phe Gly His Thr Ala Thr Glu Lys
      210     215     220
Val Gly Pro Lys Ala Leu Ala Gln Tyr Leu Lys Gly Ala Gly Leu Glu
225     230     235     240
Ser Val Val Phe Leu Asp Thr Asp Asn Pro Phe
      245     250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 352:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 341 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(346080..347102)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 352:

```

Val Cys Trp Tyr Asp Phe Thr Arg Ile Ser Met Ile Arg Thr Ala Phe
1      5      10      15
Phe Gln Asp Lys Glu Cys Phe Pro Leu Glu Ala Leu Arg Ser Trp Phe
      20      25      30
Leu Glu Ser Lys Arg Ser Phe Pro Trp Arg Asp Ser Pro Thr Pro Tyr
      35      40      45
Arg Val Trp Val Ser Glu Val Met Leu Gln Gln Thr Arg Ala Glu Val

```

```

      50      55      60
Val Val Pro Tyr Phe Leu Lys Trp Met Glu Arg Phe Pro Thr Leu Gln
65      70      75      80
Asp Leu Ala Gln Ala Arg Glu Ser Asp Val Val Gln Leu Trp Glu Gly
      85      90      95
Leu Gly Tyr Tyr Ser Arg Ala Arg Asn Leu Leu Ala Gly Ala Arg Val
      100      105      110
Ile Thr Glu Ile Phe Gly Gly Glu Ile Pro Asn Asp Leu Ala Leu Leu
      115      120      125
Ser Ser Ile Lys Gly Ile Gly Ser Tyr Thr Ala Asn Ala Ile Leu Ala
      130      135      140
Phe Ala Phe Lys Gln Lys Asn Pro Ala Val Asp Gly Asn Val Leu Arg
145      150      155      160
Val Met Ser Arg Leu Phe Ala Ile Glu Glu Ser Ile Asp Arg Met Asn
      165      170      175
Thr Arg Arg Glu Ile Thr Gly Leu Cys Glu Ser Leu Leu Pro Asp Gln
      180      185      190
Asp Pro Gln Val Ile Ala Glu Ser Phe Ile Glu Leu Gly Ala Arg Ile
      195      200      205
Cys Lys Lys Gln Pro Leu Cys Glu Gln Cys Pro Leu Arg Ser Phe Cys
      210      215      220
Thr Ala Tyr Arg Gln Gly Thr Met Glu Gln Tyr Pro Val Arg Asn Thr
225      230      235      240
Arg Ala Ala Ile Ser Arg Leu Phe Arg Ala Val Val Ile Val Leu Tyr
      245      250      255
Lys Asp Gln Val Leu Met Thr Lys Arg Glu Glu Lys Glu Ile Met Ala
      260      265      270
Gly Leu Tyr Glu Phe Pro Tyr Tyr Gln Leu Pro Lys Glu Asp Cys Cys
      275      280      285
Asp Ile Glu Lys Ile Ile His Leu Val Gln Lys Asp Tyr Gly Glu Thr
      290      295      300
Leu His Phe Val Ser Ser Leu Pro Ser Gln Lys Gln Val Phe Thr Xaa
305      310      315      320
Ile Ala Leu His Tyr Ser His Met Phe Ser Thr Xaa Asn Ile Xaa Tyr
      325      330      335
Arg Ile Ala Thr Arg
      340

```

(2) INFORMATIONS POUR LA SEQ ID NO: 353:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 347113..347940

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 353:

```

Trp Ile Met Gln Glu Phe Ile Gly Thr Ala Asp Arg His Ile Arg Leu
1      5      10      15
Ser Ser Phe Leu Arg Thr Ser Leu Pro His Leu Pro Lys Lys Thr Ile
      20      25      30
Leu Glu Ser Val Arg Tyr His Gly Cys Arg Val Asn Gly Arg Ile Glu
      35      40      45

```

```

Arg Phe Glu Ser Tyr Lys Leu Gln Pro Gly Asp Arg Val Ser Leu Gln
 50          55          60
Ile Ile Glu His Ser Ser Pro Gln Leu Leu Trp Glu Asp Glu His Leu
65          70          75          80
Cys Ile Tyr Asn Lys Pro Ala Lys Gln Thr Ser Glu Asp Leu Ala His
          85          90          95
Gln Leu Asn Val His Leu Val His Arg Leu Asp Arg Asp Thr Ser Gly
          100          105          110
Cys Ile Leu Phe Ala Lys His Ala Lys Ala Ser Ser Leu Ile Thr Gln
          115          120          125
Leu Phe Lys Asn Arg Glu Ile Asp Lys Arg Tyr Ile Ala Leu Val Phe
          130          135          140
Gly Gln Pro Arg Gln Glu Ser Gly Ile Ile Thr Thr Tyr Thr Ala Pro
145          150          155          160
Cys Tyr Arg Arg Thr Gly Ala Val Leu Phe Gly Asn Thr Asp Gln Asn
          165          170          175
Ser Gly Lys Ile Thr Ile Thr Lys Trp Glu Ile Leu Thr Arg Tyr Pro
          180          185          190
Lys Tyr Thr Leu Leu Leu Cys Arg Pro Val Thr Gly Arg Thr His Gln
          195          200          205
Ile Arg Leu His Met Lys Thr Ile Gly His Pro Ile Val Gly Asp Val
          210          215          220
Asp Tyr Gly Asn Gln Glu Gln Pro Lys Asn Val Val Arg Thr Leu Leu
225          230          235          240
His Ala Ala Ser Leu Ala Phe Ile Ser Pro Phe Ser Asn Glu Lys Ile
          245          250          255
Glu Ile Ser Ser Leu Thr Pro Ser Gln Asp Pro Tyr Pro Phe Tyr Ala
          260          265          270
Asp Phe Arg Pro
          275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 354:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 673 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(348146..350164)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 354:

```

Asn Phe Leu Leu Lys Ile Lys Asn Pro Tyr Lys Asn Pro Gly Val Lys
 1          5          10          15
Gly Met Ser Phe Gly Ile Gly Ser Ala Cys Ser Ser Leu Trp Ser Arg
          20          25          30
Leu Cys Gly Ser Ser Gly Ser Glu Gly Asn Ser Glu Glu Gly Val Thr
          35          40          45
Ser Ser Gly Ser Asp Ala Ala Ser Gly Ser Gly Ala Ala Ser Ala Val
          50          55          60
Cys Gln Gln Pro Thr Ser Ser Ala Ser Thr Glu Gly Asn Gly Pro Ser
65          70          75          80
Val Gln Ile Pro Met Val Gly Thr Tyr Ser Ala Asn Val Gln Ser Leu
          85          90          95
Val Asn Gln Gly His Gly Gly Arg Gly Phe Val Asn Arg Cys Tyr Gln

```

100 105 110
 Lys Tyr Ser Ala Ser Gly Val Ser Leu Thr Ser Ile Ser Ile Gly Ala
 115 120 125
 Gly Asp Ser Val Asp Gly Pro Leu Pro Ser Val Val Ile Thr Gln Gln
 130 135 140
 Pro Gln Gly Ser Gly Ser Ser Ala Arg Gly Ala Gly Ser Leu Gln Met
 145 150 155 160
 Gly Ala Val Leu Ser Gly Met Ser Thr Leu Thr Gly Asn Ser Ile Phe
 165 170 175
 Asp Leu Phe Gly Glu Ser Gln Ile Thr Asn Leu Ile Gly Asp Ala Val
 180 185 190
 Asp Gly Thr Ser Thr Ser Ser Ser Pro Leu Arg Asp Ala Thr Lys Gly
 195 200 205
 Ala Ser Thr Ala Asp Leu Ile Ala Leu Phe Leu Ala Leu Gly Gly Ser
 210 215 220
 Gly Ser Gln Gly Val Asn Ser Pro Leu Val Ala Thr Leu Leu Ser Arg
 225 230 235 240
 Tyr Ser Leu Ser Gly Ser Leu Asp Ala Lys Lys Leu Gln Glu Leu Leu
 245 250 255
 Glu Ala Leu Lys Lys Leu Gln Asn Asp Ala Pro Thr Ser Asp Gly Ala
 260 265 270
 Arg Pro Gly Leu Gly Glu Cys Cys Thr His Leu Cys Gly Ala Leu Ser
 275 280 285
 Ser Ser Pro Asn Pro Ile Val Ser Ala Val Gly Ile Ala Gly Thr Gly
 290 295 300
 Leu Thr Glu Leu Leu Met Leu Ala Ala Gln Ser Gln Arg Val Arg Lys
 305 310 315 320
 Cys Ala Leu Leu Cys His Asp Ala Cys Lys Pro Cys Cys Ala Ser Ala
 325 330 335
 Cys Gly Tyr Pro Ser Cys Gly Cys Ala Asp Gly Glu Gly Gly Cys Gly
 340 345 350
 Ser Phe Gly Ala Leu Val Cys Ser Cys Ala Glu Leu Trp Cys Cys Gln
 355 360 365
 Glu Ser Pro Ala Glu Glu Ala Asn Leu Glu Glu Tyr Ala Arg Lys Leu
 370 375 380
 Lys Asp Leu Glu Met Ala Val Gly Ser Thr Thr Phe Met Leu Gly Leu
 385 390 395 400
 His Asn Leu Gly Ile Ser Phe Ser Asp Leu Val Lys Gly Asn Phe Thr
 405 410 415
 Asn Leu Pro Thr Pro Glu Gln Leu Glu Thr Ala Cys Lys Asp Ala Val
 420 425 430
 Ser Ser Leu Gly Lys Leu Met Met Arg Ile Thr His Glu Lys Trp Leu
 435 440 445
 Gly Arg Leu Cys Ser Cys Ala Gly Ile Leu Asp Asn Pro Phe Trp Lys
 450 455 460
 Arg Ala Leu Cys Ser Gly Leu Ala Gly Gly Thr His Met Leu Ser Leu
 465 470 475 480
 Gln Asp Leu Thr Ser Arg Val Lys Val Ile Thr Ser Ser Gly Asn Lys
 485 490 495
 Gln Glu Ala Glu Asn Leu Asp Leu Glu Leu Leu Leu Pro Ala Leu Ser
 500 505 510
 Ser Leu Gln Val Thr Gly Thr Glu Glu Asp Cys Asp Asp Glu Gly Gln
 515 520 525
 Gly Leu Asn Thr Asp Gln Leu Thr Met Leu Leu Cys Lys Phe Cys Ser
 530 535 540
 Val Leu Ser Ala Ala Ile Gly Asn Asp Arg Arg Pro Ile Trp Leu Thr
 545 550 555 560
 Pro Lys Gln Ile Thr Glu Ile Leu Cys Val Cys Met Val Met Ser Gly
 565 570 575

```

Ile Ser Ile Val Gly Gly Pro Ser Asn Gln Ser Ala Glu Tyr Gln Glu
                    580                    585                    590
Phe Gln Asn Thr Val Met Gln Glu Ser Leu Thr His Leu Gln Ser Ser
                    595                    600                    605
Leu Arg Val Ser Lys Arg Thr Asn Asn Arg Thr Arg Ala Glu Val Arg
                    610                    615                    620
Lys Leu Val Val Lys Tyr Glu Ala Gln Ser Ser Phe Leu Ser Leu Leu
625                    630                    635                    640
Glu Gly Leu Arg Asp Pro Asn Ser Lys Glu Ser Lys Asp Leu Met Arg
                    645                    650                    655
Glu Cys Phe Ala Ser Trp Ala Gln Lys Ala Gly Val Gln Ser Ser Ser
                    660                    665                    670
Ile

```

(2) INFORMATIONS POUR LA SEQ ID NO: 355:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 287 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 350423..351283

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 355:

```

Leu Met Leu Lys Ile Asp Leu Thr Gly Lys Ile Ala Phe Ile Ala Gly
1                    5                    10                    15
Ile Gly Asp Asp Asn Gly Tyr Gly Trp Gly Ile Ala Lys Met Leu Ala
                    20                    25                    30
Glu Ala Gly Ala Thr Ile Leu Val Gly Thr Trp Val Pro Ile Tyr Lys
                    35                    40                    45
Ile Phe Ser Gln Ser Trp Glu Leu Gly Lys Phe Asn Ala Ser Arg Glu
50                    55                    60
Leu Ser Asn Gly Glu Leu Thr Phe Ala Lys Ile Tyr Pro Met Asp
65                    70                    75                    80
Ala Ser Phe Asp Thr Pro Glu Asp Ile Pro Gln Glu Ile Leu Glu Asn
                    85                    90                    95
Lys Arg Tyr Lys Asp Leu Ser Gly Tyr Thr Val Ser Glu Val Val Glu
                    100                    105                    110
Gln Val Lys Lys Asp Phe Gly His Ile Asp Ile Leu Val His Ser Leu
                    115                    120                    125
Ala Asn Ser Pro Glu Ile Ala Lys Pro Leu Leu Asp Thr Ser Arg Lys
                    130                    135                    140
Gly Tyr Leu Ala Ala Leu Ser Thr Ser Ser Tyr Ser Phe Ile Ser Leu
145                    150                    155                    160
Leu Ser His Phe Gly Pro Ile Met Asn Ala Gly Ala Ser Thr Ile Ser
                    165                    170                    175
Leu Thr Tyr Leu Ala Ser Met Arg Ala Val Pro Gly Tyr Gly Gly Gly
                    180                    185                    190
Met Lys Pro Ala Lys Ala Ala Leu Glu Ser Asp Thr Lys Val Leu Ala
                    195                    200                    205
Trp Glu Ala Gly Arg Arg Trp Gly Val Arg Val Asn Thr Ile Ser Ala
210                    215                    220
Gly Pro Leu Ala Ser Arg Ala Gly Lys Ala Ile Gly Phe Ile Glu Arg

```

```

225          230          235          240
Met Val Asp Tyr Tyr Gln Asp Trp Ala Pro Leu Pro Ser Pro Met Glu
          245          250          255
Ala Glu Gln Val Gly Ala Ala Ala Ala Phe Leu Val Ser Pro Leu Leu
          260          265          270
Ala Gln Leu Arg Glu Lys Leu Ser Met Trp Ile Thr Glu Pro Met
          275          280          285

```

(2) INFORMATIONS POUR LA SEQ ID NO: 356:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(351314..352207)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 356:

```

Met Ser Leu Gln Lys Leu Leu Val Thr Asp Ile Asp Gly Thr Ile Thr
1          5          10          15
His Gln Ser His Leu Leu His Asp Arg Val Val Lys Ala Leu His Gln
          20          25          30
Tyr Tyr Asp Ser Gly Trp Gln Leu Phe Phe Leu Thr Gly Arg Tyr Phe
          35          40          45
Ser Tyr Ala Tyr Pro Leu Phe Gln Asn Phe Ser Val Pro Phe Leu Leu
          50          55          60
Gly Ser Gln Asn Gly Ser Ser Val Trp Ser Ser Thr Asp Lys Glu Phe
65          70          75          80
Ile Tyr Phe Arg Ser Leu Ser Arg Asp Phe Leu Cys Val Leu Glu Lys
          85          90          95
Tyr Phe Glu Asp Leu Asp Leu Ile Ala Cys Ile Glu Ser Gly Ala Ser
          100          105          110
Asn Arg Asp Val Tyr Phe Arg Lys Gly Leu Gly Lys Thr Ser Gln Glu
          115          120          125
Leu Lys Ala Ile Leu Asp Ala Val Tyr Phe Pro Thr Pro Glu Ala Ala
130          135          140
Arg Leu Leu Val Asp Val Gln Gly His Leu Ser Glu Glu Phe Ser Tyr
145          150          155          160
Glu Asp Phe Ala Ile Ala Lys Phe Phe Gly Glu Arg Glu Glu Val Lys
          165          170          175
Lys Ile Met Asp Arg Phe Ile Gln Ser Pro Glu Val Ser Ser Gln Val
          180          185          190
Thr Met Asn Tyr Met Arg Trp Pro Phe Asp Phe Lys Tyr Ala Val Leu
          195          200          205
Leu Leu Thr Leu Lys Asp Val Ser Lys Gly Phe Ala Val Asp Gln Val
          210          215          220
Val Gln Thr Phe Tyr Lys Glu Asn Lys Pro Phe Ile Met Ala Ser Gly
225          230          235          240
Asp Asp Val Asn Asp Ile Asp Leu Leu Ser Arg Gly Asp Phe Lys Ile
          245          250          255
Val Ile Gln Thr Ala Pro Glu Glu Met His Gly Leu Ala Asp Phe Leu
          260          265          270
Ala Pro Pro Ala Lys Asp Leu Gly Ile Leu Ser Ala Trp Glu Ala Gly
          275          280          285

```

Met Phe Gly Val Gly Ile Asp Ile Ile Glu Ile Asp Arg Ile Arg Lys
1 5 10 15
Ser Tyr Gln Thr Tyr Gly Asp Arg Phe Leu Lys Lys Ile Phe Thr Glu

```

                20                25                30
Gly Glu Arg Val Tyr Cys Phe Ser Lys Ser Asn Pro Tyr Ala Ser Leu
      35                40                45
Ala Ala Arg Phe Ala Ala Lys Glu Ala Val Ala Lys Ala Leu Gly Thr
      50                55                60
Gly Ile Gly Lys Leu Leu Lys Trp Lys Glu Ile Glu Met Arg Arg Asp
65      70                75                80
Ser Arg Gln Pro Gln Val Val Val Pro Glu Ala Leu Leu Cys Ser Leu
      85                90                95
Gly Val Lys Arg Val Leu Leu Ser Val Ser His Ser Arg Glu Tyr Ala
      100               105               110
Thr Ala Val Ala Ile Ala Glu
      115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 359:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 183 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(353670..354218)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 359:

```

Val Leu Ala Lys Gly Arg Asn Thr Cys Ala Val Cys Asp Gly Ala Ser
1      5      10      15
Pro Ile Phe Arg Asp Lys Asp Leu Phe Val Val Gly Gly Gly Asp Ser
      20      25      30
Ala Leu Glu Ala Met Phe Leu Thr Arg Tyr Gly Lys Arg Val Phe
      35      40      45
Val Val His Arg Arg Asp Thr Leu Arg Ala Ser Lys Val Met Val Asn
50      55      60
Lys Ala Gln Ala Asn Glu Lys Ile Phe Phe Leu Trp Asn Ser Glu Ile
65      70      75      80
Val Lys Ile Ser Gly Asp Thr Leu Val Arg Ser Ile Asp Ile Tyr Asn
      85      90      95
Asn Val Asp Lys Thr Thr Thr Thr Met Glu Ala Ala Gly Val Phe Phe
100      105      110
Ala Ile Gly His Gln Pro Asn Thr Ala Phe Leu Gly Gly Gln Val Ala
115      120      125
Leu Asp Glu Asn Gly Tyr Ile Ile Thr Glu Lys Gly Ser Ser Arg Thr
130      135      140
Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Tyr Tyr
145      150      155      160
Arg Gln Ala Ile Thr Ser Ala Gly Ser Gly Cys Met Ala Ala Leu Asp
      165      170      175
Val Glu Arg Phe Leu Glu Asn
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 360:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 155 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(354140..354604)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 360:

```

Met Thr His Ala Lys Leu Val Ile Ile Gly Ser Gly Pro Ala Gly Tyr
1      5      10      15
Thr Ala Ala Ile Tyr Ala Ser Arg Ala Leu Leu Thr Pro Val Leu Phe
      20      25      30
Glu Gly Phe Phe Ser Gly Ile Ala Gly Gly Gln Leu Met Thr Thr Thr
      35      40      45
Glu Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Val Leu Gly His Gln
      50      55      60
Leu Met Asp Leu Met Lys Thr Gln Ala Gln Arg Phe Gly Thr Gln Val
      65      70      75      80
Leu Ser Lys Asp Ile Thr Ala Val Asp Phe Ser Val Arg Pro Phe Val
      85      90      95
Leu Lys Ser Gly Glu Glu Thr Phe Thr Cys Asp Ala Cys Ile Ile Ala
      100      105      110
Thr Gly Ala Ser Ala Lys Arg Leu Ser Ile Pro Gly Ala Gly Asp Asn
      115      120      125
Glu Phe Trp Gln Lys Gly Val Thr Leu Ala Leu Phe Val Thr Glu Pro
      130      135      140
Leu Pro Phe Phe Val Thr Lys Ile Cys Leu Leu
      145      150      155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 361:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 538 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 355059..356672

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 361:

```

Leu Tyr Ala Ile His Gly Phe Thr Ala Thr Glu Glu Glu Pro Thr Ser
1      5      10      15
Glu Val His Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Ser
      20      25      30
Lys Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile
      35      40      45
Pro Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Thr Val Gly Ala
      50      55      60
Glu Val Glu Val Tyr Leu Asp Gln Thr Glu Asp Asp Glu Gly Lys Val
      65      70      75      80
Val Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile
      85      90      95
Leu Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg

```

100 105 110
 Lys Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu
 115 120 125
 Pro Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr
 130 135 140
 Val Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Asp Arg
 145 150 155 160
 Arg Asn Val Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile
 165 170 175
 Ser Lys Lys Ala Glu Leu Ile Glu Gln Ile Thr Ile Gly Glu Arg Arg
 180 185 190
 Lys Gly Ile Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu
 195 200 205
 Asp Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg
 210 215 220
 Ile Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val
 225 230 235 240
 Ile Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu
 245 250 255
 Lys Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro
 260 265 270
 Pro Gly Lys Arg Val Arg Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly
 275 280 285
 Ala Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Val Ser
 290 295 300
 Glu Met Ser Trp Val Lys Asn Ile Val Asp Pro Asn Glu Val Val Asn
 305 310 315 320
 Lys Gly Asp Glu Val Glu Val Val Val Leu Ser Ile Gln Lys Asp Glu
 325 330 335
 Gly Lys Ile Ser Leu Gly Leu Lys Gln Thr Lys His Asn Pro Trp Asp
 340 345 350
 Asn Ile Glu Glu Lys Tyr Pro Ile Gly Leu Arg Val Thr Ala Glu Ile
 355 360 365
 Lys Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile
 370 375 380
 Glu Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser
 385 390 395 400
 His Pro Ser Glu Leu Phe Lys Lys Gly Asn Thr Val Glu Ala Val Ile
 405 410 415
 Leu Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln
 420 425 430
 Leu Thr Pro Asn Pro Trp Asp Glu Ile Glu Ala Met Phe Pro Val Gly
 435 440 445
 Ser Asp Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe
 450 455 460
 Val Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu
 465 470 475 480
 Ser Glu Lys Pro Phe Ala Lys Ile Glu Asp Val Leu Ser Ile Gly Asp
 485 490 495
 Lys Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val
 500 505 510
 Ser Leu Ser Ile Lys Glu Phe Leu Ala His Gly Gly Asp Ala Gly His
 515 520 525
 Asp Ala Glu Glu Glu Ser Ser Asp Arg Asp
 530 535

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 195 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 356793..357377

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 362:

```

Met Asn Lys Asp Leu Val Ala Ile Phe Asp Tyr Met Glu Arg Glu Lys
1      5      10      15
Gly Ile Gln Arg Ser Thr Ile Val Gly Ala Ile Glu Ser Ala Leu Lys
      20      25      30
Ile Ala Ala Lys Lys Thr Leu Arg Asp Asp Ala Asn Val Ser Val Ser
      35      40      45
Ile Asn Pro Arg Thr Gly Asp Ile Glu Val Phe Cys Glu Lys Gln Ile
      50      55      60
Val Glu Lys Cys Gln Asn Pro Ser Lys Glu Ile Pro Leu Asp Lys Ala
      65      70      75      80
Arg Glu Tyr Asp Pro Asp Cys Gln Ile Gly Gln Tyr Met Asp Val Pro
      85      90      95
Phe Ile Ser Asp Gln Phe Gly Arg Ile Ala Ala His Ala Ala Arg Gln
      100      105      110
Ile Ile Gly Gln Lys Leu Arg His Ala Glu Arg Asp Val Ile Tyr Glu
      115      120      125
Glu Tyr Arg His Arg Lys Asn Glu Ile Ile Ser Gly Val Val Lys Ser
      130      135      140
Phe Ala Arg Gly Ala Asn Leu Val Val Asp Leu Gly Lys Val Glu Gly
      145      150      155      160
Leu Leu Pro Ala Arg Phe Tyr Pro Lys Thr Glu Lys His Lys Val Gly
      165      170      175
Asp Lys Ile Tyr Ala Leu Leu Tyr Glu Tyr Arg Asn Leu Lys Met Val
      180      185      190
Glu Leu Lys
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 363:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 256 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 357326..358093

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 363:

```

Asp Leu Cys Ala Ser Leu Arg Val Gln Glu Ser Glu Asn Gly Gly Ala
1      5      10      15
Glu Val Ile Leu Ser Arg Ser His Pro Glu Phe Val Lys Gln Leu Phe
      20      25      30
Val Gln Glu Val Pro Glu Leu Glu Glu Gly Ser Val Glu Ile Val Lys

```

```

          35          40          45
Ile Ala Arg Glu Ala Gly Tyr Arg Thr Lys Met Ala Val Arg Ser Ser
50          55          60
Asp Pro Gln Thr Asp Ala Val Gly Ala Phe Val Gly Met Arg Gly Ser
65          70          75          80
Arg Ile Lys Asn Ile Ile Arg Glu Leu Asn Asp Glu Lys Ile Asp Val
85          90          95
Val Asn Tyr Ser Pro Val Ser Thr Glu Leu Leu Gln Asn Leu Leu Tyr
100          105          110
Pro Val Glu Ile Gln Lys Ile Ala Ile Leu Glu Asp Asp Lys Val Ile
115          120          125
Ala Ile Ile Val Gln Asp Ser Asp Tyr Ala Thr Val Ile Gly Lys Arg
130          135          140
Gly Ile Asn Ala Arg Leu Ile Ser Gln Ile Leu Gly Tyr Glu Leu Glu
145          150          155          160
Val Gln Arg Met Ser Glu Tyr Asn Lys Leu Leu Glu Ile Gln Arg Leu
165          170          175
Gln Leu Ala Glu Phe Glu Asp Pro Arg Leu Asp Gln Pro Leu Glu Val
180          185          190
Glu Gly Ile Asn Thr Leu Ile Val Gln Asn Leu Glu His Ala Gly Tyr
195          200          205
Asp Thr Ile Arg Lys Ile Leu Leu Ala Ser Ala Ser Glu Leu Ala Ser
210          215          220
Val Pro Gly Ile Ser Leu Glu Leu Ala Tyr Lys Ile Leu Glu Gln Val
225          230          235          240
Ser Lys Tyr Gly Glu Gly Lys Val Asp Glu Lys Pro Gln Xaa Glu Asp
245          250          255

```

(2) INFORMATIONS POUR LA SEQ ID NO: 364:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 897 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 358053..360743

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 364:

```

Met Glu Lys Ala Lys Leu Thr Lys Asn Leu Lys Xaa Lys Ile Lys Asn
1          5          10          15
Ala Gln Leu Thr Lys Ala Xaa Gly Leu Asp Lys Leu Lys Gln Lys Leu
20          25          30
Ala Gln Ala Gly Ser Ser Asp Thr Lys Asn Ser Pro Ala Ser Lys Ala
35          40          45
Gln Thr Lys Glu Lys Ser Ser Lys Lys Thr Ala Gly Thr Pro Ala Pro
50          55          60
Ala Pro Glu Val Asp Leu Gly Ala Thr Glu Ser Thr Ala Arg Arg Ile
65          70          75          80
Arg Ala Lys Asp Arg Ser Ser Phe Ala Ala Glu Pro Thr Val Thr Thr
85          90          95
Ala Leu Pro Gly Asp Ala Ser His Leu Thr Leu Asp Ala Ile Pro Ala
100          105          110
Ile Lys Ala Pro Glu Ile Thr Ser Val Thr Gln Lys Glu Gln Thr Leu
115          120          125

```

Arg Glu Cys Thr Asp Thr Ser Ser Val Gln Gln Glu Glu Lys Lys Glu
 130 135 140
 Ser Ser Glu Glu Thr Ser Pro Glu Thr Pro Glu Arg Ile Glu Glu Thr
 145 150 155 160
 Pro Ile Ile Arg Thr Arg Thr Glu Pro Lys Ser Val Val Ser Ile Lys
 165 170 175
 Pro Lys Phe Gly Pro Thr Gly Lys His Ile Asn His Leu Leu Ala Lys
 180 185 190
 Thr Phe Lys Ala Pro Ala Lys Glu Thr Lys Ala Ala Ser Thr Glu Glu
 195 200 205
 Thr Thr Gln Gln Gln Pro Arg Gln Asn Asp Ala Ala Ser His Asn Asn
 210 215 220
 Lys Gln Gln Pro Ser Gly Thr Ser Ser Arg Pro Ala Ser Ser Ala Pro
 225 230 235 240
 Ser Tyr Arg Arg Glu Ser Thr Ser Asn Asn Asn Asn Asn Ala Lys Arg
 245 250 255
 Gly Ser Glu Arg Asp Arg Ser Lys Arg Ser Asp Glu Ser Val Lys Ala
 260 265 270
 Phe Thr Gly Arg Asp Arg Tyr Gly Leu Asn Glu Gly Ser Ser Glu Glu
 275 280 285
 Asp Lys Trp Arg Lys Lys Arg Val His Lys Thr Lys Lys Gln Ala Glu
 290 295 300
 Glu His Val Val Gln Cys Pro Ala His Ile Lys Ile Ala Leu Pro Ile
 305 310 315 320
 Thr Val Lys Asp Leu Ala Ala Glu Met Lys Leu Lys Ala Ser Glu Leu
 325 330 335
 Ile Gln Lys Leu Phe Ile His Gly Met Thr Tyr Val Val Asn Asp Val
 340 345 350
 Leu Asp Ser Gln Thr Val Val Glu Tyr Ile Gly Leu Glu Phe Gly Cys
 355 360 365
 Thr Ile Glu Ile Asp Ser Ser Ala Lys Glu Lys Leu Cys Leu Val Glu
 370 375 380
 Asn Thr Val Arg Asp Glu Val Asn Ala Thr Asp Pro Glu Lys Leu Ile
 385 390 395 400
 Ile Arg Ser Pro Ile Val Ala Phe Met Gly His Val Asp His Gly Lys
 405 410 415
 Thr Thr Ile Ile Asp Ala Leu Arg Gln Ser Asn Met Ala Ala Ser Glu
 420 425 430
 Ala Gly Ala Ile Thr Gln His Thr Gly Ala Phe Lys Cys Thr Thr Pro
 435 440 445
 Val Gly Glu Ile Thr Val Leu Asp Thr Pro Gly His Glu Ala Phe Ser
 450 455 460
 Ala Met Arg Ala Arg Gly Ala Glu Val Cys Asp Ile Val Val Leu Val
 465 470 475 480
 Val Ala Gly Asp Glu Gly Ile Lys Glu Gln Thr Ile Glu Ala Ile Glu
 485 490 495
 His Ala Lys Gly Ala Asn Ile Thr Ile Val Val Ala Ile Asn Lys Cys
 500 505 510
 Asp Lys Pro Lys Leu Gln Cys Arg Asn Ser Val Pro Ser Val Ser Arg
 515 520 525
 Ile Arg Ser Leu Leu Pro Glu Ala Trp Gly Gly Ser Ile Ala Thr Ile
 530 535 540
 Asn Thr Ser Ala Lys Thr Gly Glu Gly Leu Gln Asp Leu Leu Glu Met
 545 550 555 560
 Leu Ala Leu Gln Ala Glu Val Leu Glu Leu Lys Ala Asp Pro Ser Ala
 565 570 575
 Arg Ala Arg Gly Leu Val Ile Glu Ser Glu Leu His Lys Gly Leu Gly
 580 585 590
 Ala Val Ala Thr Val Leu Val Gln Asn Gly Thr Leu His Leu Gly Glu

595 600 605
 Ala Leu Val Phe Asn Asp Cys Tyr Gly Lys Val Lys Thr Met His Asp
 610 615 620
 Glu His Asn Gln Leu Leu Gln Ser Ala Thr Pro Ser Thr Pro Val Leu
 625 630 635 640
 Ile Thr Gly Leu Ser Ala Ile Pro Lys Ala Gly Asp Pro Phe Ile Val
 645 650 655
 Val Lys Asn Glu Lys Val Ala Lys Glu Ile Ile Ser Ala Arg Leu Ala
 660 665 670
 Gly Gln Gln Arg Ser Ala Ala Leu Gln Lys Lys Arg Pro Asn Phe Asp
 675 680 685
 Ala Val Leu Gln Asn Lys Lys Thr Leu Lys Leu Ile Ile Lys Ala Asp
 690 695 700
 Val Gln Gly Ser Ile Glu Ala Leu Ala His Ser Ile Leu Asn Ile Arg
 705 710 715 720
 Ser Glu Lys Val Asp Val Glu Ile Leu Ser Ser Gly Val Gly Asp Ile
 725 730 735
 Ser Glu Ser Asp Ile Arg Leu Ala Ser Ala Ser Lys Ala Thr Val Ile
 740 745 750
 Gly Phe His Thr Ser Val Glu Ser His Ala Glu Pro Leu Ile Lys Asn
 755 760 765
 Leu Asn Val Lys Val Cys Leu Phe Asp Ile Ile Tyr His Ala Val Asp
 770 775 780
 Ala Ile Lys Glu Ile Met Thr Gly Leu Leu Asp Pro Ile Ala Glu Glu
 785 790 795 800
 Lys Asn Leu Gly Ala Ala Glu Ile Lys Ala Thr Phe Lys Ser Ser Gln
 805 810 815
 Leu Gly Thr Ile Tyr Gly Cys Leu Val Thr Glu Gly Thr Val Val Arg
 820 825 830
 Asn Gln Lys Ile Arg Ile Ile Arg Asp Lys Glu Val Leu Trp Lys Gly
 835 840 845
 Ser Leu Ser Ser Leu Lys Arg Leu Lys Glu Asp Val Lys Glu Val Lys
 850 855 860
 Lys Gly Met Glu Cys Gly Ile Leu Leu Asp Asn Tyr Gln Gln Ala Gln
 865 870 875 880
 Val Gly Asp Ile Leu Gln Cys Tyr Glu Val Ile Tyr His Pro Gln Thr
 885 890 895
 Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 365:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 360753..361121

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 365:

Met Ala Glu Asn Arg Arg Met Lys Lys Val Asn Ala Met Leu Arg Glu
 1 5 10 15
 Ala Ile Ala Lys Val Ile Leu Lys Asp Val Lys His Pro Lys Ile Ser
 20 25 30

```

Asn Arg Trp Ile Thr Ile Thr Arg Val Ser Leu Ser Arg Asp Leu Gln
    35          40          45
Ser Ala Cys Val Tyr Val Ser Ile Met Pro His Glu Asn Ser Gln Glu
    50          55          60
Glu Thr Leu Ala Ala Leu Lys Ala Ser Ala Gly Phe Ile Ala Phe Gln
    65          70          75          80
Ala Ser Lys Asp Leu Val Leu Lys Tyr Phe Pro Asp Leu Asn Phe Tyr
    85          90          95
Val Glu Asp Ile Phe Ser Pro Gln Asp His Ile Glu Ser Leu Leu Leu
    100          105          110
Lys Ile Ala Glu Gln Asp Lys Lys Thr Asn Pro
    115          120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 366:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 361183..361884

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 366:

```

Ile Glu Gly Val Leu Leu Val Asp Lys Pro Gln Gly Arg Thr Ser Phe
1          5          10          15
Ser Leu Ile Arg Ser Leu Val Arg Leu Ile Gly Val Lys Lys Ile Gly
    20          25          30
His Ala Gly Thr Leu Asp Pro Phe Ala Thr Gly Val Met Val Met Leu
    35          40          45
Ile Gly Arg Lys Phe Thr Arg Leu Ser Asp Ile Met Leu Phe Glu Asp
    50          55          60
Lys Glu Tyr Ala Ala Val Ala His Leu Gly Thr Thr Thr Asp Thr Tyr
    65          70          75          80
Asp Cys Asp Gly Lys Ile Val Gly Arg Ser Lys Lys Val Pro Thr Met
    85          90          95
Asp Glu Val Leu Thr Cys Thr Ser Tyr Phe Gln Gly Glu Ile Gln Gln
    100          105          110
Val Pro Pro Met Phe Ser Ala Lys Lys Val Gln Gly Lys Lys Leu Tyr
    115          120          125
Glu Tyr Ala Arg Gln Gly Leu Ser Ile Glu Arg Arg Phe Ala Thr Val
    130          135          140
Thr Val Asn Leu Arg Leu Val Lys Tyr Glu Tyr Pro Arg Leu His Phe
    145          150          155          160
Val Val Gln Cys Ser Lys Gly Thr Tyr Ile Arg Ser Ile Ala His Glu
    165          170          175
Leu Gly Asn Met Leu Gly Cys Gly Ala Tyr Leu Glu Glu Leu Arg Arg
    180          185          190
Leu Arg Ser Gly Ser Phe Ser Ile Asp Gln Cys Ile Asp Gly Asn Leu
    195          200          205
Leu Asp Glu Pro Glu Phe Asn Val Ser Pro Tyr Leu Arg Asp Ala Asn
    210          215          220
Gly Leu Ile Leu Gln Pro Ala Pro Val Leu
    225          230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 367:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 307 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 361826..362746

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 367:

Met	Tyr	Leu	Leu	Ile	Tyr	Val	Met	Gln	Met	Asp	Leu	Phe	Tyr	Ser	Leu	1	5	10	15
Leu	Pro	Ser	Ser	Asn	Pro	Ile	Glu	Ser	Val	Thr	Ile	Xaa	Phe	Phe	Asp	20	25	30	
Gly	Cys	Xaa	Leu	Xaa	His	Gln	Ala	Leu	Leu	Ser	Phe	Leu	Thr	Lys	Phe	35	40	45	
Pro	Gly	Lys	Ser	Gly	Val	Ile	Thr	Phe	Ser	Gln	His	Pro	Glu	His	Thr	50	55	60	
Leu	Ser	Asn	Ser	Pro	Pro	Glu	Thr	Ile	Thr	Ser	Leu	Glu	Glu	Arg	Ile	65	70	75	80
Gln	Leu	Leu	Ala	Gly	Cys	Gly	Ile	Asp	Tyr	Leu	Ala	Val	Leu	Pro	Phe	85	90	95	
Asn	Gln	Glu	Ile	Ala	Asn	Gln	Glu	Ala	Glu	Leu	Phe	Ile	Gln	Ser	Ile	100	105	110	
Tyr	Lys	Thr	Leu	His	Pro	Ser	Arg	Ile	Val	Leu	Gly	Tyr	Asp	Ser	Arg	115	120	125	
Leu	Gly	Lys	Gly	Gly	Leu	Gly	Thr	Ala	Gln	Thr	Leu	Arg	Pro	Phe	Ala	130	135	140	
Ala	Ser	Leu	Gly	Ile	Ser	Leu	Glu	Glu	Val	Pro	Pro	Leu	Gln	Ile	Glu	145	150	155	160
Gly	Thr	Ile	Val	Ser	Ser	Arg	Lys	Ile	Arg	Gln	Phe	Leu	Arg	Glu	Lys	165	170	175	
Asp	Leu	Cys	Ser	Ala	Glu	Lys	Phe	Leu	Gly	Arg	Pro	Phe	Ala	Tyr	Thr	180	185	190	
Gly	Lys	Val	Ala	His	Gly	Arg	Gly	Ile	Gly	Thr	Ser	Phe	Gly	Tyr	Ala	195	200	205	
Thr	Ile	Asn	Leu	Pro	Leu	Thr	His	Ser	Leu	Leu	Pro	Leu	Gly	Val	Tyr	210	215	220	
Thr	Cys	Thr	Ile	Val	Ile	Glu	Gly	Phe	Ser	Tyr	Ala	Gly	Val	Met	Asn	225	230	235	240
Leu	Gly	Met	Ala	Pro	Thr	Met	Gln	Arg	His	Gln	Leu	Cys	Leu	Glu	Ala	245	250	255	
His	Ile	Leu	Asp	Phe	Ser	Glu	Asp	Leu	Tyr	Asp	Lys	Ser	Ile	Thr	Val	260	265	270	
Ile	Leu	Glu	Gln	Phe	Leu	Arg	Glu	Glu	Lys	Leu	Phe	Ser	Ser	Lys	Asp	275	280	285	
Glu	Leu	Val	Leu	Ala	Ile	Gln	Glu	Asp	Ile	Arg	Gln	Ala	Arg	Leu	Asn	290	295	300	
Lys	Asn	Arg														305			

(2) INFORMATIONS POUR LA SEQ ID NO: 368:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(362816..363853)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 368:

```

Met Gly Gln Thr Glu Cys Gly Ile Val Gly Leu Pro Asn Val Gly Lys
1      5      10      15
Ser Gly Leu Phe Asn Ala Leu Thr Gly Ala Gln Val Ala Ser Cys Asn
20      25      30
Tyr Pro Phe Cys Thr Ile Asp Pro Asn Val Gly Ile Val Pro Val Ile
35      40      45
Asp Pro Arg Leu Glu Thr Leu Ala Arg Ile Ser Gln Ser Gln Lys Ile
50      55      60
Ile Tyr Ala Asp Met Lys Phe Val Asp Ile Ala Gly Leu Val Lys Gly
65      70      75      80
Ala Ala Ser Gly Ala Gly Leu Gly Asn Arg Phe Leu Ser His Ile Arg
85      90      95
Glu Thr His Ala Ile Ala His Val Val Arg Cys Phe Asp Asn Asp Asp
100     105     110
Ile Thr His Val Ser Gly Lys Ile Asp Pro Glu Glu Asp Ile Ala Val
115     120     125
Ile Asn Leu Glu Leu Val Leu Ala Asp Phe Ser Ser Ala Thr Ser Val
130     135     140
Arg Glu Lys Leu Gly Lys Gln Ala Lys Gly Lys Lys Asp Ile Gly Gln
145     150     155     160
Leu Leu Pro Leu Leu Asp Arg Val Val Asp His Leu Glu Ser Gly Asn
165     170     175
Pro Val Arg Thr Leu Ser Leu Ser Leu Glu Glu Lys Val Leu Leu Lys
180     185     190
Pro Tyr Pro Phe Leu Thr Gly Lys Pro Met Leu Tyr Ile Ala Asn Ile
195     200     205
Asp Glu Asp Ser Leu Thr Asp Leu Asp Asn Pro Tyr Val Gln Lys Val
210     215     220
Arg Glu Ile Ala Lys Arg Glu Glu Ala Asn Val Val Pro Ile Cys Val
225     230     235     240
Lys Leu Glu Glu Glu Ile Leu Ser Leu Pro Leu Glu Glu Arg Gln Asp
245     250     255
Phe Leu His Ser Leu Gly Leu Gln Glu Ser Gly Leu Asn Arg Leu Val
260     265     270
Ala Ser Ala Tyr His Thr Leu Gly Leu Ile Ser Tyr Phe Thr Thr Gly
275     280     285
Pro Gln Glu Thr Arg Ala Trp Thr Ile Ser Lys Gly Val Thr Ala Ala
290     295     300
Glu Ala Ala Gly Glu Ile His Ser Asp Ile Gln Arg Gly Phe Ile Arg
305     310     315     320
Ala Glu Val Val Thr Met Glu Asp Ile Val Ala Tyr Asp Gly Arg Ala
325     330     335
Gly Ala Arg Glu Ala Gly Lys Leu Arg Ala
340     345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 369:

Met	Gly	Glu	Lys	Thr	Glu	Lys	Ala	Thr	Pro	Lys	Arg	Leu	Arg	Asp	Ala
1				5					10					15	
Arg	Lys	Lys	Gly	Gln	Val	Ala	Lys	Ser	Gln	Asp	Phe	Pro	Ser	Ala	Ile
			20					25					30		
Thr	Phe	Ile	Val	Ser	Met	Phe	Leu	Thr	Phe	Ser	Leu	Ala	Ser	Phe	Phe
		35					40					45			
Ala	Glu	His	Leu	Gly	Ser	Phe	Leu	Val	Ser	Ile	Phe	Lys	Thr	Ala	Pro
	50					55					60				
Gln	Asn	His	Asp	Pro	His	Leu	Ala	Ile	Tyr	Tyr	Leu	Lys	Asn	Cys	Leu
65					70					75					80
Ile	Leu	Ile	Leu	Thr	Val	Ser	Leu	Pro	Leu	Leu	Gly	Ala	Val	Gly	Phe
				85					90					95	
Val	Gly	Leu	Leu	Ile	Gly	Phe	Leu	Ile	Val	Gly	Pro	Thr	Phe	Ser	Thr
			100					105					110		
Glu	Val	Phe	Lys	Pro	Asp	Leu	Lys	Lys	Phe	Asn	Pro	Ile	Asp	Asn	Leu
		115					120					125			
Lys	Gln	Lys	Phe	Lys	Val	Lys	Thr	Phe	Ile	Glu	Leu	Leu	Lys	Ser	Ile
	130					135					140				
Phe	Lys	Ile	Ser	Gly	Ala	Ala	Leu	Ile	Leu	Tyr	Ile	Val	Leu	Lys	Asn
145					150					155					160
Arg	Val	Glu	Leu	Val	Ile	Glu	Thr	Ala	Gly	Val	Pro	Pro	Leu	Val	Thr
				165					170					175	
Ala	Gln	Val	Phe	Lys	Glu	Ile	Leu	Tyr	Lys	Ala	Val	Thr	Ser	Ile	Gly
			180					185					190		
Leu	Phe	Phe	Leu	Val	Val	Ala	Val	Ile	Asp	Leu	Val	Tyr	Gln	Arg	His
		195					200					205			
Ser	Phe	Ala	Lys	Glu	Leu	Lys	Met	Glu	Lys	Phe	Glu	Val	Lys	Gln	Glu
	210					215					220				
Phe	Lys	Asp	Thr	Glu	Gly	Asn	Pro	Glu	Ile	Lys	Gly	Arg	Arg	Arg	Gln
225					230					235					240
Ile	Ala	Gln	Glu	Ile	Ala	Tyr	Glu	Asp	Thr	Ser	Ser	Gln	Ile	Lys	His
				245					250					255	
Ala	Ser	Ala	Val	Val	Ser	Asn	Pro	Lys	Asp	Ile	Ala	Val	Ala	Ile	Gly
			260					265					270		
Tyr	Met	Pro	Glu	Lys	Tyr	Lys	Ala	Pro	Trp	Ile	Ile	Ala	Met	Gly	Val
		275					280						285		
Asn	Leu	Arg	Ala	Lys	Arg	Ile	Ile	Ala	Glu	Ala	Glu	Lys	Tyr	Gly	Val
	290					295					300				
Pro	Ile	Met	Arg	Asn	Val	Pro	Leu	Ala	His	Gln	Leu	Leu	Asp	Glu	Gly
305					310					315					320
Lys	Glu	Leu	Lys	Phe	Ile	Pro	Glu	Thr	Thr	Tyr	Glu	Ala	Val	Gly	Glu
				325					330					335	
Ile	Leu	Leu	Tyr	Ile	Thr	Ser	Leu	Asn							

(2) INFORMATIONS POUR LA SEQ ID NO: 370:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 365198..365587

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 370:

Met	Asn	Lys	Leu	Leu	Asn	Phe	Val	Ser	Arg	Thr	Phe	Gly	Gly	Asp	Ala
1			5						10					15	
Ala	Leu	Asn	Met	Ile	Asn	Lys	Ser	Ser	Asp	Leu	Ile	Leu	Ala	Met	Trp
		20					25						30		
Met	Leu	Gly	Val	Val	Leu	Met	Ile	Ile	Leu	Pro	Leu	Pro	Pro	Ala	Met
	35					40						45			
Val	Asp	Phe	Met	Ile	Thr	Ile	Asn	Leu	Ala	Ile	Ser	Val	Phe	Leu	Leu
	50				55					60					
Met	Val	Ala	Leu	Tyr	Ile	Pro	Ser	Ala	Leu	Gln	Leu	Ser	Val	Phe	Pro
65				70					75					80	
Ser	Leu	Leu	Leu	Ile	Thr	Thr	Met	Phe	Arg	Leu	Gly	Ile	Asn	Ile	Ser
			85				90						95		
Ser	Ser	Arg	Gln	Ile	Leu	Leu	His	Ala	Tyr	Ala	Gly	His	Val	Ile	Gln
		100				105						110			
Ala	Ser	Glu	Thr	Ser	Ser	Leu	Glu	Thr	Met	Ser	Leu	Asp	Leu	Leu	
		115				120					125				
Ser	Ser														
	130														

(2) INFORMATIONS POUR LA SEQ ID NO: 371:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 614 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 365479..367320

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 371:

His	Phe	Phe	Leu	Pro	Thr	Asn	Ser	Pro	Ser	Cys	Leu	Cys	Trp	Ser	Arg
1			5						10					15	
Asp	Pro	Ser	Phe	Gly	Asp	Phe	Val	Val	Gly	Gly	Asn	Tyr	Val	Val	Gly
		20					25						30		
Phe	Ile	Ile	Phe	Leu	Ile	Ile	Thr	Ile	Ile	Gln	Phe	Ile	Val	Val	Thr
	35					40					45				
Lys	Gly	Ala	Glu	Arg	Val	Ala	Glu	Val	Ala	Ala	Arg	Phe	Arg	Leu	Asp
	50				55					60					
Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Arg	Ala	Gly

65 Met Ile Asp Ala Thr Gln Ala Arg Asp Lys Arg Ser Gln Ile Gln Lys
 70 85 90 95
 Glu Ser Glu Leu Tyr Gly Ala Met Asp Gly Ala Met Lys Phe Ile Lys
 100 105 110
 Gly Asp Val Ile Ala Gly Ile Val Ile Ser Leu Ile Asn Ile Val Gly
 115 120 125
 Gly Leu Val Ile Gly Val Thr Met Lys Gly Met Thr Met Ala Gln Ala
 130 135 140
 Ala His Ile Tyr Thr Leu Ile Thr Ile Gly Asp Gly Leu Val Ser Gln
 145 150 155 160
 Ile Pro Ser Leu Leu Ile Ser Leu Thr Ala Gly Ile Val Thr Thr Arg
 165 170 175
 Val Ser Ser Asp Lys Asp Thr Asn Leu Gly Lys Glu Ile Ser Ser Gln
 180 185 190
 Leu Val Lys Glu Pro Arg Ala Leu Leu Leu Ser Ala Gly Ala Thr Leu
 195 200 205
 Gly Ile Gly Phe Phe Lys Gly Phe Pro Leu Trp Ser Phe Ala Leu Met
 210 215 220
 Ala Val Leu Phe Ala Val Leu Gly Ile Leu Leu Ile Thr Lys Lys Asn
 225 230 235 240
 Ser Pro Gly Lys Lys Gly Gly Ala Ser Ser Thr Thr Thr Val Gly Ala
 245 250 255
 Ala Asp Gly Ala Ala Ala Ser Gly Glu Asn Ser Asp Asp Tyr Ala Leu
 260 265 270
 Thr Leu Pro Val Ile Leu Glu Leu Gly Lys Asp Leu Ser Lys Leu Ile
 275 280 285
 Gln Gln Arg Thr Lys Ser Gly Gln Ser Phe Val Asp Asp Met Ile Pro
 290 295 300
 Lys Met Arg Gln Ala Leu Tyr Gln Asp Ile Gly Ile Arg Tyr Pro Gly
 305 310 315 320
 Ile His Val Arg Thr Asp Ser Pro Ser Leu Glu Gly Asn Asp Tyr Met
 325 330 335
 Ile Leu Leu Asn Glu Val Pro Tyr Val Arg Gly Lys Ile Pro Pro Asn
 340 345 350
 His Val Leu Thr Asn Glu Val Glu Glu Asn Leu Ser Arg Tyr Asn Leu
 355 360 365
 Pro Phe Ile Thr Tyr Lys Asn Ala Ala Gly Leu Pro Ser Thr Trp Val
 370 375 380
 Ser Thr Asp Ala Leu Thr Ile Leu Glu Lys Ala Ala Ile Lys Tyr Trp
 385 390 395 400
 Ser Pro Leu Glu Val Ile Ile Leu His Leu Ser Tyr Phe Phe His Arg
 405 410 415
 Asn Ser Gln Glu Phe Leu Gly Ile Gln Glu Val Arg Ser Met Ile Glu
 420 425 430
 Phe Met Glu Arg Ser Phe Pro Asp Leu Val Lys Glu Val Thr Arg Leu
 435 440 445
 Ile Pro Leu Gln Lys Leu Thr Glu Ile Phe Lys Arg Leu Val Gln Glu
 450 455 460
 Gln Ile Ser Ile Lys Asp Leu Arg Thr Ile Leu Glu Ser Leu Ser Glu
 465 470 475 480
 Trp Ala Gln Thr Glu Lys Asp Thr Val Leu Leu Thr Glu Tyr Val Arg
 485 490 495
 Ser Ser Leu Lys Leu Tyr Ile Ser Phe Lys Phe Ser Gln Gly Gln Ser
 500 505 510
 Ala Ile Ser Val Tyr Leu Leu Asp Pro Glu Ile Glu Glu Met Ile Arg
 515 520 525
 Gly Ala Ile Lys Gln Thr Ser Ala Gly Ser Tyr Leu Ala Leu Asp Pro
 530 535 540

```

Asp Ser Val Asn Leu Ile Leu Lys Ser Met Arg Met Thr Ile Thr Pro
545                               550                               555                               560
Thr Pro Pro Gly Gly Gln Pro Pro Val Leu Leu Thr Ala Ile Asp Val
                               565                               570                               575
Arg Arg Tyr Val Arg Lys Leu Ile Glu Thr Glu Phe Pro Asp Ile Ala
                               580                               585                               590
Val Ile Ser Tyr Gln Glu Val Leu Pro Glu Ile Arg Ile Gln Pro Leu
                               595                               600                               605
Gly Arg Ile Gln Ile Phe
610

```

(2) INFORMATIONS POUR LA SEQ ID NO: 372:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 421 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 367341..368603

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 372:

```

Met Thr Ala Ser Gly Gly Ala Gly Gly Leu Gly Ser Thr Gln Thr Val
1                               5                               10                               15
Asp Val Ala Arg Ala Gln Ala Ala Ala Thr Gln Asp Ala Gln Glu
                               20                               25                               30
Val Ile Gly Ser Gln Glu Ala Ser Glu Ala Ser Met Leu Lys Glu Cys
                               35                               40                               45
Glu Asp Leu Ile Asn Pro Ala Ala Ala Thr Arg Ile Xaa Lys Lys Glu
                               50                               55                               60
Glu Lys Phe Glu Ser Leu Glu Ala Arg Arg Lys Xaa Thr Ala Asp Lys
65                               70                               75                               80
Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Gly Asp Thr Pro Leu
                               85                               90                               95
Glu Asp Arg Phe Thr Glu Asp Leu Ser Glu Val Ser Gly Glu Asp Phe
                               100                              105                              110
Arg Gly Leu Lys Asn Ser Phe Asp Asp Asp Ser Ser Ser Asp Glu Ile
                               115                              120                              125
Leu Asp Ala Leu Thr Ser Lys Phe Ser Asp Pro Thr Ile Lys Asp Leu
130                              135                              140
Ala Leu Asp Tyr Leu Ile Gln Ile Ala Pro Ser Asp Gly Lys Leu Lys
145                              150                              155                              160
Ser Ala Leu Ile Gln Ala Lys His Gln Leu Met Ser Gln Asn Pro Gln
                               165                              170                              175
Ala Ile Val Gly Gly Arg Asn Val Leu Leu Ala Ser Glu Thr Phe Ala
                               180                              185                              190
Ser Arg Ala Asn Thr Ser Pro Ser Ser Leu Arg Ser Leu Tyr Phe Gln
                               195                              200                              205
Val Thr Ser Ser Pro Ser Asn Cys Ala Asn Leu His Gln Met Leu Ala
210                              215                              220
Ser Tyr Ser Pro Ser Glu Lys Thr Ala Val Met Glu Phe Leu Val Asn
225                              230                              235                              240
Gly Met Val Ala Asp Leu Lys Ser Glu Gly Pro Ser Ile Pro Pro Ala
                               245                              250                              255
Lys Leu Gln Val Tyr Met Thr Glu Leu Ser Asn Leu Gln Ala Leu His

```

260 265 270
 Ser Val Asp Ser Phe Phe Asp Arg Asn Ile Gly Asn Leu Glu Asn Ser
 275 280 285
 Leu Lys His Glu Gly His Ala Pro Ile Pro Ser Leu Thr Thr Gly Asn
 290 295 300
 Leu Thr Lys Thr Phe Leu Gln Leu Val Glu Asp Lys Phe Pro Ser Ser
 305 310 315 320
 Ser Lys Ala Gln Lys Ala Leu Asn Glu Leu Val Gly Pro Asp Thr Gly
 325 330 335
 Pro Gln Thr Glu Val Leu Asn Leu Phe Phe Arg Ala Leu Asn Gly Cys
 340 345 350
 Ser Pro Arg Ile Phe Ser Gly Ala Glu Lys Lys Gln Gln Leu Ala Ser
 355 360 365
 Val Ile Thr Asn Thr Leu Asp Ala Ile Asn Ala Asp Asn Glu Asp Tyr
 370 375 380
 Pro Lys Pro Gly Asp Phe Pro Arg Ser Ser Phe Ser Ser Thr Pro Pro
 385 390 395 400
 His Ala Pro Val Pro Gln Ser Glu Ile Pro Thr Ser Pro Thr Ser Thr
 405 410 415
 Gln Pro Pro Ser Pro
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 373:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 146 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 368644..369081

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 373:

Met Gln Asn Gln Phe Glu Gln Leu Leu Thr Glu Leu Gly Thr Gln Ile
 1 5 10 15
 Asn Ser Pro Leu Thr Pro Asp Ser Asn Asn Ala Cys Ile Val Arg Phe
 20 25 30
 Gly Tyr Asn Asn Val Ala Val Gln Ile Glu Glu Asp Gly Asn Ser Gly
 35 40 45
 Phe Leu Val Ala Gly Val Met Leu Gly Lys Leu Pro Glu Asn Thr Phe
 50 55 60
 Arg Gln Lys Ile Phe Lys Ala Ala Leu Ser Ile Asn Gly Ser Pro Gln
 65 70 75 80
 Ser Asn Ile Lys Gly Thr Leu Gly Tyr Gly Glu Ile Ser Asn Gln Leu
 85 90 95
 Tyr Leu Cys Asp Arg Leu Asn Met Thr Tyr Leu Asn Gly Glu Lys Leu
 100 105 110
 Ala Arg Tyr Leu Val Leu Phe Ser Gln His Ala Asn Ile Trp Met Gln
 115 120 125
 Ser Ile Ser Lys Gly Glu Leu Pro Asp Leu His Ala Leu Gly Met Tyr
 130 135 140
 His Leu
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 374:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 388 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 369088..370251

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 374:

Met	Pro	Ser	Leu	Ser	Gln	Ser	Arg	Arg	Ile	Ile	Gln	Gln	Ser	Ser	Ile	1	5	10	15
Arg	Lys	Ile	Trp	Asn	Gln	Ile	Asp	Thr	Ser	Pro	Lys	His	Gly	Val	Cys	20	25	30	
Val	Pro	Leu	Phe	Ser	Leu	His	Thr	Gln	Glu	Ser	Cys	Gly	Ile	Gly	Glu	35	40	45	
Phe	Leu	Asp	Leu	Ile	Pro	Met	Ile	Asp	Trp	Cys	Ile	Ser	Cys	Gly	Phe	50	55	60	
Gln	Ile	Leu	Gln	Ile	Leu	Pro	Ile	Asn	Asp	Thr	Gly	Ser	Cys	Ser	Ser	65	70	75	80
Pro	Tyr	Asn	Ser	Ile	Ser	Ser	Ile	Ala	Leu	Asn	Pro	Leu	His	Leu	Ser	85	90	95	
Ile	Ser	Ala	Leu	Pro	Tyr	Lys	Glu	Glu	Val	Pro	Ala	Ala	Glu	Thr	Arg	100	105	110	
Ile	Arg	Glu	Met	Gln	Gln	Leu	Ser	Gln	Leu	Pro	Gln	Val	His	Tyr	Glu	115	120	125	
Lys	Val	Arg	Ser	Met	Lys	Arg	Asp	Phe	Phe	Gln	Glu	Tyr	Tyr	Arg	Val	130	135	140	
Cys	Lys	Gln	Lys	Lys	Leu	Thr	Asp	His	Pro	Asp	Phe	Tyr	Ala	Phe	Cys	145	150	155	160
Glu	Gln	Glu	Lys	Tyr	Trp	Leu	His	Pro	Tyr	Ala	Leu	Phe	Arg	Ser	Ile	165	170	175	
Arg	Glu	His	Leu	Asp	Asn	Leu	Pro	Ile	Asn	His	Trp	Pro	Thr	Thr	Tyr	180	185	190	
Thr	Asp	Leu	Ser	Gln	Ile	Thr	Glu	His	Glu	Arg	Thr	Phe	Ala	Glu	Asp	195	200	205	
Ile	Gln	Phe	His	Ser	Tyr	Leu	Gln	Tyr	Leu	Cys	Phe	Gln	Gln	Met	Thr	210	215	220	
Gln	Val	Arg	Glu	His	Ala	Asn	Cys	Lys	Ser	Cys	Leu	Ile	Lys	Gly	Asp	225	230	235	240
Ile	Pro	Ile	Leu	Ile	Ser	Lys	Asp	Ser	Cys	Asp	Val	Trp	Phe	Tyr	Arg	245	250	255	
His	Tyr	Phe	Ser	Ser	Ser	Glu	Ser	Val	Gly	Ala	Pro	Pro	Asp	Leu	Tyr	260	265	270	
Asn	Ala	Glu	Gly	Gln	Asn	Trp	His	Leu	Pro	Ile	Tyr	Asn	Met	Lys	Thr	275	280	285	
Leu	Gln	Gln	Asp	Asn	Tyr	Leu	Trp	Trp	Lys	Glu	Arg	Leu	Arg	Tyr	Ala	290	295	300	
Glu	Asn	Phe	Tyr	Ser	Leu	Tyr	Arg	Leu	Asp	His	Ile	Val	Gly	Leu	Phe	305	310	315	320
Arg	Phe	Trp	Val	Trp	Asp	Glu	Ser	Gly	Cys	Gly	Arg	Phe	Glu	Pro	His	325	330	335	
Asp	Pro	Lys	Asp	Tyr	Leu	Ala	Gln	Gly	Gln	Asp	Ile	Leu	Ser	His	Leu	340	345	350	
Leu	Thr	Ser	Ser	Ser	Met	Leu	Pro	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Ile				

(2) INFORMATION POUR LA SEQ ID NO: 375:

(A) LONGUEUR: 89 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 370820..371086

[illegible]

(A) LONGUEUR: 538 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 371203..372816

Tyr 1	Asp	Val	Phe	Ser 5	Leu	Arg	Ser	Leu	Val 10	Asp	Tyr	Leu	Arg	Ser 15	Gln
His	Glu	Leu	Ile	Asp	Ile	His	Val	Pro	Val	Asp	Pro	His	Leu	Glu	Ile
			20					25					30		
Ala	Glu	Ile	His	Arg	Arg	Val	Val	Glu	Arg	Glu	Gly	Pro	Ala	Leu	Leu
		35					40					45			
Phe	His	Gln	Val	Lys	Gly	Ser 55	Pro	Phe	Pro	Val	Leu	Thr	Asn	Leu	Phe
	50										60				
Gly	Thr	Arg	Arg	Arg	Val	Asp	Leu	Leu	Phe	Pro	Asp	Leu	Ser	Ser	Asp
65					70					75					80

Leu Phe Glu Gln Ile Ile His Leu Leu Ser Ser Pro Pro Ser Phe Ser
 85 90 95
 Ser Leu Trp Lys His Arg Ser Leu Phe Lys Arg Gly Ile Ser Ala Leu
 100 105 110
 Gly Met Arg Lys Arg His Leu Arg Ser Ser Pro Phe Leu Tyr Gln Asp
 115 120 125
 Ala Pro Asn Leu Ser Gln Leu Pro Met Leu Thr Ser Trp Pro Glu Asp
 130 135 140
 Gly Gly Pro Phe Leu Thr Leu Pro Leu Val Tyr Thr Gln Ser Pro Glu
 145 150 155 160
 Asn Gly Val Pro Asn Leu Gly Met Tyr Arg Met Gln Arg Phe Asp Lys
 165 170 175
 Glu Thr Leu Gly Leu His Phe Gln Ile Gln Lys Gly Gly Gly Ala His
 180 185 190
 Phe Phe Glu Ala Glu Gln Lys Lys Gln Asn Leu Pro Val Thr Val Phe
 195 200 205
 Leu Ser Gly Asn Pro Phe Leu Ile Leu Ser Ala Ile Ala Pro Leu Pro
 210 215 220
 Glu Asn Val Pro Glu Leu Leu Phe Cys Ser Phe Leu Gln Asn Lys Lys
 225 230 235 240
 Leu Ser Phe Val Glu Lys His Pro Gln Ser Gly His Pro Leu Leu Cys
 245 250 255
 Asp Ser Glu Phe Ile Leu Thr Gly Glu Ala Val Ala Gly Glu Arg Arg
 260 265 270
 Pro Glu Gly Pro Phe Gly Asp His Phe Gly Tyr Tyr Ser Leu Thr His
 275 280 285
 Asp Phe Pro Ile Phe Lys Cys Asn Cys Leu Tyr His Lys Lys Asp Ala
 290 295 300
 Ile Tyr Pro Ala Thr Val Val Gly Lys Pro Phe Gln Glu Asp Phe Phe
 305 310 315 320
 Leu Gly Asn Lys Leu Gln Glu Leu Leu Ser Pro Leu Phe Pro Leu Ile
 325 330 335
 Met Pro Gly Val Gln Asp Leu Lys Ser Tyr Gly Glu Ala Gly Phe His
 340 345 350
 Ala Leu Ala Ala Ala Ile Val Lys Glu Arg Tyr Trp Lys Glu Ala Leu
 355 360 365
 Arg Ser Ala Leu Arg Ile Leu Gly Glu Gly Gln Leu Ser Leu Thr Lys
 370 375 380
 Phe Leu Trp Ile Thr Asp Gln Ser Val Asp Leu Glu Asn Phe Ser Ser
 385 390 395 400
 Leu Leu Glu Cys Val Leu Glu Arg Met Asn Phe Asp Arg Asp Leu Leu
 405 410 415
 Ile Leu Ser Glu Thr Ala Asn Asp Thr Leu Asp Tyr Thr Gly Ser Gly
 420 425 430
 Phe Asn Lys Gly Ser Lys Gly Ile Phe Leu Gly Val Gly Ala Pro Ile
 435 440 445
 Arg Ser Leu Pro Arg Arg Tyr Arg Gly Pro Ser Leu Pro Gly Ile Ser
 450 455 460
 Gln Ile Gly Val Phe Cys Arg Gly Cys Leu Val Leu Glu Thr Ser Leu
 465 470 475 480
 Gln Gln Leu Asp Ile Pro Ala Leu Leu Lys Asp Pro His Leu Ala Asp
 485 490 495
 Trp Pro Leu Val Ile Leu Val Glu Asp Leu Ser Ser Ala Leu Ser Ser
 500 505 510
 Thr Lys Glu Phe Ile Trp Glu Asn Ile Tyr Thr Ile Phe Ser Cys Asn
 515 520 525
 Arg Phe Thr His Pro Cys Lys Ser Asn His
 530 535

(2) INFORMATIONS POUR LA SEQ ID NO: 377:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 137 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 373119..373529

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 377:

```

Asn Glu Lys Asn Lys Thr Leu Ile Ser Lys Ile Met Phe Ser Leu Val
1      5      10      15
Ser Leu Phe Val Gly Gly Phe Leu Leu Lys Ala Pro Ala Pro Thr Gln
20      25      30
Ser Ala Asp Thr Phe Gln Thr Leu Ile Glu Ser Lys Glu Pro Val Ile
35      40      45
Phe Thr Lys Gln Cys Gly Asp Asn Val Thr Gln Ile Leu Cys Asp Ala
50      55      60
Ile Asp Ser Ala Lys Lys Asp Ile Phe Leu Xaa Ile Tyr Asp Leu Ser
65      70      75      80
Ala Pro Ala Ile Thr Thr Ser Leu Lys Lys Gln Val Ser Ala Arg Ile
85      90      95
Pro Val Cys Ile His Tyr Gln Arg Ile Ser Lys Asn Ala Glu Phe Ser
100     105     110
Gln Ser Pro Tyr Leu Thr Pro Trp Glu Asn Ile Leu Pro Cys Thr Glu
115     120     125
Asn Ser Cys Ile Lys Lys Leu Trp Gln
130     135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 378:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 197 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 373614..374204

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 378:

```

Lys Ala Gln Lys Phe Val Ile Leu Leu Lys Arg Lys Pro Leu Val Gly
1      5      10      15
Ala Leu Leu Thr Ile Asn Ser Ser Ser Ile Val Ser Phe Asp Gly Gly
20      25      30
Ser Ser Ala Ala Leu Glu Thr Val Leu His His Ile Arg Ser Ala Lys
35      40      45
Glu Ser Ile Gln Val Gly Met Phe Ala Leu Thr Leu Pro Gln Ile Ile
50      55      60
Ala Glu Leu Asn Ala Ala Gln Asn Cys Gly Val Asp Val Val Ile Leu
65      70      75      80

```

```

Val Asp Lys Gly Tyr Lys Ser Phe Thr Val Gln Gln Ile Lys Gln Leu
      85                      90                      95
Glu His Pro Ser Leu Ser Ile Tyr Glu Lys Val Thr Pro Tyr Gln Leu
      100                    105                    110
His His Lys Phe Gly Ile Phe Asp Lys Lys Thr Leu Ile Thr Gly Ser
      115                    120                    125
Val Asn Trp Ser Glu Asn Gly Phe Leu Ile Asn Thr Glu Asp Met Ile
      130                    135                    140
Val Ile Glu Asn Leu Thr Glu Lys Gln Gln Ser Lys Ile Gln Ala Ile
      145                    150                    155                    160
Trp Glu Gly Leu Val Arg Glu Cys Ala Leu Tyr Tyr Ser Pro Asp Gln
      165                    170                    175
Glu Glu Lys Glu Lys Asp Pro Leu Ile Ile Pro Phe Pro Pro Ser Glu
      180                    185                    190
Lys Lys Gln Ala Ala
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 379:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(374224..374736)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 379:

```

Asn Glu Arg Asn Arg Gly Cys Arg Arg Arg Phe Met Arg Ile Ile Pro
1      5      10      15
Phe Asp Pro Tyr Gly Ser Met Ala Phe Gln Ala Ile Ala Lys Asp Pro
      20      25      30
Gln Glu Arg Lys Asn Gly Ser Ile Ser Glu Lys Ile Ser Glu Glu Ile
      35      40      45
Ala Arg Asn Glu Ala Leu Arg Met Ala Leu Leu Ala Ile Ala Asp Gln
      50      55      60
Glu Asp Lys Glu Lys Lys Gln Lys His Arg Phe Lys Ile Leu Thr Lys
65      70      75      80
Lys Gln Thr Arg Met Leu Leu Gly Gln Leu Arg His Phe Arg Leu Asp
      85      90      95
Phe Gln Lys Leu Gln Ala Gly Val Val Ile Glu Trp Ser Trp Asp Asp
      100     105     110
Lys Ser Lys Arg Ser Lys Ser Leu Gly Ser Arg Ile Thr Arg Lys Ser
      115     120     125
Lys Lys Thr Ile Cys Ile Ser Ala Ala Ala Gln Ala Ile Ala His
      130     135     140
Ala Ala Glu Ala Trp Val Ile Ala Arg Asn Glu Gly Ile Leu Glu Met
145     150     155     160
Thr Leu Ser Leu Phe Gln His Lys Asp Asn Glu
      165     170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 380:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(374703..376391)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 380:

(xi) DESCRIPTION OF THE SEQUENCE

Glu Lys Ile Met Ser Ile Ser Gly Ser Gly Asn Val Ser Pro Ala Thr
1 5 10 15
Pro Asp Phe Asp Pro Ser Ile Leu Met Gly Arg Gln Ala Ala Ser Ala
20 25 30
His Ala Ala Lys Glu Ala Ser Gly Ala Ser Lys Ala Thr Glu Thr Ser
35 40 45
Ala Ala Glu Gln Gln Ala Leu Ile Ser Ser Gly Thr Glu Leu Asp Tyr
50 55 60
Val Thr Asp Leu Gln Gln Ser Glu Gly Lys Tyr Lys Lys Thr Leu Asp
65 70 75 80
Lys Thr Ser Lys Ser Pro Lys Thr Lys Leu Lys Gly Asn Phe Ser Lys
85 90 95
Val Arg Ala Gly Thr Lys Gly Phe Leu Thr Gly Phe Gly Thr Arg Ala
100 105 110
Ser Arg Ile Ser Ala Arg Lys Ala Glu Asn Asn Gly Glu Gly Met Ser
115 120 125
Met Ile Pro Ser Gln Met Glu Tyr Val Lys Lys Lys Gly Asn Arg Val
130 135 140
Ser Pro Glu Met Gln Asn Phe Tyr Leu Gly Ala Ser Gly Leu Trp Ser
145 150 155 160
Pro Thr Ser Asp Val Ser Ser Lys Thr Glu Asn Arg Leu Gly Ala Thr
165 170 175
Ala Leu Ser Thr Thr Pro Ser Leu Thr Thr Met Gln Asp Pro Val Ser
180 185 190
Ile Glu His Leu Ser Ser Gly Glu Ile Thr Ala Leu Ala Ser Phe Asn
195 200 205
Pro Asn Val Arg Ala Ala Ser Leu Asn Glu Gln Thr Ile Asn Ala Trp
210 215 220
Thr Glu Ala Arg Leu Gly Gly Glu Met Val Ser Thr Leu Leu Asp Pro
225 230 235 240
Asn Ile Glu Thr Ser Ser Leu Leu Arg Arg Ala Pro Thr Val Ser Asn
245 250 255
Glu Gly Met Val Asp Val Ser Asp Met Gly Asn Gln Thr Thr Ser Leu
260 265 270
Ser Met Glu Gly Leu Val Asn Thr Val Val Asp Asp Pro Ala Ser Ala
275 280 285
Glu Glu Glu Lys Lys Thr Gly Glu Leu Ser Leu Glu Glu Met Ala Ala
290 295 300
Met Ala Lys Met Met Ala Ala Leu Leu Ser Ser Gly Gln Gly Met Ala
305 310 315 320
Val Phe Ile Ala Ser Ser Thr Pro Ser Ser Gly Ser Thr Gln Phe Pro
325 330 335
Glu Pro Lys Phe Ser Gly Thr Ile Pro His His Phe Ser Lys Lys Glu
340 345 350
Asp Asn Glu Thr Ile Trp Gly Leu Asp Ser Gln Ile Gly Ser Ile Ala
355 360 365
Phe Asp Thr Arg Arg Glu Asn Asn Ala Ser Pro Leu Pro Thr Thr Ser
370 375 380

```

Leu His Glu Glu Ala Ser Tyr Arg Phe Pro Val Gly Glu Ala Pro Leu
385          390          395          400
Asp Val Asn Glu Ile Pro Phe Ala Val Gln His Ser Thr Val Phe Ser
          405          410          415
Glu Glu Thr Ala Asn Thr Glu Gln Ala Leu Ile Gln Asn Glu Ser Leu
          420          425          430
Gly Glu Ile Pro Val Ser Ala Glu Val Val Gly Gln Asp Thr Val Ser
          435          440          445
Ser Ala Tyr Gln Phe Pro Ser His Leu Gly Met Ala Val Leu Ala Ser
          450          455          460
Val Pro Leu Ser Thr Glu Asp Tyr Lys Thr Ala Val Glu His Arg Lys
465          470          475          480
Gly Pro Gly Gly Pro Pro Asp Pro Leu Ile Tyr Gln Tyr Arg Asn Val
          485          490          495
Ala Val Asp Pro Ala Ile Ile Phe Gln Ser Pro Ser Pro Phe Ser Val
          500          505          510
Ser Ser Arg Phe Ser Val Gln Gly Lys Pro Glu Ala Val Ala Val Tyr
          515          520          525
Asn Asp Asp Gln Glu Glu Ala Ala Gly Gly Asn Arg Asp Ser Asp Glu
          530          535          540
Gly Lys Asp Gln Glu Gln Asp Lys Thr Arg Glu Thr Glu Asp Ala Gly
545          550          555          560
Gly Asp Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 381:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(376748..377038)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 381:

```

Met Lys Lys Arg Ser Ser Arg Lys Leu Ala Gln Val Ile Gly Arg Lys
1          5          10          15
Thr Gly Asn Tyr Phe Pro Ala Ser Ile Glu Gly Glu Thr Lys Lys Glu
          20          25          30
His Lys Arg Tyr Tyr Ser Thr Ala Ser Lys Glu Lys Glu Ser Leu Arg
          35          40          45
Lys Arg Ala Lys Glu Phe Asp Val Leu Val His Ser Leu Leu Asp Lys
          50          55          60
His Val Pro Gln Asn Ser Asp Gln Val Leu Ile Phe Thr Tyr Gln Asn
          65          70          75          80
Gly Phe Val Glu Thr Asp Phe His Asn Phe Gly Arg Tyr Ser Val Lys
          85          90          95
Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 382:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 295 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 377853..378737

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 382:

Asn	His	Leu	Thr	Lys	Tyr	Leu	Cys	Met	Leu	Leu	Lys	Gly	Ala	Pro	Ala
1				5					10					15	
Ala	Asp	His	Ile	Leu	Ala	Thr	Ile	Lys	Glu	Asn	Ile	Arg	Ala	Cys	Ser
			20					25					30		
Lys	Ala	Pro	Gly	Leu	Ala	Val	Val	Leu	Ile	Gly	Asn	Asn	Pro	Ala	Ser
			35				40					45			
Glu	Ile	Tyr	Val	Asn	Met	Lys	Ile	Lys	Arg	Ala	Thr	Asp	Leu	Gly	Met
			50			55					60				
Val	Ser	Lys	Ser	Tyr	Arg	Lys	Pro	Ser	Asp	Ala	Thr	Leu	Ser	Asp	Ile
65					70				75					80	
Leu	Ala	Leu	Ile	His	Gln	Leu	Asn	Asn	Asp	Glu	Asn	Ile	His	Gly	Ile
				85					90				95		
Leu	Val	Gln	Leu	Pro	Leu	Pro	Lys	His	Leu	Asp	Ala	Gln	Ala	Ile	Leu
			100					105					110		
Ser	Thr	Ile	Thr	Pro	Asp	Lys	Asp	Val	Asp	Gly	Leu	His	Pro	Val	Asn
		115					120					125			
Val	Gly	Lys	Leu	Leu	Leu	Gly	Glu	Thr	Asp	Gly	Phe	Ile	Pro	Cys	Thr
		130				135					140				
Pro	Ala	Gly	Ile	Val	Glu	Leu	Cys	Lys	Tyr	Tyr	Glu	Ile	Pro	Leu	His
145					150					155				160	
Gly	Lys	His	Val	Val	Ile	Leu	Gly	Arg	Ser	Asn	Ile	Val	Gly	Lys	Pro
			165						170					175	
Leu	Ala	Ala	Leu	Leu	Met	Gln	Arg	His	Ala	Asp	Thr	Asn	Ala	Ser	Val
			180					185					190		
Thr	Leu	Leu	His	Ser	Gln	Ser	Glu	His	Leu	Thr	Glu	Ile	Thr	Arg	Thr
		195					200					205			
Ala	Asp	Ile	Leu	Ile	Ser	Ala	Ile	Gly	Val	Pro	Leu	Phe	Val	Asn	Lys
		210				215					220				
Glu	Met	Ile	Ala	Glu	Lys	Thr	Val	Ile	Met	Asp	Val	Gly	Thr	Ser	Arg
225					230					235				240	
Ile	Pro	Ala	Ala	Asn	Pro	Lys	Gly	Tyr	Ile	Leu	Val	Gly	Asp	Val	Asp
			245					250					255		
Phe	Asn	Asn	Val	Val	Pro	Val	Cys	Arg	Ala	Ile	Thr	Pro	Val	Pro	Gly
			260					265					270		
Gly	Val	Gly	Pro	Met	Thr	Val	Ala	Met	Leu	Met	Arg	Asn	Thr	Trp	Glu
		275					280						285		
Ser	Phe	Leu	Arg	His	Thr	Ser									
		290				295									

(2) INFORMATIONS POUR LA SEQ ID NO: 383:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 141 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 383:

(2) INFORMATION POUR LA SEQ ID NO: 384:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 379017..379403

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 384:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 385:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 123 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(379641..380009)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 385:

Gln Glu Gln Lys Leu Asn Ser Leu Arg Asp His Gly Gly Asn Leu Gly
 1 5 10 15
 Asp Ala Tyr Val Thr Ile Ser Lys Gly Glu Ala Trp Leu Leu Gln Ser
 20 25 30
 Ser Ile Ala Pro Tyr Arg Phe Gly Asn Ile Asn Asn His Glu Glu Arg
 35 40 45
 Arg Lys Arg Lys Leu Leu Leu His Lys Tyr Glu Ile His Lys Leu Asp
 50 55 60
 Ala Arg Ile Ser Gln Lys Gly Leu Thr Val Val Pro Leu Ser Phe Phe
 65 70 75 80
 Phe Ser Lys Gly Phe Val Lys Val Arg Ile Gly Cys Cys Arg Gly Lys
 85 90 95
 Lys Ala His Asp Lys Arg Gln Ser Ile Ile Glu Arg Glu Lys Asn Arg
 100 105 110
 Glu Leu Ala Ala Ala Met Lys Arg Ser Cys Arg
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 386:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 366 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 380373..381470

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 386:

Met Lys Phe Val Ile Ser Arg Asn Glu Leu Gly Asn Leu Ile Lys Lys
 1 5 10 15
 Val Gln Asn Val Val Pro Gln Ser Thr Pro Ile Pro Val Leu Thr His
 20 25 30
 Val Leu Ile Glu Ser Cys Asn Asp Glu Leu Val Phe Thr Ala Thr Asp
 35 40 45
 Leu Thr Val Ser Thr Arg Cys Val Val Lys Ala Lys Val Tyr Glu Ser
 50 55 60
 Gly Ser Val Thr Ile Pro Ser Arg Arg Phe Phe Gln Leu Ile Arg Glu
 65 70 75 80
 Leu Thr Glu Ala Asn Ile Glu Val Ala Ala His Ser Gly Glu Met Ala
 85 90 95


```

Thr Ile Thr Ser Gly Ser Ser Cys Phe Arg Leu Leu Ser Met Gly Lys
      100      105      110
Glu Asp Phe Pro Met Leu Pro Asp Met Gln Asn Ala Leu Arg Phe Thr
      115      120      125
Leu Asp Ser Glu Arg Leu Lys Asp Met Phe Gln Arg Thr Ser Phe Ala
      130      135      140
Val Ser Arg Glu Glu Ser Arg Tyr Val Leu Thr Gly Val Leu Leu Ser
      145      150      155      160
Ile Ala Asn Gly Thr Met Thr Val Val Gly Thr Asp Gly Lys Arg Leu
      165      170      175
Ala Lys Ile Asp Thr Glu Ile Ser Leu Asp Pro Ser Phe Ser Gly Asp
      180      185      190
Tyr Ile Ile Pro Ile Lys Ala Val Glu Glu Ile Ile Arg Met Ser Ser
      195      200      205
Glu Asp Val Gln Ser Thr Ile Phe Leu Asp Gln Thr Lys Ile Ala Val
      210      215      220
Glu Cys Gly Asn Thr Leu Leu Val Thr Lys Leu Leu Ser Gly Glu Phe
      225      230      235      240
Pro Asp Phe Ser Pro Val Ile Ser Thr His Ser Ser Val Gln Leu Asp
      245      250      255
Leu His Arg Glu Glu Leu Ile Ser Leu Leu Lys Gln Val Ala Leu Phe
      260      265      270
Thr Asn Glu Ser Ser His Ser Val Lys Phe Ser Phe Ser Pro Gly Glu
      275      280      285
Leu Thr Leu Thr Ala Asn Cys Thr Lys Val Gly Glu Gly Lys Val Ser
      290      295      300
Met Ala Val Asn Tyr Thr Gly Glu Thr Leu Glu Ile Ala Phe Asn Pro
      305      310      315      320
Phe Phe Phe Leu Asp Ile Leu Lys His Ser Arg Asp Glu Leu Val Gln
      325      330      335
Leu Gly Ile Ser Asp Ser Tyr Asn Pro Gly Ile Ile Thr Asp Ser Thr
      340      345      350
Arg Ser Leu Phe Val Ile Met Pro Met Arg Leu His Asp Asp
      355      360      365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 387:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 381473..382567

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 387:

```

Met Arg Val Leu Ser Leu Phe Leu Lys Asp Phe Arg Asn Tyr Thr Asp
1      5      10      15
Leu Arg Leu Glu Leu Gly Pro Glu Met Asn Ser Ile Phe Gly Leu Asn
      20      25      30
Ala Gln Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Ile Leu Ser Leu
      35      40      45
Gly Arg Ser Phe Arg Thr Ser Arg Leu Thr Asp Ala Ile Arg Phe Gly
      50      55      60
Ala Ser His Phe Phe Ile Glu Ala Val Phe Ser His Lys Glu Val Phe

```

```

65              70              75              80
His Thr Leu Ser Ile Gln Val Asp Lys Lys Gly Lys Lys Ile Leu Phe
85              90              95
Asp Gly Ala Pro Ile Thr Lys Leu Ser Glu Leu Val Gly Leu Phe Pro
100             105             110
Val Ile Leu Phe Ser Ile Lys Asp Ile Ala Ile Ile Glu Gly Ser Pro
115             120             125
Ser Glu Arg Arg Arg Phe Leu Asp Leu Leu Leu Ala Gln Ala Ser Asp
130             135             140
Lys Tyr Thr Glu His Ile Ser Leu Tyr His Lys Ala Leu Asp Gln Arg
145             150             155
Asn Ala Ser Ile Lys Ala Gln Asn Gln Lys Ala Ile Ser Ala Trp Asn
165             170             175
Ser Pro Leu Ile Ala Tyr Gly Ser Leu Val Ala Phe Leu Arg Asn Glu
180             185             190
Cys Thr Lys Lys Leu Asn Thr Ile Phe Gln Thr Leu Trp Asp Asn Thr
195             200             205
Leu Lys Glu Thr Leu Ser Leu Arg Tyr Glu Ser Ser Leu Ile Thr Glu
210             215             220
Glu Ser Pro Thr Leu Asn Asp Ile Ala Ser Asn Tyr Tyr Glu Gln Leu
225             230             235
Arg Ile Ala Asn Thr Lys Asp Leu Asp Leu Gly Tyr Thr Met Val Gly
245             250             255
Pro His Arg Asp Glu Leu Leu Leu Thr Ile Asn Asp Leu Pro Val Ala
260             265             270
Lys Phe Ser Ser Glu Gly Gln Lys His Ser Leu Leu Ala Val Leu Arg
275             280             285
Phe Ala Glu Cys Val Tyr Leu Gln Glu Glu Phe Cys Ile His Pro Leu
290             295             300
Leu Cys Met Asp Asp Ile His Ala Cys Leu Asp Gln Gln Arg Leu Asp
305             310             315
Gln Leu Leu Gln Leu Ser Asn Ser Leu Gly Gln Val Val Thr Thr Ser
325             330             335
Thr Ile Cys Pro Asp His Arg Ser Thr Thr Ser Cys Ile Phe His Val
340             345             350
Thr Gln Ala Gln Val Ser Leu Val Ala Pro Gln Ser Leu
355             360             365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 388:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 333 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 382704..383702

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 388:

```

Asn Asn Ile Asn Arg Cys Cys Glu Met Lys Asn Phe Leu Leu Thr Ile
1              5              10             15
Leu Phe Leu Leu Met Gly Thr Ser Leu Leu Ala Asp Pro Ser Val Ile
20             25             30
Gln Thr Leu Thr Ser Gly Val Ala Gly Val Asn Ser Ile Arg Glu Glu
35             40             45

```

```

Lys Glu Ser Val Val Cys Val His Ala Phe Leu Arg Ser Tyr Gly Ser
 50      55      60
Leu Lys Pro Ile Gly Arg Val Leu Glu Lys Glu Asn Tyr Asp Val Phe
65      70      75      80
Ile Trp Asn Tyr Glu Thr Arg Lys Phe Thr Leu Glu Lys His Ala Glu
      85      90      95
His Leu Val Arg Leu Leu Asn Lys Ile Ala Glu Leu Lys Pro Gly Ile
      100      105      110
Pro Ile Asn Phe Val Thr His Ser Val Gly Gly Val Ile Val Arg Val
      115      120      125
Ala Leu Ala His Pro Asp Cys Pro Glu Glu Ala Lys Lys Gly Lys Ala
130      135      140
Val Leu Met Ala Pro Pro Asn Ala Gly Ser Thr Leu Ala Arg Arg Tyr
145      150      155      160
Ser Arg Ser Ser Leu Val Gln Phe Val Phe Gly Arg Lys Leu Gly Met
      165      170      175
Gln Leu Leu Thr Tyr Ser Pro Glu His Met Leu Asn Ile Ala Lys Met
      180      185      190
Pro Ser Ser Val Asp Val Leu Val Leu Ser Gly Thr Lys Lys Ser Lys
      195      200      205
Phe Leu Leu Phe Gln Leu Glu Asp Asn Asp Gly Lys Val Cys Val
210      215      220
Thr Glu Thr Arg Leu Asp Thr Pro His Gln Asn Tyr Ile Ile Asp Ala
225      230      235      240
Asn His Thr Tyr Ile Ile Thr Asn Lys Thr Ser Leu Phe Leu Met Arg
      245      250      255
Glu Phe Leu Arg Asn Gly Ser Arg Ser Ser Ala Leu Thr Gln Val Pro
      260      265      270
Glu Glu Ile Glu Ala Ser Ile Gln Gln Ser Pro Lys Ala Lys Val Asn
      275      280      285
Lys Glu Lys Ser Lys Asp Ile Tyr Val Ile His Cys Leu Gly Ala His
290      295      300
Pro Tyr Ser Leu Tyr Gly Phe Pro Lys Ser Arg Thr Ser Pro Asn Glu
305      310      315      320
Asn Ser Arg Lys Val Leu Glu Gly Gln Glu Tyr Lys Lys
      325      330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 389:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(383655..383945)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 389:

```

Trp Leu Ser Gly Pro Val Gly Ile Val Arg Ile Leu His Thr Gly Trp
1      5      10      15
Ser Val Gly Ile Pro Glu Ala Leu Ala Trp Ile Gly Leu Ile Ser Val
      20      25      30
Asn Leu Ala Val Leu Asn Leu Leu Pro Ile Pro Val Leu Asp Gly Gly
      35      40      45
Tyr Ile Leu Leu Cys Leu Trp Glu Ile Leu Ser Arg Arg Arg Leu Asn

```

```

      50              55              60
Met Arg Leu Val Glu Lys Ala Leu Val Pro Phe Met Ile Leu Leu Val
65              70              75              80
Leu Phe Phe Val Phe Leu Thr Leu Gln Asp Leu Ser Arg Val Phe Val
      85              90              95
Gly

```

(2) INFORMATIONS POUR LA SEQ ID NO: 390:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 423 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(383949..385217)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 390:

```

Val Ala Leu Glu Ala Asp Phe Cys Phe Ser Arg Arg Pro Leu Ala Asn
1              5              10              15
Leu Leu Val Ala Ile Phe Val Phe Gly Ile Leu Tyr Phe Ser Gly Gly
      20              25              30
Arg Thr Lys Ser Phe Ser Glu His Thr Ser Ile Val Gly Trp Val His
      35              40              45
Pro Ser Leu Glu Gln Gln Gly Leu His Ala Gly Asp Gln Ile Phe Phe
      50              55              60
Cys Asn Gly Gln Pro Tyr Ser Gly His Lys Met Ala Phe Ser Ser Ser
65              70              75              80
Leu Leu Glu Arg Lys Leu Ser Leu Gln Gly Gln His Pro Ala Tyr Phe
      85              90              95
Ser Glu Ser Glu Ala Phe Ser Leu Glu Ala Pro Phe Asn Pro Asp Met
      100              105              110
Glu Gly Val Pro Cys Leu Gly Ala Ser Tyr Leu Leu Tyr Arg Gly Ser
      115              120              125
Asp Pro Leu Pro Glu Lys Ser Pro Leu Val Asp Ala Gly Leu Ser Glu
      130              135              140
Gly Asp Arg Leu Val Trp Met Asp Gly Leu Leu Val Phe Ser Gly Ala
145              150              155              160
Gln Val Ser Gln Met Leu Asn Glu Lys Gln Ser Phe Leu Arg Val Glu
      165              170              175
Arg Gln Gly Lys Val Val Phe Val Arg Gln Ala Arg Val Leu Ala Gly
      180              185              190
Asp Leu Thr Leu Thr Pro Tyr Phe Lys Asn Glu Leu Ile Asp Cys Gln
      195              200              205
Tyr Glu Ala Gly Leu Lys Gly Lys Trp Ala Ser Leu Tyr Met Leu Pro
      210              215              220
Tyr Ile Ile Asn Gly Asp Gly Phe Val Glu Ser Lys Val Lys Leu Leu
225              230              235              240
Asn Asn Glu Arg Val Ser Leu Asp Tyr Asn Leu Glu Leu Gly Asp Lys
      245              250              255
Ile Val Ala Val Asp Gly Ile Pro Val Met Ser Asn Ala Asp Ile Leu
      260              265              270
Arg Leu Val Gln Asp His Arg Val Ser Leu Ile Phe Gln Arg Met Ser
      275              280              285

```

```

Pro Glu Gln Leu Thr Val Leu Glu Gln Lys Ala Ala Asp Gln Ala Phe
 290                295                300
Ile Asn Ser Tyr Asp Met Asp Asp Leu Leu Arg Val Ala Glu Ser Val
305                310                315                320
Gly Glu Glu Arg Glu Val Ser Arg Leu Gly Asp Tyr Arg Leu Val Thr
                325                330                335
Arg Val Gln Pro Arg Pro Trp Ala His Ile Tyr Ser Glu Ala Leu Leu
                340                345                350
Asp Lys Gln Arg Ala Leu Ala Ser Lys Phe Arg Asp Glu Gln Glu Arg
                355                360                365
Arg Tyr Tyr Leu Glu Arg Ile Glu Ala Glu Asn Gln Arg Ile Ser Leu
                370                375                380
Gly Ile Pro Leu Arg Ser Ser Arg Ser Val Gln Ser Gly Ser Leu Gly
385                390                395                400
Ile Asp Gly Gly Ile Arg Phe Arg Gln Leu Lys Asp Cys Glu Ser Leu
                405                410                415
Gly Asp Gly Ala Gly Glu Pro
                420

```

(2) INFORMATIONS POUR LA SEQ ID NO: 391:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(385178..385507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 391:

```

Met Thr Ile Ile Tyr Phe Val Leu Ala Ala Leu Ala Leu Gly Phe Leu
 1                5                10                15
Ile Leu Ile His Glu Leu Gly His Leu Leu Ala Ala Lys Ala Val Gly
                20                25                30
Met Ser Val Glu Ser Phe Ser Ile Gly Phe Gly Pro Ala Leu Val Arg
                35                40                45
Lys Lys Ile Gly Ser Val Glu Tyr Arg Ile Gly Ala Ile Pro Phe Gly
                50                55                60
Gly Tyr Val Arg Ile Lys Gly Met Asp Arg Asn Asp Lys Asp Asn Ser
65                70                75                80
Gly Asp Lys Glu Lys Thr Val Tyr Asp Ile Pro Glu Gly Phe Phe Ser
                85                90                95
Lys Ser Pro Trp Lys Arg Ile Phe Val Leu Ala Ala Gly Leu
                100                105                110

```

(2) INFORMATIONS POUR LA SEQ ID NO: 392:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 380 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(385706..386845)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 392:

```

Leu Leu Lys His Leu Ala Leu Ile Gly Ser Thr Gly Ser Ile Gly Arg
1      5      10      15
Gln Val Leu Gln Val Val Arg Ser Ile Pro Asp Thr Phe Ile Ile Glu
      20      25      30
Thr Leu Ala Ala Tyr Gly Arg Asn Gln Glu Ala Leu Ile Ser Gln Ile
      35      40      45
Arg Glu Phe Asn Pro Arg Val Val Ala Val Arg Glu Glu Thr Thr Tyr
      50      55      60
Lys Glu Leu Arg Lys Leu Phe Pro His Ile Glu Ile Leu Leu Gly Glu
      65      70      75      80
Glu Gly Leu Val Ser Val Ala Thr Glu Pro Ser Val Thr Ile Thr Ile
      85      90      95
Val Ala Ser Ser Gly Ile Asp Ala Leu Pro Ala Val Ile Ala Ala Ile
      100      105      110
Arg Gln Lys Lys Thr Ile Ala Leu Ala Asn Lys Glu Ser Leu Val Ala
      115      120      125
Ala Gly Glu Leu Val Thr Thr Leu Ala Arg Glu Asn Gly Val Gln Ile
      130      135      140
Leu Pro Ile Asp Ser Glu His Asn Ala Leu Phe Gln Cys Leu Glu Gly
      145      150      155      160
Arg Asp Ser Ser Thr Ile Lys Lys Leu Leu Leu Thr Ala Ser Gly Gly
      165      170      175
Pro Leu Arg Asn Lys Ser Lys Glu Glu Leu Gln Lys Val Ser Leu Gln
      180      185      190
Glu Val Leu Arg His Pro Val Trp Asn Met Gly Pro Lys Ile Thr Val
      195      200      205
Asp Ser Ser Thr Leu Val Asn Lys Gly Leu Glu Ile Ile Glu Ala Phe
      210      215      220
Trp Leu Phe Gly Leu Glu Ala Val Glu Ile Glu Ala Val Ile His Pro
      225      230      235      240
Gln Ser Leu Val His Gly Met Val Glu Phe Cys Asp Gly Thr Ile Leu
      245      250      255
Ser Val Met Lys Pro Pro Ser Met Leu Phe Pro Ile Gln His Val Leu
      260      265      270
Thr Phe Pro Glu Arg Ser Pro Ala Ile Gly Pro Gly Phe Asp Phe Leu
      275      280      285
Ser Asn Arg Thr Leu Glu Phe Phe Pro Ile Asp Glu Asp Arg Phe Pro
      290      295      300
Ser Val His Leu Ala Lys Arg Val Leu Leu Glu Lys Gly Ser Met Gly
      305      310      315      320
Cys Phe Phe Asn Gly Ala Asn Glu Ala Leu Val His Arg Phe Leu Ala
      325      330      335
Gly Glu Ile Ser Trp His Gln Ile Val Pro Lys Leu Gln Ala Leu Val
      340      345      350
Asp Gln His Arg Val Gln Ser Cys Leu Ser Leu Glu Glu Ile Leu Ser
      355      360      365
Val Asp Ala Glu Ala Arg Ala Arg Ala Gln Glu Cys
      370      375      380

```

(2) INFORMATIONS POUR LA SEQ ID NO: 393:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 167 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 386127..386627

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 393:

Gly	Trp	Ile	Thr	Ala	Ser	Ile	Ser	Thr	Ala	Ser	Ser	Pro	Asn	Ser	Gln
1				5					10				15		
Lys	Ala	Ser	Ile	Ile	Ser	Lys	Pro	Leu	Phe	Thr	Lys	Val	Glu	Glu	Ser
			20					25					30		
Thr	Val	Ile	Leu	Gly	Pro	Ile	Phe	Gln	Thr	Gly	Cys	Arg	Lys	Thr	Ser
			35				40					45			
Cys	Lys	Glu	Thr	Phe	Cys	Asn	Ser	Ser	Phe	Asp	Leu	Phe	Leu	Asn	Gly
	50					55					60				
Pro	Pro	Glu	Ala	Val	Asn	Asn	Asn	Phe	Leu	Met	Val	Glu	Glu	Ser	Leu
65					70					75					80
Pro	Ser	Lys	His	Trp	Lys	Ser	Ala	Leu	Cys	Ser	Leu	Ser	Met	Gly	Arg
			85						90					95	
Ile	Cys	Thr	Pro	Phe	Ser	Leu	Ala	Lys	Val	Val	Thr	Asn	Ser	Pro	Ala
			100					105					110		
Ala	Thr	Asn	Asp	Ser	Leu	Leu	Ala	Lys	Ala	Ile	Val	Phe	Phe	Cys	Arg
		115					120					125			
Ile	Ala	Ala	Met	Thr	Ala	Gly	Lys	Ala	Ser	Ile	Pro	Asp	Glu	Ala	Thr
	130					135					140				
Met	Val	Ile	Val	Thr	Glu	Gly	Ser	Val	Ala	Thr	Glu	Thr	Asn	Pro	Ser
145					150					155					160
Ser	Pro	Lys	Arg	Ile	Ser	Ile									
				165											

(2) INFORMATIONS POUR LA SEQ ID NO: 394:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 167 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(386872..387372)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 394:

Gly	Pro	Ser	Leu	Ser	Leu	Val	Met	Arg	Xaa	Phe	Thr	Lys	Thr	Asp	Ile
1				5					10					15	
Leu	Pro	Ile	Phe	Leu	Val	Leu	Leu	Ile	Asn	Leu	Gly	Ile	Ser	Tyr	Cys
			20					25					30		
Phe	Phe	Ser	Ser	Phe	Val	Cys	Val	Ser	Phe	Asp	Thr	Ile	Phe	Ala	Phe
		35				40						45			
Ser	Leu	Gly	Ile	Arg	Val	Arg	Leu	Val	Asp	Tyr	Leu	Val	Met	Leu	Leu
	50					55					60				
Leu	Ser	Ala	Ser	Ile	Val	Gly	Ala	Phe	Lys	Ala	Val	Gly	Val	Leu	Met
65				70					75						80
Ser	Leu	Ala	Phe	Leu	Leu	Ile	Pro	Gly	Leu	Ile	Ala	Lys	Leu	Ile	Ala

(2) INFORMATION POUR LA SEQ ID NO: 395:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(387338..387724)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 395:

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 396:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(387816..388250)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 396:

```

Leu Phe Ser Arg Asp Glu Glu His Leu Leu Lys Ile Phe Trp Tyr Leu
1           5           10           15
Arg Glu Gln Asn Thr Tyr Gln Val Gly Val Arg Asp Phe Val Arg Ser
          20           25           30
Arg Lys Tyr Gln Glu Tyr Phe Gly Asp Lys Val Phe Pro Arg Phe Arg
          35           40           45
Met Phe Leu Leu Cys Lys Lys Gly Leu Val Ser Cys Ser Glu His Gln
          50           55           60
Trp Ser Leu Thr Asp Lys Gly Leu Ala Arg Ala Lys Leu Val Arg
65           70           75           80
Ala His Arg Leu Trp Glu Ser Tyr Leu Val Ser Gln Leu Gly Phe Asn
          85           90           95
Lys Asn Glu Val His His Phe Ala Glu Glu Met Glu His Val Leu Thr
          100          105          110
Asp Glu Leu Asp Ser Thr Leu Ser Gln Met Leu Gln Asp Pro Asp Tyr
          115          120          125
Asp Pro His Gln Arg Glu Ile Pro Lys Arg Thr Arg Lys Ser Asp Gly
130          135          140
Cys
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 397:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 311 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(388237..389169)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 397:

```

Met Leu Ser Cys Ile Phe Gln Asp Thr Ile Phe Leu Ser Ser Phe Leu
1           5           10           15
Ala Val Ser Leu Ile Cys Met Thr Thr Ala Leu Trp Gly Thr Ile Leu
          20           25           30
Leu Val Glu Arg Gln Pro Leu Leu Ser Glu Ser Leu Ser His Ala Cys
          35           40           45
Tyr Pro Gly Leu Leu Ile Gly Ala Leu Leu Ser Tyr Lys Val Pro Ala
          50           55           60
Phe Ser Asp Ser Leu Trp Val Ile Ile Phe Phe Gly Cys Leu Ala Ser
65           70           75           80
Val Leu Gly Cys Leu Gly Ile Ser Phe Leu Glu Lys Lys Leu Ala Met
          85           90           95
His Lys Asp Ser Ala Leu Cys Leu Val Leu Val Ser Phe Phe Gly Val
          100          105          110
Gly Val Ile Leu Val Ser Tyr Val Lys Asp Cys Cys Pro Leu Leu Tyr
          115          120          125
Asn Lys Ile Asn Ala Tyr Leu Tyr Gly Gln Ala Ala Thr Leu Gly Tyr
130          135          140
Thr Glu Ala Lys Leu Ala Leu Ile Ile Phe Cys Leu Ser Ala Val Val
145          150          155          160
Leu Trp Trp Trp Tyr Arg Gln Ile Ser Val Ala Ile Phe Asp Arg Glu

```

				165					170				175				
Phe	Ala	Tyr	Ser	Cys	Gly	Leu	Arg	Thr	Arg	Thr	Ala	Glu	Leu	Val	Val		
			180					185					190				
Leu	Val	Phe	Ile	Ser	Leu	Val	Ile	Val	Ser	Gly	Val	Arg	Ser	Val	Gly		
		195					200					205					
Ile	Leu	Leu	Ile	Ser	Ala	Met	Phe	Val	Ala	Pro	Pro	Leu	Ser	Ala	Arg		
	210				215				220								
Gln	Leu	Ser	Asp	Arg	Leu	Ser	Thr	Ile	Leu	Ile	Leu	Ser	Ser	Ile	Phe		
225					230				235						240		
Gly	Gly	Ile	Cys	Gly	Ala	Leu	Gly	Cys	Tyr	Phe	Ser	Val	Ala	Phe	Thr		
			245					250						255			
Cys	Gln	Thr	Val	Val	Glu	Gly	Lys	Pro	Ile	Ser	Ile	Ile	Leu	Pro	Thr		
		260					265						270				
Gly	Pro	Leu	Val	Val	Phe	Phe	Ala	Gly	Val	Leu	Val	Phe	Leu	Cys	Leu		
	275						280					285					
Ile	Phe	Ser	Trp	Lys	Thr	Gly	Trp	Ile	Thr	Arg	Tyr	Phe	Arg	Arg	Lys		
	290					295					300						
Met	Val	Leu	Ile	Phe	Ser	Arg											
305					310												

(2) INFORMATIONS POUR LA SEQ ID NO: 398:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(389173..389955)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 398:

Leu	Phe	Leu	Asn	Arg	Asp	Asn	Ala	Ile	Ala	Trp	Ser	Val	Glu	Asp	Leu		
1			5				10						15				
Cys	Val	Asn	Tyr	Asp	His	Ser	Asp	Val	Leu	Cys	His	Ile	Thr	Phe	Ser		
		20					25					30					
Leu	Pro	Ala	Gly	Asp	Leu	Ala	Ala	Ile	Ile	Gly	Pro	Asn	Gly	Ala	Gly		
	35					40						45					
Lys	Ser	Thr	Leu	Leu	Lys	Ala	Ser	Leu	Gly	Leu	Ile	Arg	Ala	Ser	Ser		
	50				55						60						
Gly	Gln	Ser	Leu	Phe	Phe	Gly	Gln	Arg	Phe	Ser	Lys	Ala	His	His	Arg		
65				70					75					80			
Ile	Ala	Tyr	Met	Pro	Gln	Arg	Ala	Ser	Val	Asp	Trp	Asp	Phe	Pro	Met		
			85					90					95				
Thr	Val	Leu	Asp	Leu	Val	Leu	Met	Gly	Cys	Tyr	Gly	Tyr	Lys	Gly	Ile		
		100					105					110					
Trp	Asn	Arg	Ile	Ser	Thr	Asp	Asp	Arg	Gln	Glu	Ala	Met	Arg	Ile	Leu		
	115					120						125					
Glu	Arg	Val	Gly	Leu	Glu	Ala	Phe	Ala	Asn	Arg	Gln	Ile	Gly	Lys	Leu		
	130				135					140							
Ser	Gly	Gly	Gln	Gln	Gln	Arg	Ala	Phe	Leu	Ala	Arg	Ser	Leu	Met	Gln		
145				150					155					160			
Lys	Ala	Asp	Leu	Tyr	Leu	Met	Asp	Glu	Leu	Phe	Ser	Ala	Ile	Asp	Met		
		165						170					175				
Ala	Ser	Tyr	Gln	Met	Val	Val	Asp	Val	Leu	Gln	Glu	Leu	Lys	Ser	Glu		
			180					185					190				

Gly Lys Thr Ile Val Val Ile His His Asp Leu Ser Asn Val Arg Lys
 195 200 205
 Leu Phe Asp His Val Ile Leu Leu Asn Lys His Leu Val Cys Ser Gly
 210 215 220
 Ser Val Glu Glu Cys Leu Thr Lys Glu Ala Ile Phe Gln Ala Tyr Gly
 225 230 235 240
 Cys Glu Leu Glu Leu Leu Asp Tyr Thr Leu Lys Leu Ser Arg Gly Lys
 245 250 255
 Tyr Gln Gly Ser Cys
 260

(2) INFORMATIONS POUR LA SEQ ID NO: 399:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 317 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(389945..390895)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 399:

Lys Leu Ile Leu Arg Gly Leu Leu Cys Leu Ala Gly Cys Phe Leu Met
 1 5 10 15
 Asn Ser Cys Ser Ser Ser Arg Gly Asn Gln Pro Ala Asp Glu Ser Ile
 20 25 30
 Tyr Val Leu Ser Met Asn Arg Met Ile Cys Asp Cys Val Ser Arg Ile
 35 40 45
 Thr Gly Asp Arg Val Lys Asn Ile Val Leu Ile Asp Gly Ala Ile Asp
 50 55 60
 Pro His Ser Tyr Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met
 65 70 75 80
 Ser Gln Leu Ile Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser
 85 90 95
 Leu Arg Lys His Leu Glu Gly Asn Pro Lys Val Phe Asp Phe Gly Gln
 100 105 110
 Arg Leu Leu Asn Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe
 115 120 125
 Pro Asp Pro His Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val
 130 135 140
 Lys Glu Val Ala Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu
 145 150 155 160
 Asp Phe Gln Lys Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu
 165 170 175
 Asp Arg Trp Ala Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg
 180 185 190
 Tyr Leu Val Thr Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr
 195 200 205
 Leu Ser Ser Asp Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys
 210 215 220
 Ile Ser Pro Glu Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp
 225 230 235 240
 Ile Met Arg Val Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val
 245 250 255
 Phe Leu Glu Asp Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser

(2) INFORMATION POUR LA SEQ ID NO: 400:

(A) LONGUEUR: 99 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 391514..391810

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 400:

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 401:

(A) LONGUEUR: 529 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 392410..393996

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 401:

Asn	Met	Thr	Gln	Thr	Ala	Glu	Lys	Pro	Phe	Gly	Lys	Leu	Arg	Ser	Phe
1				5					10					15	
Leu	Trp	Pro	Ile	His	Met	His	Glu	Leu	Lys	Lys	Val	Leu	Pro	Met	Phe
			20					25					30		
Leu	Met	Phe	Phe	Cys	Ile	Ser	Phe	Asn	Tyr	Thr	Ile	Leu	Arg	Asp	Thr
		35					40					45			

Lys Asp Thr Leu Ile Val Thr Ala Pro Gly Ser Gly Ala Glu Ala Ile
 50 55 60
 Pro Phe Ile Lys Leu Trp Leu Val Val Pro Ser Ala Val Val Phe Met
 65 70 75 80
 Leu Ile Tyr Ala Lys Leu Ser Asn Ile Leu Asn Lys Gln Ala Leu Phe
 85 90 95
 Phe Ala Val Leu Ser Pro Phe Val Val Phe Phe Ala Leu Phe Pro Val
 100 105 110
 Val Ile Tyr Pro Cys Arg His Ile Leu His Pro Thr Ala Phe Ala Asp
 115 120 125
 Thr Leu Gln Ser Ile Leu Pro Ser Gly Phe Met Gly Phe Ile Ala Met
 130 135 140
 Leu Arg Asn Trp Thr Phe Ala Val Phe Tyr Val Leu Ser Glu Leu Trp
 145 150 155 160
 Gly Ser Val Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile
 165 170 175
 Thr Lys Ile Ser Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Val Gly
 180 185 190
 Ala Asn Val Ala Leu Leu Ile Ser Gly Pro Ala Ile Ile Trp Ser Ser
 195 200 205
 Lys Leu Arg Ala Ser Leu Gly Glu Gly Val Asp Pro Trp Gly Val Ser
 210 215 220
 Leu Tyr Phe Leu Met Ala Met Phe Leu Cys Ser Cys Ala Ile Ile Ala
 225 230 235 240
 Ala Cys Tyr Trp Trp Met Asn Arg Tyr Val Leu Thr Asp Pro Arg Phe
 245 250 255
 Tyr Asn Pro Ala Glu Leu Lys Ala Lys Lys Ser Lys Pro Lys Met Ser
 260 265 270
 Met Gly Glu Ser Phe Ser Tyr Leu Leu Arg Ser Pro Tyr Met Leu Leu
 275 280 285
 Leu Ala Leu Leu Val Ile Cys Tyr Gly Ile Cys Ile Asn Leu Val Glu
 290 295 300
 Val Thr Trp Lys Ser Gln Leu Lys Met Gln Phe Pro Asn Pro Asn Asp
 305 310 315 320
 Tyr Ser Ala Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser
 325 330 335
 Val Phe Val Met Leu Phe Ile Gly Gly Asn Val Ile Arg Arg Phe Gly
 340 345 350
 Trp Leu Thr Gly Ala Leu Val Thr Pro Ile Met Val Leu Val Thr Gly
 355 360 365
 Ala Val Phe Phe Ala Leu Val Ile Phe Arg Asp His Ala Thr Gly Leu
 370 375 380
 Val Ala Ala Leu Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly
 385 390 395 400
 Ala Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp
 405 410 415
 Ala Thr Lys Glu Leu Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val
 420 425 430
 Lys Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser
 435 440 445
 Gly Gly Ser Leu Ile Gln Gln Gly Leu Leu Val Val Cys Gly Ser Ile
 450 455 460
 Gly Ala Met Thr Pro Phe Leu Ala Val Ala Leu Phe Ala Ile Ile Met
 465 470 475 480
 Val Trp Leu Thr Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Ala
 485 490 495
 Ser Ala Ala Lys Glu Gln Glu Leu Xaa Glu Ala Ala Ala Ala Glu Lys
 500 505 510
 Glu Ala Ser Ser Ala Ala Lys Glu Ser Ala Pro Ala Ile Glu Gly Val

525

- (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 402:

Thr 1	Arg	Leu	Lys 5	Thr 5	Leu	Lys	Pro	Tyr	Lys 10	Ile	Glu	Asn	Ile	Arg 15	Asn
Phe	Ser	Ile	Ile 20	Ala	His	Ile	Asp	His 25	Gly	Lys	Ser	Thr 30	Ile	Ala	Asp
Arg	Leu	Leu 35	Glu	Ser	Thr	Ser	Thr 40	Ile	Glu	Gln	Arg	Glu 45	Met	Arg	Glu
Gln	Leu	Leu 50	Asp	Ser	Met	Asp 55	Leu	Glu	Arg	Glu	Arg 60	Gly	Ile	Thr	Ile
Lys 65	Ala	His	Pro	Val 70	Thr	Met	Thr	Tyr	Glu	Tyr 75	Glu	Gly	Glu	Thr	Tyr 80
Glu	Leu	Asn	Leu 85	Ile	Asp	Thr	Pro	Gly	His 90	Val	Asp	Phe	Ser	Tyr 95	Glu
Val	Ser	Arg	Ser 100	Leu	Ala	Ala	Cys	Glu 105	Gly	Ala	Leu	Leu	Ile 110	Val	Asp
Ala	Ala	Gln 115	Gly	Val	Gln	Ala 120	Gln	Ser	Leu	Ala	Asn	Val 125	Tyr	Leu	Ala
Leu	Glu	Arg 130	Asp	Leu	Glu	Ile 135	Ile	Pro	Val	Leu	Asn 140	Lys	Ile	Asp	Leu
Pro 145	Ala	Ala	Gln	Pro	Glu	Ala 150	Ile	Lys	Lys	Gln 155	Ile	Glu	Glu	Phe	Ile 160
Gly	Leu	Asp	Thr 165	Ser	Asn	Thr	Ile	Ala 170	Cys	Ser	Ala	Lys	Thr	Gly 175	Gln
Gly	Ile	Pro 180	Glu	Ile	Leu	Glu	Ser	Ile 185	Ile	Arg	Leu	Val 190	Pro	Pro	Pro
Lys	Pro	Pro 195	Gln	Glu	Thr	Glu	Leu 200	Lys	Ala	Leu	Ile 205	Phe	Asp	Ser	His
Tyr	Asp 210	Pro	Tyr	Val	Gly	Ile 215	Met	Val	Tyr	Val	Arg 220	Val	Ile	Ser	Gly
Glu 225	Ile	Lys	Lys	Gly	Asp 230	Arg	Ile	Thr	Phe	Met 235	Ala	Thr	Lys	Gly	Ser 240
Ser	Phe	Glu	Val 245	Leu	Gly	Ile	Gly	Ala 250	Phe	Leu	Pro	Glu	Ala 255	Thr	Leu
Met	Glu	Gly 260	Ser	Leu	Arg	Ala	Gly 265	Gln	Val	Gly	Tyr	Phe 270	Ile	Ala	Asn
Leu	Lys 275	Lys	Val	Lys	Asp	Val 280	Lys	Ile	Gly	Asp	Thr 285	Val	Thr	Thr	Val
Lys	His 290	Pro	Ala	Lys	Glu	Pro 295	Leu	Glu	Gly	Phe 300	Lys	Glu	Ile	Lys	Pro
Val 305	Val	Phe	Ala	Gly	Ile 310	Tyr	Pro	Ile	Asp 315	Ser	Ser	Asp	Phe	Asp	Thr 320

```

Leu Lys Asp Ala Leu Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr
              325              330              335
Ile Glu Gln Glu Ser Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly
              340              345              350
Phe Leu Gly Leu Leu His Leu Glu Ile Ile Phe Glu Arg Ile Ser Arg
              355              360              365
Glu Phe Asp Leu Asp Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys
              370              375              380
Val Val Leu Lys Asn Gly Lys Thr Leu Phe Ile
385              390              395

```

(2) INFORMATIONS POUR LA SEQ ID NO: 403:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 228 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 395309..395992

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 403:

```

Arg Tyr Leu Gln Ser Arg Leu Lys Lys Trp Gln Asn Pro Phe Tyr Leu
1              5              10              15
Ile Thr Gln Gln His Ile Leu Thr Gln Leu Leu Leu Asn Thr Trp Lys
              20              25              30
Ser Leu Gly Ser Ile Val Asn Ile Ile Thr Pro Gln Glu Tyr Leu Ser
              35              40              45
Asn Ile Met Ser Leu Cys Met Asp Lys Arg Gly Ile Cys Leu Lys Thr
              50              55              60
Asp Met Leu Asp Gln His Arg Leu Val Leu Ser Tyr Glu Leu Pro Leu
65              70              75              80
Asn Glu Ile Val Ser Asp Phe Asn Asp Lys Leu Lys Ser Val Thr Lys
              85              90              95
Gly Tyr Gly Ser Phe Asp Tyr Arg Leu Gly Asp Tyr Lys Lys Gly Ala
              100              105              110
Ile Ile Lys Leu Glu Ile Leu Ile Asn Asp Glu Ala Val Asp Ala Phe
              115              120              125
Ser Cys Leu Val His Arg Asp Lys Ala Glu Ser Lys Gly Arg Ser Ile
              130              135              140
Cys Glu Lys Leu Val Asp Val Ile Pro Pro Gln Leu Phe Lys Ile Pro
145              150              155              160
Ile Gln Ala Ala Ile Asn Lys Lys Ile Ile Ala Arg Glu Thr Ile Arg
              165              170              175
Ala Leu Ala Lys Asn Val Thr Ala Lys Cys Tyr Gly Gly Asp Ile Thr
              180              185              190
Arg Lys Arg Lys Leu Trp Asp Lys Gln Lys Lys Gly Lys Lys Arg Met
              195              200              205
Lys Glu Phe Gly Lys Val Ser Ile Pro Asn Thr Ala Phe Val Glu Val
210              215              220
Leu Lys Met Glu
225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 404:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 160 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(396059..396538)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 404:

```

Phe Glu Asp Val Arg Glu Ala Leu Tyr Ala Ala Lys Ile Ile Ser Tyr
1      5      10      15
Ala Gln Gly Phe Met Leu Leu Lys Gln Val Ser Gln Asp Lys Gly Trp
20      25      30
Asp Leu Asn Leu Gly Glu Leu Ala Leu Ile Trp Arg Gly Gly Cys Ile
35      40      45
Ile Gln Ser Ala Phe Leu Asp Lys Ile His Gln Gly Phe Glu Asn Ser
50      55      60
Pro Glu Ala His Ser Leu Ile Leu Gln Asp Tyr Phe Lys Lys Val Leu
65      70      75      80
Phe Asp Ser Glu Thr Gly Phe Arg Arg Ala Val Leu His Ala Ile Gly
85      90      95
Ser Gly Val Ala Ile Pro Cys Leu Ser Ser Ala Leu Ser Phe Tyr Asp
100     105     110
Gly Tyr Arg Thr Val Asp Ser Pro Leu Phe Leu Val Gln Gly Leu Arg
115     120     125
Asp Tyr Phe Gly Ala His Gly Tyr Glu Arg Arg Asp Cys Pro Arg Gly
130     135     140
Glu Phe Tyr His Thr Asp Trp Leu Glu Thr Lys Lys Thr Phe Arg Ala
145     150     155     160

```

(2) INFORMATIONS POUR LA SEQ ID NO: 405:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 322 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(396542..397507)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 405:

```

Glu Gly Ser Val Ala Pro Asn Thr Asp Ile Gly Leu Ile Gly Leu Ala
1      5      10      15
Val Met Gly Lys Asn Leu Val Leu Asn Met Val Asp His Gly Phe Ser
20      25      30
Val Ser Val Tyr Asn Arg Ser Pro Ala Lys Thr Glu Glu Phe Leu Lys
35      40      45
Asp His Gly Glu Ser Gly Ala Leu Gln Gly Phe Thr Thr Ile Gln Glu
50      55      60
Phe Val Gln Ser Leu Lys Arg Pro Arg Lys Ile Met Ile Met Ile Lys
65      70      75      80

```



```

Ala Gly Ala Pro Val Asp Glu Met Ile Ala Ser Leu Leu Pro Phe Leu
      85                      90
Glu Glu Gly Asp Ile Leu Ile Asp Gly Gly Asn Ser Tyr Tyr Leu Asp
      100                    105
Ser Glu Arg Arg Tyr Val Asp Leu Lys Lys Glu Gly Ile Leu Phe Val
      115                    120
Gly Met Gly Val Ser Gly Gly Glu Glu Gly Ala Arg Lys Gly Pro Ser
      130                    135
Ile Met Pro Gly Gly Asn Ile Asp Ala Trp Pro Ala Ile Ala Pro Ile
      145                    150
Phe Gln Ser Ile Ala Ala Gln Val Gly Gly Arg Pro Cys Cys Ser Trp
      165                    170
Ile Gly Thr Gly Ala Gly His Phe Val Lys Ala Val His Asn Gly
      180                    185
Ile Glu Tyr Gly Asp Ile Gln Leu Ile Cys Glu Thr Tyr Glu Ile Leu
      195                    200
Lys Thr Arg Leu Asn Leu Ser Leu Glu Gln Ile Gly Asn Ile Phe Phe
      210                    215
Glu Trp Asn Gln Thr Asp Leu Asn Ser Tyr Leu Leu Gly Ala Ala Ala
      225                    230
Ala Val Leu Ile Ala Lys Asp Glu Asn Gly Asn Ala Ile Ala Ser Thr
      245                    250
Ile Leu Asp Val Ala Gly Gln Lys Gly Thr Gly Arg Trp Val Ala Glu
      260                    265
Asp Ala Ile Lys Ala Gly Val Pro Met Ser Leu Ile Ile Glu Ser Val
      275                    280
Leu Ala Arg Tyr Leu Ser Thr Trp Lys Glu Val Arg Thr Lys Ala Ala
      290                    295
Gln Glu Phe Pro Gly Phe Leu Phe Xaa Val Asn Leu His Lys Lys Leu
      305                    310
Leu Pro
      315                    320

```

(2) INFORMATIONS POUR LA SEQ ID NO: 406:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 451 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(397401..398753)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 406:

```

Ile Phe Met Gln Gln Leu Ile Asp Asn Leu Lys Lys Arg Gly Ile Leu
1      5      10      15
Asp Asn Ser Ser Ala Gly Leu Glu Ser Leu Thr Val Pro Val Ser Ala
      20      25      30
Tyr Leu Gly Phe Asp Pro Thr Ala Pro Ser Leu His Ile Gly His Trp
      35      40      45
Ile Gly Ile Cys Phe Leu Arg Arg Leu Ala Ala Tyr Gly Ile Thr Pro
      50      55      60
Val Ala Leu Val Gly Gly Ala Thr Gly Met Ile Gly Asp Pro Ser Gly
      65      70      75      80
Lys Ser Val Glu Arg Ser Leu Leu Asp Gln Ala Gln Val Leu Asp Asn

```

(2) INFORMATION POUR LA SEQ ID NO: 407:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 260 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(398909..399688)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 407:

```

Phe Val Lys Glu Ile Phe Phe Val Lys Thr His Asp Leu Ala Asp Thr
1          5          10          15
Trp Gln Leu Tyr Trp Ser Thr Lys Glu Ile His His Arg Asp Val Leu
          20          25          30
Ile Glu Ser Tyr Leu Pro Leu Val Lys Asn Val Ala His Arg Leu Ala
          35          40          45
Ser Gly Met Pro Ser His Val Lys Met Glu Asp Leu Tyr Ala Leu Gly
50          55          60
Val Glu Gly Leu Ile Arg Ala Val Glu Arg Phe Asp Pro Glu Lys Ser
65          70          75          80
Lys Arg Phe Glu Ser Tyr Ala Leu Phe Ile Ile Lys Ala Ala Ile Ile
          85          90          95
Asp Gly Leu Arg Lys Gln Asp Trp Val Pro Arg Ser Val Tyr Gln Arg
          100          105          110
Ala Asn Arg Leu Ala Asp Ala Met Asp Ser Leu Arg Gln Thr Leu Gly
          115          120          125
Lys Glu Pro Thr Asp Gly Glu Leu Cys Glu Tyr Leu Asn Ile Ser Gln
130          135          140
Gln Glu Leu Ser His Trp Phe Ser Ser Ser Arg Pro Ala Leu Val Leu
145          150          155          160
Ser Leu Asn Asp Asp Phe Ser Cys Gln Asp Asp Asp Glu Gly Leu Ala
          165          170          175
Leu Glu Glu Arg Ile Ala Asp Glu Arg Ala Glu Thr Gly Tyr Asp Val
          180          185          190
Ile Arg Lys Lys Glu Ala Ile Ser Ile Leu Thr Glu Ala Leu Leu Ala
          195          200          205
Leu Asp Glu Lys Glu Arg Gln Val Met Ala Leu Tyr Tyr Tyr Asp Asp
210          215          220
Leu Val Leu Lys Glu Ile Gly Lys Ile Leu Gly Val Ser Glu Ser Arg
225          230          235          240
Val Ser Gln Ile His Ser Lys Ala Leu Leu Lys Leu Arg Gly Thr Leu
          245          250          255
Ser Ser Leu Leu
          260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 408:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 130 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(399778..400167)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 408:

```

Met Tyr Met Ala Leu Lys Ser Lys Asn Ser Gln Glu Leu Val Glu Cys
1          5          10          15
Val Arg Lys Tyr Leu Gly Lys Gln Ile Gly Leu Ser Leu Trp Asn Arg
          20          25          30
Gln Asp Val Leu Glu Val Ile Thr Ile Asp Ser Leu Val Glu Gln Phe

```

```

          35          40          45
Val Arg Asp Ser Gln Glu Lys Val Val Leu Asp Leu Asn Glu Lys Val
  50          55          60
Val Ala Gln Val Lys His Leu Leu Arg Val Gly Glu Gly Asn Phe Arg
  65          70          75          80
Ala Ile Val Thr Gly Ser Glu Thr Arg Lys Glu Leu Lys Arg Ile Val
          85          90          95
Asp Pro Tyr Phe Pro Asp Leu Leu Val Leu Ala His Ser Glu Leu Pro
          100          105          110
Glu Glu Ile Pro Ile Thr Leu Leu Gly Ala Val Ser Asp Glu Val Leu
          115          120          125
Leu Ser
  130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 409:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 397 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(400034..401224)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 409:

```

Gly Ile Ser Phe Pro Leu Gly Ala Ser Arg Leu Ala Leu Thr Val Cys
  1          5          10          15
Leu Leu Leu Phe Leu Val Asn Phe Leu Val Ile Thr Lys Gly Ala Glu
  20          25          30
Arg Ile Ala Glu Val Arg Ala Arg Phe Ser Leu Glu Ala Leu Pro Gly
  35          40          45
Lys Gln Met Ser Leu Asp Ala Asp Ile Ala Ala Gly Arg Ile Gly Tyr
  50          55          60
Ser Arg Ala Ser Val Lys Lys Ser Ser Leu Leu Glu Glu Ser Asp Tyr
  65          70          75          80
Phe Ser Ala Met Glu Gly Val Phe Arg Phe Val Lys Gly Asp Ala Ile
          85          90          95
Met Ser Trp Val Leu Leu Gly Val Asn Ile Leu Ala Ala Leu Phe Leu
          100          105          110
Gly Arg Ala Thr His Val Gly Asp Leu Trp Leu Thr Val Leu Gly Asp
          115          120          125
Ala Leu Val Ser Gln Ile Pro Ala Leu Leu Thr Ser Cys Ala Ala Ala
          130          135          140
Thr Leu Ile Ala Lys Val Gly Glu Lys Glu Ser Leu Ala Gln His Leu
          145          150          155          160
Leu Asp Tyr Tyr Glu Gln Ser Arg Gln Ser Phe Leu Phe Ile Ala Leu
          165          170          175
Ile Leu Cys Gly Met Ala Cys Ile Pro Gly Ala Pro Lys Ala Leu Ile
          180          185          190
Leu Gly Phe Ser Val Leu Leu Phe Leu Gly Tyr Lys Asn Pro Ser Ser
          195          200          205
Gly Glu Thr Leu Leu Phe Gln Lys Glu Arg Val Glu Phe Val Leu Pro
          210          215          220
Asp Glu Gly Val Gly Asn Pro Ala Asn Leu Tyr Lys Asp Ala Arg Asn
          225          230          235          240

```

(2) INFORMATION POUR LA SEQ ID NO: 410:

(A) LONGUEUR: 82 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 401776..402021

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 410:

(2) INFORMATION POUR LA SEQ ID NO: 411:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 365 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 402126..403220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 411:

```

Glu Phe Met Phe Thr Ser Leu Ser Ala Ile Gln Asn Ala Ile Arg Pro
1      5      10      15
Ser Cys Gln Leu Pro Val Leu Thr Pro Arg Arg Ala Leu Ile Thr Ser
20      25      30
Leu Ala Ser Gly Ile Ile Leu Gly Leu Ala Gly Cys Val Val Gly Val
35      40      45
Leu Ala Ser Leu Pro Ala Leu Ile Ala Val Ser Ala Val Ile Leu Gly
50      55      60
Val Ser Leu Phe Ala Ser Gly Leu Phe Leu Cys Arg Tyr Val Cys Pro
65      70      75      80
Pro Lys Ile Val Ser Arg Arg Pro Ser Thr Glu Leu Pro Ala Glu Pro
85      90      95
Thr Pro Glu Leu Pro Glu Ile Lys Arg Pro Lys Pro Ile Ala Pro Pro
100     105     110
Pro Pro Asp Phe Ile Pro Pro Lys Pro Leu Arg Arg Thr Ile Gly Glu
115     120     125
Met Leu Phe Gly Trp Asn Cys Ile Glu Ser Ile Arg Gln Met Pro Phe
130     135     140
Phe Leu Ala Asn Asp Lys Thr Pro Leu Phe Phe Arg Asn Pro Ser Ala
145     150     155     160
Arg Phe Arg Ala Trp Asn Ile Pro Phe Thr His Thr Ile Phe Val Ser
165     170     175
Thr Ser Gly Gln Phe Ser Ser Leu Arg Met Gln Ser Asn Leu Pro Ala
180     185     190
Ala Ile Ala Asn Ala Thr Gln Ser Ala Ala Phe Ala Lys Arg Gly Gln
195     200     205
Gly Gly Leu Gly Val Asn Asp Ala Phe Pro Ala Val Leu Thr Asp Lys
210     215     220
Cys Trp Glu Glu Ser Lys Pro Glu Ser Gly Ile Leu Leu Pro Gly Glu
225     230     235     240
Cys Ser Ser Ala Thr Trp Glu Asp Lys Asn His Leu Val Pro Cys Trp
245     250     255
Asp Glu Glu Thr Lys Thr Tyr Asn Lys Pro Leu Leu Phe Ile Gln Met
260     265     270
Leu Ala Pro Lys Ala Ser Met Ser Lys Ser Cys Tyr Glu Ile Thr Leu
275     280     285
Arg Ala Tyr Thr Ala Cys Phe Glu Glu Ala Ile Arg Cys Gly Cys Arg
290     295     300
Met Ile Gln Ile Pro Leu Ile Ala Ser Phe Gly Asp Phe Val Pro Arg
305     310     315     320
Ala Leu Ser Lys Arg Pro Lys Trp Ile Glu Ser Ala Lys Leu Ala Leu
325     330     335
Leu His Ala Val Glu Lys Thr Ala Lys Lys His Ala Ser Lys Asp Leu
340     345     350
Val Ile Val Leu Thr Asn Ile Pro Gln Pro Val Asn Leu
355     360     365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 412:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 611 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 403348..405180

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 412:

Gln	Lys	Leu	Phe	Val	Gly	His	Leu	Val	Met	Ala	Thr	Pro	Cys	Ile	Gln
1				5					10					15	
Asn	Ala	Phe	Arg	Arg	Lys	Thr	Leu	Pro	Val	Arg	Ile	Gly	Asp	Leu	Phe
			20					25					30		
Val	Gly	Ser	Glu	His	Ser	Ile	Lys	Ile	Gln	Ser	Met	Thr	Thr	Thr	Ala
		35					40					45			
Thr	Thr	Asp	Val	Asp	Gly	Thr	Val	Arg	Gln	Ile	Cys	Ala	Leu	Gln	Glu
	50					55					60				
Leu	Gly	Cys	Asp	Ile	Val	Arg	Val	Thr	Val	Gln	Gly	Leu	Arg	Glu	Val
65					70					75					80
His	Ala	Cys	Glu	His	Ile	Lys	Asp	Arg	Leu	Ile	Gln	Gln	Asn	Ile	Ser
				85					90					95	
Ile	Pro	Leu	Val	Ala	Asp	Ile	His	Phe	Phe	Pro	Gln	Ala	Ala	Ile	His
			100					105					110		
Val	Val	Asp	Cys	Val	Asp	Lys	Val	Arg	Ile	Asn	Pro	Gly	Asn	Tyr	Val
		115					120					125			
Asp	Lys	Arg	Asn	Met	Phe	Thr	Gly	Lys	Ile	Tyr	Ser	Asp	Glu	Gln	Tyr
	130					135					140				
Ala	His	Ser	Leu	Glu	His	Leu	Met	Asn	Lys	Phe	Ser	Pro	Leu	Val	Glu
145					150					155					160
Lys	Cys	Lys	Arg	Leu	Gly	Lys	Ala	Met	Arg	Ile	Gly	Val	Asn	His	Gly
				165					170					175	
Ser	Leu	Ser	Glu	Arg	Val	Thr	Gln	Arg	Tyr	Gly	Asn	Thr	Ile	Glu	Gly
			180					185					190		
Met	Val	Tyr	Ser	Ala	Leu	Glu	Tyr	Ala	Glu	Val	Cys	Val	Ala	Met	Asp
		195					200					205			
Tyr	His	Asp	Val	Ile	Phe	Ser	Met	Lys	Ser	Ser	Asn	Pro	Lys	Val	Met
	210					215						220			
Val	Ala	Ala	Tyr	Arg	Ser	Leu	Ala	Tyr	Glu	Leu	Asp	Gln	Arg	Glu	Trp
225					230					235					240
Ser	Tyr	Pro	Leu	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Ser	Gly	Thr	Ala
				245					250					255	
Gly	Ile	Val	Lys	Ser	Ala	Val	Gly	Ile	Gly	Thr	Leu	Leu	Ser	Glu	Gly
			260				265						270		
Leu	Gly	Asp	Thr	Ile	Arg	Cys	Ser	Leu	Thr	Gly	Ser	Pro	Ile	Asn	Glu
		275					280					285			
Ile	Pro	Ile	Cys	Ile	Asp	Leu	Lys	Gln	Thr	Thr	Thr	Glu	Leu	Ser	Glu
	290					295						300			
Arg	Trp	Gly	Glu	Ala	Asp	Asn	Pro	Phe	Ala	Ile	His	Ser	Ser	Lys	Gln
305					310					315					320
Leu	Gly	Thr	Arg	Asn	Thr	Leu	Asn	Thr	Pro	Pro	Trp	Asp	Asn	Val	Tyr
				325					330					335	
Gly	Leu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Gln	Leu	Leu	Thr	Ala	Glu	Pro
			340				345						350		
Ile	Glu	Leu	Leu	Gln	Cys	Leu	Gly	Ile	Asp	Thr	Thr	Thr	Gly	Lys	Ile
		355					360					365			
Asp	Pro	Thr	Thr	Pro	Glu	Gly	Val	Val	Val	Pro	Lys	Ala	Met	Arg	Ser
	370					375					380				
Ser	Pro	Ile	Val	Ser	Glu	Ile	Glu	Lys	His	Leu	Leu	Val	Phe	Asn	Lys
385					390					395					400
Glu	Asp	Ala	Pro	Ile	Leu	Asn	Pro	Met	Asn	Glu	Glu	Glu	Trp	Leu	Ser

405 410 415
 Glu Glu Thr Leu Ser Ala Pro Phe Val Tyr Phe Glu Val Thr Asp Ile
 420 425 430
 His Thr Ala Arg Arg Phe Phe Ser Leu Arg Gln His Ser Thr Gln Pro
 435 440 445
 Val Cys Leu Ser Phe Ser Leu Asp Pro His Leu Ser Lys Asn Glu Ala
 450 455 460
 Ile Ile Asp Leu Ser Ala Arg Leu Gly Ala Leu Leu Leu Asp Gly Leu
 465 470 475 480
 Gly Ser Cys Val Leu Leu Asp Phe Val Asp Ile Lys Leu Ser Arg Thr
 485 490 495
 Leu Gly Phe Leu Ile Leu Gln Ser Ala Asn Ile Arg Ser Val Thr Val
 500 505 510
 Glu Tyr Val Ser Cys Pro Gly Cys Gly Arg Thr Leu Phe Asp Leu Leu
 515 520 525
 Ala Val Ser Gln Arg Ile Arg Glu Arg Thr Lys His Leu Pro Gly Gly
 530 535 540
 Leu Lys Ile Ala Val Met Gly Cys Ile Val Asn Gly Pro Gly Glu Met
 545 550 555 560
 Ala Asp Ala Asp Phe Gly Tyr Val Gly Ser Lys Pro Gly Met Ile Asp
 565 570 575
 Leu Tyr Val Lys His Lys Cys Val Lys Ser Cys Ile Pro Ile Glu Asn
 580 585 590
 Ala Glu Glu Glu Leu Val Gln Leu Leu Lys Glu His Gly Val Trp Lys
 595 600 605
 Glu Pro Glu
 610

(2) INFORMATIONS POUR LA SEQ ID NO: 413:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 171 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(403276..403788)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 413:

Ala Met Arg Val Leu Leu Ile Arg Val Asn Phe Pro Ser Lys His Ile
 1 5 10 15
 Thr Leu Ile Tyr Ile Val Ser Trp Ile Asp Thr His Phe Ile Tyr Thr
 20 25 30
 Ile His Asn Met Tyr Gly Cys Leu Arg Lys Glu Met Asp Ile Cys Tyr
 35 40 45
 Lys Arg Asp Gly Asn Val Leu Leu Asn Gln Ala Val Phe Asn Val Leu
 50 55 60
 Ala Cys Met Asn Leu Ser Gln Thr Leu Tyr Arg Asn Thr Asn Asp Val
 65 70 75 80
 Ala Thr Gln Leu Leu Gln Ser Thr Asn Leu Ser Asn Arg Ser Ile His
 85 90 95
 Ile Cys Gly Gly Cys Ser Arg His Arg Leu Asp Phe Asp Gly Val Leu
 100 105 110
 Thr Thr Asn Lys Lys Ile Ser Asp Ser Tyr Trp Glu Gly Phe Ala Ser
 115 120 125


```

Lys Arg Ile Leu Tyr Thr Gly Cys Cys His Asp Glu Val Ser Tyr Lys
 130          135          140
Gln Phe Leu Lys Leu Ala Gly Thr Val Pro Ala Glu Ser Leu Ser Pro
145          150          155          160
Glu Gly Phe Gly Gly Leu Arg Lys Tyr Lys Leu
          165          170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 414:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 252 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 405165..405920

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 414:

```

Met Glu Arg Ala Arg Ile Gly Ser Leu Met Thr Leu Pro Ser Glu Ala
 1          5          10          15
Leu Arg Lys Gln Thr Phe Pro Glu Leu Glu Tyr Leu Pro Ile Arg His
          20          25          30
Gly Ile Phe Pro Lys Gln Asp Asp Lys Glu Glu Ala Ser Gln Val Ser
          35          40          45
Asp Glu Val Ile Ser Ser Ser Leu Gly Gly Asn Asp Phe Cys Asn Ala
          50          55          60
Arg Gln Val His Gly Thr Ser Val Arg Tyr Val Thr Pro Lys Thr Pro
          65          70          75          80
Lys Arg Ala Pro Ala Asp Gly Leu Phe Thr Thr Thr Pro Leu Leu Ser
          85          90          95
Leu His Ile Tyr His Ala Asp Cys Gln Ala Ala Ile Phe Tyr Asp Pro
          100          105          110
Glu Asn His Val Ile Ala Asn Val His Ala Gly Trp Arg Gly Leu Val
          115          120          125
Gly Asn Ile Tyr Ala Val Thr Val Arg Leu Leu Lys Lys Thr Phe Asn
          130          135          140
Thr Arg Pro Gln Asp Leu Ile Val Ala Ile Ser Pro Ser Leu Gly Pro
          145          150          155          160
Asp Met Ala Val Tyr Pro Asp Tyr Lys Arg Leu Phe Pro Ser Ser Phe
          165          170          175
Phe Pro Leu Met Pro Lys Glu Asn His Leu Asp Phe Arg Ala Val Ala
          180          185          190
Arg Lys Gln Leu Leu Ser Glu Gly Leu Ser Ser Asn His Ile Phe Ile
          195          200          205
Ser Glu Arg Cys Thr Cys Ser Glu Ser Asn Thr Phe Phe Ser Phe Arg
          210          215          220
Ser Trp Lys Ser Arg His Gln Gln Asp Pro Ser Ala Ile Arg Ser Arg
          225          230          235          240
Lys Asn Asn Val Thr Ala Val Leu Leu Leu Pro Arg
          245          250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 415:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(405955..407049)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 415:

Met	Ser	Ile	Glu	Val	Arg	Ile	Pro	Asn	Ile	Ala	Glu	Ser	Ile	Ser	Glu
1				5				10						15	
Val	Thr	Ile	Ser	Ala	Leu	Leu	Ile	Pro	Ser	Gly	Asp	Leu	Val	Gln	Glu
			20					25					30		
Asn	Gln	Gly	Ile	Leu	Glu	Ile	Glu	Ser	Asp	Lys	Val	Asn	Gln	Leu	Ile
		35					40					45			
Tyr	Ala	Pro	Cys	Ser	Gly	Arg	Val	Glu	Trp	Ser	Val	Ser	Val	Gly	Asp
	50					55					60				
Thr	Val	Ala	Val	Gly	Ser	Val	Val	Gly	Ile	Ile	Ser	Glu	Ala	Glu	Lys
65					70					75					80
Ser	Gln	Asp	Thr	Ala	Pro	Ile	His	Glu	Gln	Met	Pro	Phe	Ser	Leu	Val
				85					90					95	
Glu	Gln	Glu	Ser	Asp	Ala	Gln	Ile	Ile	Ala	Phe	Pro	Ser	Ser	Val	Arg
			100					105						110	
Gln	Asp	Pro	Pro	Ala	Glu	Gly	Lys	Thr	Phe	Val	Pro	Leu	Lys	Glu	Ile
		115					120					125			
Gln	Pro	Ala	Ser	Ser	Asp	His	Arg	Glu	Ser	Arg	Glu	Ser	Met	Ser	Ala
	130						135					140			
Ile	Arg	Lys	Thr	Ile	Ser	Arg	Arg	Leu	Val	Gln	Ser	Leu	His	Asp	Ser
145					150					155					160
Ala	Met	Leu	Thr	Thr	Phe	Asn	Glu	Ile	His	Met	Gly	Pro	Leu	Ile	Ala
				165					170					175	
Leu	Arg	Lys	Glu	Arg	Gln	Glu	Asp	Phe	Val	Ala	Lys	Tyr	Gly	Val	Lys
			180					185						190	
Leu	Gly	Phe	Met	Ser	Phe	Phe	Val	Arg	Ala	Val	Val	Asp	Ser	Leu	Lys
		195					200					205			
Lys	Tyr	Pro	Arg	Val	Asn	Ala	Tyr	Ile	Glu	Asp	Asn	Glu	Ile	Val	Tyr
	210					215						220			
Arg	His	Tyr	Tyr	Asp	Ile	Ser	Ile	Ala	Ile	Gly	Thr	Asp	Arg	Gly	Leu
225					230					235					240
Val	Val	Pro	Val	Ile	Arg	Asn	Cys	Asp	Gln	Leu	Ser	Ser	Gly	Glu	Ile
				245					250					255	
Glu	Leu	Gln	Leu	Ala	Asp	Leu	Ala	Ser	Arg	Ala	Arg	Glu	Gly	Lys	Leu
			260					265						270	
Ala	Ile	His	Glu	Leu	Glu	Gly	Gly	Gly	Phe	Thr	Ile	Thr	Asn	Gly	Gly
		275					280						285		
Val	Tyr	Gly	Ser	Leu	Leu	Ser	Thr	Pro	Ile	Ile	Asn	Pro	Pro	Gln	Val
	290					295					300				
Gly	Ile	Leu	Gly	Met	His	Lys	Ile	Glu	Lys	Arg	Pro	Val	Val	Arg	Glu
305					310					315					320
Asp	Ala	Ile	Val	Ile	Ala	Asp	Met	Met	Tyr	Val	Ala	Met	Ser	Tyr	Asp
				325					330					335	
His	Arg	Ile	Ile	Asp	Gly	Lys	Glu	Ala							

(2) INFORMATIONS POUR LA SEQ ID NO: 416:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 906 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(407056..409773)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 416:

Ile	Arg	Leu	Met	Asp	Ser	Asp	Phe	Ala	Arg	His	Val	His	Ser	Ser	Asp
1				5				10					15		
Ile	Asp	Trp	Ile	Glu	Ser	Leu	Phe	Glu	Arg	Phe	Glu	Lys	His	Glu	Pro
		20						25					30		
Met	Asp	Ser	Ser	Trp	Lys	Tyr	Phe	Glu	Gly	Tyr	Gln	Val	Gly	Lys	
		35					40				45				
Thr	Glu	Gly	Ser	Pro	Thr	Glu	Ser	Ser	His	Asp	Gln	Phe	Phe	Thr	Ser
	50					55					60				
Leu	Gln	Glu	Lys	Lys	Ala	His	Ser	Leu	Leu	Met	Ile	Tyr	Arg	Tyr	Tyr
65					70					75					80
Gly	Tyr	Leu	Gln	Gly	Gln	Val	Ser	Pro	Ile	Ser	Ser	Ser	Glu	Glu	Ser
				85				90					95		
Ser	Leu	Val	Thr	Glu	Lys	Val	Arg	Asn	Phe	Asp	Pro	Gln	Glu	Glu	Ile
		100						105					110		
Pro	Ser	Leu	Gly	Leu	Leu	Pro	Gln	Ser	Tyr	Val	Arg	Ile	Ala	Asp	Phe
		115					120					125			
Ile	Gln	Val	Leu	Lys	Glu	Lys	Tyr	Cys	Arg	Ser	Ile	Ser	Val	Glu	Thr
	130					135						140			
Leu	Asn	Cys	Ser	Pro	Glu	Ile	Gln	Glu	Tyr	Val	Trp	Lys	Leu	Met	Glu
145					150					155					160
Gly	Glu	Lys	Pro	Ser	Leu	Thr	Lys	Glu	Val	Leu	Leu	Ala	Arg	Tyr	Arg
				165				170						175	
Asp	Val	Lys	Arg	Ala	Val	Ala	Phe	Glu	Gly	Phe	Leu	Gln	Val	Lys	Phe
		180						185				190			
Thr	Gly	Lys	Lys	Arg	Phe	Ser	Leu	Glu	Gly	Gly	Glu	Ser	Leu	Val	Pro
		195					200					205			
Met	Leu	Glu	His	Leu	Ile	Ala	Cys	Gly	Val	Lys	Gln	Gly	Ile	Asn	Arg
	210					215					220				
Tyr	Val	Met	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Ala	Asn
225					230					235					240
Ile	Phe	Gly	Lys	Pro	Tyr	Arg	Gln	Ile	Phe	Met	Glu	Phe	Glu	Asp	Ala
			245						250					255	
Pro	Gln	Ile	Arg	Gly	Leu	Glu	Thr	Val	Gly	Asp	Val	Lys	Tyr	His	Lys
		260						265					270		
Gly	Tyr	Val	Ala	Asn	Arg	Pro	Glu	Gln	Asn	Val	Met	Met	Ala	Leu	Leu
		275					280					285			
Pro	Asn	Pro	Ser	His	Leu	Glu	Ser	Val	Asp	Pro	Val	Val	Glu	Gly	Ala
	290					295					300				
Val	Ala	Ala	Ile	Gln	His	Gln	Gly	Glu	Ala	Gly	Lys	Glu	Gln	Ala	Cys
305				310						315					320
Leu	Ala	Val	Leu	Met	His	Gly	Asp	Ala	Ala	Leu	Ala	Gly	Gln	Gly	Val
			325					330						335	
Val	Tyr	Glu	Thr	Phe	Gln	Leu	Ser	Gly	Ile	Pro	Gly	Tyr	Ser	Thr	Glu
		340						345				350			
Gly	Thr	Val	His	Ile	Val	Val	Asn	Asn	Gln	Ile	Gly	Phe	Thr	Ala	Gln

355 360 365
 Pro Arg Glu Ser Arg Ser Thr Pro Tyr Cys Thr Asp Ile Ala Lys Met
 370 375 380
 Met Gly Ile Pro Val Phe Arg Val Asn Gly Glu Asp Val Leu Ala Cys
 385 390 395 400
 Leu Gln Val Met Glu Tyr Ala Ile His Ile Arg Glu Arg Phe His Cys
 405 410 415
 Asp Val Ile Ile Asp Leu Cys Cys Tyr Arg Lys Tyr Gly His Asn Glu
 420 425 430
 Ser Asp Asp Pro Ser Val Thr Ala Pro Phe Leu Tyr Glu Glu Ile Lys
 435 440 445
 Lys Lys Lys Gln Gly Ser Glu Leu Phe Lys Glu Ile Leu Leu His His
 450 455 460
 Pro Glu Trp Asn Ile Ser Ser Asn Glu Leu Glu Arg Ile Asp Thr Glu
 465 470 475 480
 Ile Ala His Val Leu Asn Gln Glu Tyr Ala Ser Leu Lys Asp Pro Gly
 485 490 495
 Val Glu Arg Leu Asp Glu Cys Met His Cys Thr Arg Met Ala Ala Gly
 500 505 510
 Glu Leu Leu Val Asp Asn Val Asp Thr Ser Leu Asp Lys Glu Ala Leu
 515 520 525
 Phe Asp Leu Ser Ala Lys Leu Cys Asp Ile Pro Glu His Phe Ser Pro
 530 535 540
 His Ala Lys Ile Arg Ser Leu Leu Asn Lys Arg Met Ser Met Ala Asp
 545 550 555 560
 Gly Glu Ile Gly Tyr Asp Trp Gly Met Ala Glu Glu Val Ala Phe Ala
 565 570 575
 Ser Leu Leu Gln Glu Gly Phe Ser Leu Arg Leu Ser Gly Gln Asp Ser
 580 585 590
 Ile Arg Gly Thr Phe Ser Gln Arg Gln Leu Val Trp Thr Asp Val Gln
 595 600 605
 Thr Gly Asp Thr Phe Ser Pro Leu Tyr His Leu Ser Pro Ser Gln Gly
 610 615 620
 Ser Val Glu Leu Tyr Asn Ser Pro Leu Ser Glu Tyr Ala Val Leu Gly
 625 630 635 640
 Phe Glu Tyr Gly Tyr Ala Gln Gln Ala Glu Lys Thr Leu Val Ile Trp
 645 650 655
 Glu Ala Gln Phe Gly Asp Phe Ser Asn Gly Ala Gln Ile Ile Phe Asp
 660 665 670
 Gln Tyr Ile Ser Ser Gly Ile Gln Lys Trp Asp Leu His Ser Asp Val
 675 680 685
 Val Val Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser
 690 695 700
 Ser Ala Arg Ile Glu Arg Tyr Leu Gln Leu Ala Ser Asp Trp Asn Phe
 705 710 715 720
 Gln Val Val Leu Pro Ser Thr Pro Val Gln Tyr Phe Arg Ile Leu Arg
 725 730 735
 Glu His Thr Lys Arg Asp Leu Ser Leu Pro Leu Ile Ile Phe Ser Pro
 740 745 750
 Lys Met Leu Leu Arg His Pro Gln Cys Val Ser Ser Ile Ala Glu Phe
 755 760 765
 Gly Met Lys Gly Gly Phe Lys Pro Phe Leu Glu Asp Glu Asn Pro Asn
 770 775 780
 Tyr His Ala Lys Val Leu Val Leu Cys Ser Gly Lys Ile Tyr Tyr Asp
 785 790 795 800
 Tyr Arg Ala Ser Leu Pro Lys Asp Leu Glu Cys Arg Phe Ala Cys Ile
 805 810 815
 Arg Val Glu Ser Leu Tyr Pro Leu Tyr Leu Glu Asp Leu Leu Val Leu
 820 825 830

```

Ile Ser Lys Tyr Thr Glu Val His His Tyr Val Trp Leu Gln Glu Glu
      835      840      845
Pro Gln Asn Met Gly Ala Phe Ser Tyr Phe Ala Leu Ala Thr Asp Glu
      850      855      860
Ile Phe Pro Ser Lys Leu Gln Cys Val Cys Arg Pro Arg Ser Ser Ser
865      870      875      880
Thr Ala Thr Gly Ser Ala Ser Leu Ser Gln Lys Glu Leu Ser Met Leu
      885      890      895
Met Glu Thr Leu Phe Ser Ile Gly Arg Glu
      900      905

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(2) INFORMATIONS POUR LA SEQ ID NO: 417:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 295 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 410532..411416

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 417:

```

Met Asn Gly Lys Thr Pro Leu Ala Leu Tyr Ile His Ile Pro Phe Cys
1      5      10      15
Ser Lys Lys Cys His Tyr Cys Ser Phe Tyr Thr Ile Pro Tyr Lys Glu
      20      25      30
Glu Leu Met Arg Ser Tyr Cys Glu Ala Val Ile Lys Glu Gly Leu Lys
      35      40      45
Lys Leu Ala Pro Leu Arg Cys Ser His Tyr Ile Asp Thr Val Phe Phe
      50      55      60
Gly Gly Gly Thr Pro Ser Leu Val Pro Pro Ala Leu Ile Gln Asp Ile
65      70      75      80
Leu Val Ala Leu Glu Ala Gln His Ala Thr Glu Ile Thr Leu Glu Ala
      85      90      95
Asn Pro Glu Asn Leu Ser Leu Glu Tyr Ile Gln Ala Leu Ala Leu Thr
      100      105      110
Ser Ile Asn Arg Ile Ser Ile Gly Val Gln Thr Phe Asn Asp Pro Leu
      115      120      125
Leu Lys Leu Leu Gly Arg Thr His Ser Ser Ser Lys Ala Ile Glu Ala
      130      135      140
Phe Met Leu Cys Ser Gln Tyr Gly Phe Ser Asn Val Ser Ala Asp Leu
145      150      155      160
Ile Tyr Gly Leu Pro Thr Gln Ser Ile Ser Asp Phe Ile Val Asp Leu
      165      170      175
Arg Gln Ala Ile Ser Leu Pro Ile Gln His Ile Ser Ile Tyr Asn Leu
      180      185      190
Thr Ile Asp Pro His Thr Ser Phe Tyr Lys His Arg Lys Arg Ile Leu
      195      200      205
Pro Ser Ile Ala Asp Asp Asp Ser Leu Ala Glu Met Ala Leu Ala Ala
      210      215      220
Glu Glu Leu Leu Glu Asn Gln Gly Phe Thr Arg Tyr Glu Leu Ala Ser
225      230      235      240
Tyr Ala Lys Asn Gln Ala Ala Ser Lys His Asn Thr Tyr Tyr Trp Thr
      245      250      255
Ala Lys Pro Phe Leu Gly Leu Gly Val Ser Ala Ser Gln Tyr Leu His

```

Gly Ile Arg Ser Lys Asn Leu Ser Arg Ile Ser His Tyr Leu Arg Leu
 260 275 280 285 290
 Arg Ile Asn Ile Tyr Arg Leu
 290 295

(2) INFORMATIONS POUR LA SEQ ID NO: 418:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 568 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 411707..413410

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 418:

Phe Leu Ile Glu Lys Met Asn Lys Lys Glu Arg Ile Asn Lys Lys Asn
 1 5 10 15
 Ala Ser Thr Lys Ile Gln Arg Asn Thr Pro Thr Arg Ala Leu Leu Ser
 20 25 30
 Ile Gly Ser Gln Gln Leu Ser Ser Phe Thr Lys Leu Ser Phe Asn Asn
 35 40 45
 Glu Ala Lys Leu Ser Gly Val Ala Thr Pro Thr Arg Asp Thr Asp Val
 50 55 60
 Val Pro Leu Gln Tyr Leu Gln Ala Arg Tyr Leu Ser Lys Asn Asp Pro
 65 70 75 80
 Asn Pro Asp Tyr Leu Pro Ile His Gly Gly Ser Met Thr Gly Asn Ile
 85 90 95
 Asn Met Gly Thr His Ser Val Phe Asn Leu Lys Gln Pro Thr Lys Pro
 100 105 110
 Ser Ala Thr Leu Pro Glu Glu Ser Ser Lys Pro Lys Asp Pro Arg Glu
 115 120 125
 Glu Glu Gly Phe Thr Lys Lys Thr Ala Glu Lys Gln Glu Gln Ala Ile
 130 135 140
 Lys Glu Tyr Asn Thr Lys Leu Ala Glu Tyr Gln Lys Lys Ile Asp Asp
 145 150 155 160
 Tyr Asn Ala Ala Trp Glu Ala Phe Tyr Ser Glu Ala Ala Thr Val Lys
 165 170 175
 Tyr Val Lys Gly Ile Val Asp Lys Ile Leu Asn Asn Asn Lys Leu Ser
 180 185 190
 Thr Ala Leu Asn Ser Ala Thr Glu Val Glu Lys Lys Ile Ala Leu Ala
 195 200 205
 Gln Lys Ala Leu Gly Ile Glu Ile Thr Ile Asn Pro Asp Ala Asp Thr
 210 215 220
 Asp Pro Val Pro Glu Thr Pro Lys Pro Thr Pro Thr Thr Asp Thr Glu
 225 230 235 240
 Glu Lys Glu Ser Pro Pro Leu Ser Tyr Asp Asp Leu Pro Ser Val Ile
 245 250 255
 Lys Asn Ala Gln Phe Val Val Thr Gln Ser Gln Asn Lys Leu Thr Gly
 260 265 270
 Asp Leu Lys Met Thr Asn Ala Gln Ile Ala Asn Ile Lys Thr Pro Asp
 275 280 285
 Thr Gly Asp Ser Asn Tyr Ala Ala Asn Val Thr Tyr Leu Glu Ser Lys
 290 295 300

```

Leu Lys Gln Pro Lys Arg Ala Phe Leu Ser Asn Thr Leu Pro Thr Thr
305                               310                315                320
Thr Ser Ser Pro Thr Ile Ser Phe Asn Gly Tyr Ile Pro Trp Leu Ser
                               325                330                335
Thr Thr Asn Gly Ser Ser Ser Pro Thr Glu Pro Asp Phe Lys Ser Glu
                               340                345                350
Leu Ala Asp Lys Cys Phe Thr Ala Glu Gln Glu Asn Leu Lys Val Lys
                               355                360                365
Thr Ala Gly Leu Leu Val Leu Ser Val Arg Gly Thr Trp Ser Pro Thr
                               370                375                380
Thr Ala Thr Ile Ala Asp Gly Ser Thr Gln Thr Pro Lys Thr Ile Ser
385                               390                395                400
Val Asn Leu Thr Val Thr Pro Asp Asn Ser Ser Gly Thr Asn Thr Pro
                               405                410                415
Ser Ser Gly Ser Asp Ser Ser Gly Asp Ala Ser Ala Thr Thr Leu Thr
                               420                425                430
Ile Pro Leu Thr Leu Tyr Ser Arg Glu Ser Val Gln Leu Gln Leu Pro
                               435                440                445
Ile Lys Thr Ala Ser Asp Ile Lys Met Asp Thr Ser Ser Gln Thr Ser
                               450                455                460
Asn Gly Gly Ser Gly Ser Val Ser Ser Ser Ala Thr Glu Thr Leu Thr
465                               470                475                480
Ile Pro Leu Thr Leu Tyr Ser Gly Glu Ser Val Gln Leu Gln Leu Pro
                               485                490                495
Ile Thr Thr Thr Ser Ser Val Lys Met Ala Thr Thr Thr Ser Gln Thr
                               500                505                510
Ser Asn Gly Gly Gly Asp Thr Ser Ser Gln Ile Thr Leu Ser Ser Trp
                               515                520                525
Ser Trp Glu Ala Ala Leu Tyr Pro Thr Asp Val Thr Val Thr Asn Lys
                               530                535                540
Thr Thr Pro Pro Thr Thr Lys Thr Pro Ser Ser Pro Ser Pro Asn Ser
545                               550                555                560
Lys Met Ile Lys Asn Lys Ile Val
                               565

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(2) INFORMATIONS POUR LA SEQ ID NO: 419:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(412606..413433)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 419:

```

Ile Phe Asn Phe Val Asn Leu Tyr Thr Ile Leu Phe Leu Ile Ile Phe
1                               5                10                15
Glu Leu Gly Asp Gly Asp Glu Gly Val Phe Val Val Gly Gly Val Val
                               20                25                30
Leu Leu Val Thr Val Thr Ser Val Gly Tyr Arg Ala Ala Ser Gln Asp
                               35                40                45
Gln Asp Asp Ser Val Ile Cys Asp Glu Val Ser Pro Pro Pro Leu Glu
                               50                55                60
Val Trp Glu Val Val Val Ala Ile Phe Thr Leu Asp Val Val Val Ile

```

65
 Gly Ser Cys Ser Cys Thr Asp Ser Pro Glu Tyr Ser Val Arg Gly Ile
 70 75 80
 85
 Val Ser Val Ser Val Ala Glu Asp Asp Thr Glu Pro Leu Pro Pro Leu
 90 95
 100
 Glu Val Trp Glu Glu Val Ser Ile Phe Met Ser Asp Ala Val Leu Ile
 105 110
 115
 Gly Ser Cys Ser Cys Thr Asp Ser Leu Glu Tyr Ser Val Arg Gly Ile
 120 125
 130 135
 Val Ser Val Val Ala Glu Ala Ser Pro Glu Glu Ser Asp Pro Leu Leu
 140 145
 150 155
 Gly Val Leu Val Pro Leu Glu Leu Ser Gly Val Thr Val Arg Phe Thr
 160 165
 170 175
 Asp Met Val Leu Gly Val Cys Val Leu Pro Ser Ala Ile Val Ala Val
 180 185
 190
 Val Gly Leu His Val Pro Leu Thr Asp Lys Thr Ser Arg Pro Ala Val
 195 200 205
 Phe Thr Phe Arg Phe Ser Cys Ser Ala Val Lys His Leu Ser Ala Ser
 210 215 220
 Ser Leu Leu Lys Ser Gly Ser Val Gly Glu Glu Asp Pro Phe Val Val
 225 230 235 240
 Leu Ser His Gly Met Tyr Pro Leu Asn Glu Ile Val Gly Glu Leu Val
 245 250 255
 Val Val Gly Arg Val Leu Glu Arg Lys Ala Leu Leu Gly Cys Leu Ser
 260 265 270
 Leu Asp Ser Arg
 275

(2) INFORMATIONS POUR LA SEQ ID NO: 420:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 183 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 413404..413952

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 420:

Asp Ser Ile Glu Ile Tyr Glu Val Lys Asp Leu Lys Asn Glu Ile Met
 1 5 10 15
 Asn Asp Ile Lys Asn Asn Ile Ser Ser Ser Phe Trp Asn Pro Asn Lys
 20 25 30
 Val Val Thr Lys Val Leu Leu Lys Val Ser Glu Thr Gly Ile Glu Ser
 35 40 45
 Thr Pro Gly Ile Val Lys His Asn Gln Pro Ile Thr Gln Ser Glu Asn
 50 55 60
 Pro Lys Asp Pro Thr Asp Ala Val Thr Phe Lys Tyr Leu Lys Glu Asn
 65 70 75 80
 Tyr Thr Lys Glu Asn Asp Pro Asn Pro Gly Phe Leu Pro Thr Lys Gly
 85 90 95
 Gly Thr Met Thr Gly Asp Ile Asp Met Gln Gly Asn Asn Val Thr Asp
 100 105 110
 Ile Val Met Tyr Lys Gln Asn Gly Gln Gln Asp Pro Asp Asp Gly Ser
 115 120 125

Ala Val Thr Ile Gly Tyr Leu Asn Glu Lys Ala Asp Glu Ile Lys Ser
 130 135 140
 Asn Asp Lys Ile Thr Arg Val Ser Gln Ala Tyr Arg Ile Leu Thr His
 145 150 155 160
 Lys Tyr Pro Arg Tyr Thr Asn Phe Ser Val Leu Leu Lys Ile Leu Thr
 165 170 175
 Leu Ser Leu Thr Gln Ile Phe
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 421:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 424 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 413841..415112

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 421:

Gln Asn Tyr Thr Gly Val Ala Gly Leu Ser Asp Ile Asn Ser Gln Ile
 1 5 10 15
 Ser Thr Leu His Gln Leu Leu Gly Ile Ala Glu Asp Pro Asp Thr Val
 20 25 30
 Thr Asn Pro Asp Leu Leu Lys Thr Ser Gly Gly Thr Val Tyr Glu Asn
 35 40 45
 Ile Asp Met Asn Ser Asn Thr Val Ser Asp Leu Gly Thr Pro Thr Asn
 50 55 60
 Lys Asp Thr Lys Ser Ala Ile Asn Val Glu Phe Val Gln Ala Lys Ile
 65 70 75 80
 Thr Ser Pro Gln Met Ala Phe Leu Lys Asn Asn Asp Thr Asn Leu Ser
 85 90 95
 Asn Ile Thr Val Ser Glu Tyr Phe Asn Trp Leu Gln Ala Pro Thr Pro
 100 105 110
 Asn Pro Ala Pro Thr Thr Pro Asp Asn Ser Asn Thr Pro Asn Asn Pro
 115 120 125
 Pro Ser Ser Ser Asn Gly Ala Ser Ser Phe Ile Arg Glu Leu Ala Ala
 130 135 140
 Thr Thr Thr Gly Ser Thr Asp Thr Glu Ile Thr Pro Ala Ala Glu Gly
 145 150 155 160
 Thr Asp Leu Pro Asn Thr Thr Phe Ser Glu Lys Ser Pro Leu Trp Glu
 165 170 175
 Glu Phe Phe Ser Tyr Pro Asp Ser Ser Arg Ser Glu Met Val Ile Gln
 180 185 190
 Lys Thr Gly Ile Leu Thr Phe Ser Met Gln Gly Thr Trp Asn His Pro
 195 200 205
 Asn Asn Thr Thr Pro Thr Ser Thr Asp Pro Ile Ser Leu Glu Leu Thr
 210 215 220
 Val Thr Pro Pro Lys Thr Asp Thr Thr Pro Lys Ser Pro Ser Ser Ser
 225 230 235 240
 Pro Lys Lys Thr Thr Ser Glu Ala Thr Ser Ser Pro Ala Thr Asn Gly
 245 250 255
 Pro Thr Thr Ala Ser Ile Thr Lys Thr Phe Ser Arg Lys Tyr Asn Leu
 260 265 270
 Ser Ala Thr Pro Ser Pro Thr Pro Thr Thr Pro Thr Thr Pro Asp Pro

Ile Thr Lys Lys Phe Ser Leu Ala Ser Gly Gln Ser Cys Thr Leu Gln
 275 280
 290 295 300
 Ile Pro Val Gln Ala Thr Gly Ser Val Leu Lys Leu Lys Tyr Val Asn
 305 310 315 320
 Pro Asn Asn Asn Ser Ser Gly Gly Ser Ser Gly Ser Gly Gly Asp Ser
 325 330 335
 Gln Glu Glu Asn Pro Thr Ser Ser Ser Gly Thr Asn Asn Ala Pro Ala
 340 345 350
 Ser Gln Thr Ser Arg Ile Gln Ile Arg Tyr Ala Ser Thr Thr Thr Thr
 355 360 365
 Asp Ser Gly Ser Thr Thr Lys Asn Pro Ile Lys Ala Gln Ala Asp Glu
 370 375 380
 Ser Thr Pro Pro Glu Thr Thr Ser Thr Gly Ile Thr Leu Thr Ser Phe
 385 390 395 400
 Ser Trp Ser Leu Val Leu Thr Ser Gly Glu Ile Thr Lys Ala Lys Ser
 405 410 415
 Thr Pro Ser Thr Pro Ser Gln Pro
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 422:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 134 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(413978..414379)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 422:

Glu Lys Asn Ser Ser His Lys Gly Asp Phe Ser Glu Asn Val Val Phe
 1 5 10 15
 Gly Arg Ser Val Pro Ser Ala Ala Gly Val Ile Ser Val Ser Val Glu
 20 25 30
 Pro Val Val Val Ala Ala Ser Ser Leu Ile Asn Glu Glu Ala Pro Phe
 35 40 45
 Glu Glu Asp Gly Gly Leu Phe Gly Val Leu Leu Leu Ser Gly Val Val
 50 55 60
 Gly Ala Gly Phe Gly Val Gly Ala Cys Ser Gln Leu Lys Tyr Ser Glu
 65 70 75 80
 Thr Val Ile Leu Glu Arg Phe Val Ser Leu Phe Phe Arg Lys Ala Ile
 85 90 95
 Cys Gly Glu Val Ile Leu Ala Cys Thr Asn Ser Thr Leu Ile Ala Leu
 100 105 110
 Leu Val Ser Leu Phe Val Gly Val Pro Arg Ser Asp Thr Val Leu Leu
 115 120 125
 Phe Ile Ser Ile Phe Ser
 130

(2) INFORMATIONS POUR LA SEQ ID NO: 423:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 496 acides aminés

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 423:

Leu	Ile	Lys	Arg	Gln	Asn	Met	Asn	Lys	Lys	Ile	Ile	Lys	Glu	Arg	Val
1				5				10					15		
Ser	Ser	Ser	Val	Pro	Ser	Thr	Pro	Ser	Asp	Gln	Pro	Ala	Asp	Pro	Thr
			20					25					30		
Asn	Pro	Val	Thr	Lys	Met	Leu	Phe	Glu	Cys	Lys	Leu	Ser	Gln	Asn	Gln
			35				40					45			
Gly	Asp	Ala	Ser	Ala	Asp	Val	Asp	Ala	Met	Val	Thr	Thr	Ala	His	Val
	50					55					60				
Lys	Leu	Asp	Ala	Lys	Asn	Gln	Gln	Val	Arg	Lys	Val	Ala	Lys	Arg	Glu
65					70					75					80
Glu	Asp	Gln	Asn	Val	Ile	Val	Leu	Ser	Gln	Leu	Glu	Gly	Tyr	Leu	Gln
			85						90					95	
Lys	Gly	Ser	Arg	Ser	Ile	Ala	Gly	Leu	Phe	Leu	Pro	Thr	Ser	Gly	Gly
			100					105					110		
Ala	Met	Val	Gly	Asp	Ile	Asn	Met	Gly	Thr	Ser	Pro	Gly	Asn	Thr	Ile
		115					120					125			
Lys	Gly	Leu	Pro	Ser	Ser	Trp	Gly	Ser	Ala	Met	Phe	Leu	Gly	Asn	Glu
	130					135					140				
Tyr	Ala	Ala	Ser	Val	Gly	Ile	Val	Gln	Asp	Val	Val	Gly	Glu	Tyr	Arg
145					150					155					160
Ala	Arg	Leu	Asp	Asp	Leu	Ile	Asp	Arg	Ile	Thr	Lys	Tyr	Ala	Gly	Ser
			165						170					175	
Gly	Glu	Gly	Ser	Leu	Glu	Gln	Leu	Ile	Lys	Asp	Leu	Gly	Ser	Pro	Gln
			180					185					190		
Glu	Ser	Gln	Ala	Gly	Gln	Thr	Pro	Ser	Val	Thr	Leu	Glu	Lys	Pro	Thr
		195					200					205			
Asp	Ala	Lys	Trp	Leu	Leu	Leu	Ser	Ala	Lys	Asn	Ala	Met	Thr	Gly	Thr
	210					215					220				
Leu	Arg	Phe	Glu	Lys	Lys	Gln	Gly	Ala	Leu	Pro	Thr	Thr	Pro	Asp	Pro
225					230					235					240
Thr	Ile	Thr	Asn	Leu	Lys	Ala	Gly	Gly	Leu	Gly	Thr	Ile	Gly	Thr	Ala
			245						250					255	
Thr	Pro	Lys	Asp	Lys	Leu	Gln	Asn	Ile	Val	Ser	Val	Ala	Asp	Leu	Thr
			260					265					270		
Thr	Ile	Leu	Lys	Asp	Leu	Gln	Asn	Asn	Ala	Pro	Ser	Glu	Gly	Thr	Gly
		275					280					285			
Ser	His	Thr	Gly	Ser	Asp	Val	Gly	Ser	Arg	Ser	Gly	Ser	Gly	Thr	Asp
	290					295					300				
Ser	Val	Ser	Gly	Gly	Val	Ala	Gly	Ala	Ser	Val	Ser	Thr	Thr	Thr	Ala
305					310					315					320
Ser	Thr	Phe	Pro	Glu	Trp	Thr	Gly	Gln	Glu	Val	Pro	Tyr	Leu	Val	Glu
				325					330					335	
Gln	Ser	Pro	Asp	Ser	Gly	Ser	Gly	Ser	Leu	Ser	Val	Gln	Asn	Pro	Leu
			340					345					350		
Lys	Ser	Ser	Asn	Ala	Asp										

(2) INFORMATIONS POUR LA SEQ ID NO: 425:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 111 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(417721..418053)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 425:

Leu	Lys	Val	Leu	Ile	Lys	Arg	Ser	Lys	Glu	Leu	Gln	Leu	Ser	Cys	Ser
1				5					10					15	
Leu	Gly	Val	Ala	Lys	Ile	Phe	Val	Ser	Lys	Phe	Pro	Gln	Thr	Gly	Leu
			20					25					30		
Phe	Glu	Ile	Leu	Ser	Glu	Phe	Gln	Lys	Leu	Ile	Cys	Gln	Met	Gly	Asp
		35					40					45			
Lys	Glu	Ser	Ile	Glu	Ala	Ser	Asp	Ile	Gln	Ser	Phe	Val	Glu	Lys	Lys
		50				55					60				
Glu	Ala	Ile	Ser	Leu	Trp	Lys	Leu	Arg	Asp	Ala	Leu	Leu	Arg	Lys	Asp
65					70					75					80
Arg	Val	Ala	Ala	His	Ser	Leu	Met	Arg	Ser	Leu	Val	Ser	Asp	Met	Gly
			85						90					95	
Glu	Glu	Pro	Leu	Gly	Phe	Ser	Thr	Phe	Tyr	Val	Val	Ser	Thr	Ser	
			100					105					110		

(2) INFORMATIONS POUR LA SEQ ID NO: 426:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 191 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(418031..418603)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 426:

Glu	Phe	Ser	Phe	Pro	Gly	Phe	Leu	Tyr	Leu	Leu	Ala	Glu	Ser	Lys	Cys
1				5					10					15	
Leu	Lys	Lys	Ile	Lys	Ser	Gly	Asn	Lys	Lys	Asn	Asn	Pro	Arg	Ile	Ile
			20					25					30		
Gly	Phe	Trp	Arg	Trp	Ile	Met	Gly	Asn	Ser	Gln	Asn	Ser	Ile	His	Ile
		35					40					45			
Thr	Ser	Thr	Lys	Asp	Phe	Val	Gln	Tyr	Ile	Glu	Arg	Glu	Arg	Phe	Arg
		50				55					60				
Val	Ile	Val	Ile	Gly	Ser	Ser	Ser	Leu	Glu	Asp	Lys	Asp	Ile	Phe	Ser
65					70					75					80
Glu	Leu	Tyr	Ile	Ser	Gly	Arg	Lys	Ser	Phe	Phe	Asp	Gly	Gln	Arg	Leu
			85						90					95	
Leu	Gln	Gln	Glu	Leu	Leu	Ser	Trp	Thr	Asp	His	Phe	Gly	Leu	Phe	Ala

(2) INFORMATION POUR LA SEQ ID NO: 427:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(i) CARACTERISTIQUES DE LA SÉRIE
(A) LONGUEUR: 293 acides aminés

(A) LONGUEUR: 299 g
(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(418647..419525)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 427:

(xi)	DESCRIPTION DE L'ETAT															
Met	Leu	Gly	Val	Gln	Lys	Lys	Arg	Ser	Thr	Arg	Lys	Thr	Ala	Ala	Arg	15
1				5					10							
Lys	Thr	Val	Val	Arg	Lys	Pro	Ala	Ala	Lys	Lys	Thr	Ala	Ala	Lys	Lys	30
			20					25								
Ala	Pro	Val	Arg	Lys	Val	Ala	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	45
			35					40								
Val	Ala	Lys	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Xaa	Ala	60
			50				55									
Thr	Ala	Arg	Lys	Ala	Pro	Val	Arg	Xaa	Ala	Val	Ala	Lys	Lys	Thr	Val	80
65					70					75						
Ala	Arg	Lys	Thr	Val	Ala	Xaa	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	95
				85					90							
Ala	Lys	Lys	Ala	Ala	Lys	Lys	Ala	Pro	Val	Arg	Lys	Val	Ala	Ala		110
			100				105									
Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	Val	Ala	Lys	Lys	Thr	Val	Ala	Ala	125
			115				120									
Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala	Thr	Ala	Lys	Lys	Ala	Pro	Val	Arg	140
			130				135									
Lys	Ala	Val	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	Val	Ala	Lys	Lys	160
145					150					155						
Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala	Thr	Gly	Lys	Lys	175
				165					170							
Ala	Pro	Val	Arg	Lys	Val	Ala	Ala	Lys	Lys	Thr	Val	Ala	Arg	Lys	Thr	190
			180					185								
Val	Ala	Lys	Lys	Thr	Val	Ala	Ala	Arg	Lys	Pro	Val	Ala	Lys	Lys	Ala	205
			195				200									
Thr	Ala	Lys	Lys	Ala	Pro	Val	Arg	Lys	Ala	Val	Ala	Lys	Lys	Thr	Val	220
			210				215									
Ala	Lys	Arg	Val	Ala	Ser	Thr	Lys	Lys	Ser	Ser	Val	Ala	Val	Lys	Ala	240
225					230					235						
Gly	Val	Cys	Met	Lys	Lys	His	Lys	His	Thr	Ala	Ala	Cys	Gly	Arg	Val	255
				245					250							

Ala Ala Ser Gly Val Lys Val Cys Ala Ser Ala Ala Lys Arg Lys Met
 260 265 270
 Asn Pro Asn Arg Ser Arg Thr Ala His Ser Trp Arg Gln Gln Leu Met
 275 280 285
 Lys Leu Val Ala Arg
 290

(2) INFORMATIONS POUR LA SEQ ID NO: 428:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(419672..420037)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 428:

Met Val Val Ser Leu Gly Glu Ser Val Ala Gly Phe Phe Ala Asn Asn
 1 5 10 15
 Asp Val Leu Ala Arg Asp Leu Ala Glu Ala Ser Ser Glu Thr Gly Glu
 20 25 30
 Ala Leu Trp Arg Met Pro Leu Val Glu Lys Tyr Asp Gln Ala Leu His
 35 40 45
 Ser Asp Ile Ala Asp Met Lys Asn Ile Gly Ser Asn Arg Ala Gly Ser
 50 55 60
 Ile Thr Ala Ala Leu Phe Leu Gln Arg Phe Leu Glu Asp Asn Pro Val
 65 70 75 80
 Ala Trp Ala His Leu Asp Ile Ala Gly Thr Ala Tyr His Glu Lys Glu
 85 90 95
 Glu Leu Pro Tyr Pro Lys Tyr Ala Thr Gly Phe Gly Val Arg Cys Leu
 100 105 110
 Ile His Tyr Met Glu Lys Phe Leu Ser Lys
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 429:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(420245..421078)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 429:

Glu Ala Ala Val Val Asp Glu Asp Tyr Lys Leu Val Tyr Gln Asn Ala
 1 5 10 15
 Leu Ser Asn Phe Ser Gly Lys Lys Gly Glu Thr Ala Phe Leu Phe Gly
 20 25 30
 Asn Asp His Thr Lys Glu Gln Lys Ile Val Leu Leu Gly Leu Gly Lys

```

          35          40          45
Ser Glu Val Ser Gly Thr Thr Val Leu Glu Ala Tyr Ala Gln Ala
 50          55          60
Thr Thr Val Leu Arg Lys Ala Lys Cys Lys Thr Val Asn Ile Leu Phe
65          70          75          80
Pro Thr Ile Ser Gln Leu Arg Phe Ser Val Glu Glu Phe Leu Thr Asn
          85          90          95
Leu Ala Ala Gly Val Leu Ser Leu Asn Tyr Asn Tyr Pro Thr Tyr His
          100          105          110
Lys Val Asp Thr Ser Leu Pro Phe Leu Glu Lys Val Thr Val Met Gly
          115          120          125
Ile Val Ser Lys Val Gly Asp Lys Ile Phe Arg Lys Glu Glu Ser Leu
          130          135          140
Phe Glu Gly Val Tyr Leu Thr Arg Asp Leu Val Asn Thr Asn Ala Asp
          145          150          155          160
Glu Val Thr Pro Glu Lys Leu Ala Ala Val Ala Lys Gly Leu Ala Gly
          165          170          175
Glu Phe Ala Ser Leu Asp Val Lys Ile Leu Asp Arg Lys Ala Ile Leu
          180          185          190
Lys Glu Lys Met Gly Leu Leu Ala Ala Val Ala Lys Gly Ala Ala Val
          195          200          205
Glu Pro Arg Phe Ile Val Leu Asp Tyr Gln Gly Lys Pro Lys Ser Lys
          210          215          220
Asp Arg Thr Val Leu Ile Gly Lys Gly Val Thr Phe Asp Ser Gly Gly
          225          230          235          240
Leu Asp Leu Lys Pro Gly Lys Ala Met Ile Thr Met Lys Glu Asp Met
          245          250          255
Ala Gly Ala Ala Thr Val Leu Gly Ile Phe Ser Ala Phe Ser Phe Pro
          260          265          270
Trp Ser Phe Arg Ser Met
          275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 430:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 157 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(421518..421988)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 430:

```

Met Leu Phe Gly Tyr Leu Val Gly Phe Leu Ala Ala Asp Pro Glu Glu
 1          5          10          15
Arg Met Thr Ser Gly Gly Lys Arg Val Val Val Leu Arg Leu Gly Val
          20          25          30
Lys Ser Arg Val Gly Ser Lys Asp Glu Thr Val Trp Cys Arg Cys Asn
          35          40          45
Ile Trp Asn Asn Arg Tyr Asp Lys Met Leu Pro Tyr Leu Lys Lys Gly
          50          55          60
Ser Ser Val Ile Val Ala Gly Glu Leu Ser Leu Glu Ser Tyr Val Gly
          65          70          75          80
Arg Asp Gly Ser Pro Gln Ala Ser Ile Ser Val Ser Val Asp Thr Leu
          85          90          95

```



```

Lys Phe Asn Ser Gly Ser Ser Arg Pro Asp Ala Arg Gly Ser Asp Glu
      100      105      110
Gly Arg Gln Arg Ala Asn Asp Asn Val Ser Ile Gly Phe Asp Gly Glu
      115      120      125
Ser Leu Asp Thr Asp Ser Ala Leu Asp Lys Glu Val Tyr Ala Gly Phe
      130      135      140
Gly Glu Asp Gln Gln Tyr Ala Ser Glu Asp Val Pro Phe
145      150      155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 431:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 186 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 422486..423043

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 431:

```

Lys Ile Leu Leu Lys Ser Leu Lys Leu Pro Asp Val Ala Phe Asp Gln
1      5      10      15
Asn Asn Thr Cys Ile Leu Phe Val Asp Gly Glu Phe Ser Leu His Leu
      20      25      30
Thr Tyr Glu His Ser Asp Arg Leu Tyr Val Tyr Ala Pro Leu Leu
      35      40      45
Asp Gly Xaa Pro Asp Asn Pro Gln Arg Lys Leu Ala Leu Tyr Glu Lys
50      55      60
Leu Leu Glu Gly Ser Met Leu Gly Gly Gln Met Ala Gly Gly Gly Val
65      70      75      80
Gly Val Ala Thr Lys Glu Gln Leu Ile Leu Met His Cys Val Leu Asp
      85      90      95
Met Lys Tyr Ala Glu Thr Asn Leu Leu Lys Ala Phe Ala Gln Leu Phe
100      105      110
Ile Glu Thr Val Val Lys Trp Arg Thr Val Cys Ser Asp Ile Ser Val
115      120      125
Asp Glu Asn Pro Leu Leu Ile Pro Cys His Lys Cys Leu Lys Gly Val
130      135      140
Ala Glu Glu Phe Asn Leu Leu Gln Gln Glu Ser Val His Lys Ser Phe
145      150      155      160
Ala Ile Ile Gln Gln Lys Glu Glu Gly Leu Leu Pro Phe Val Phe Lys
      165      170      175
Pro Pro Pro Ser Ser Leu His Phe Phe Gly
180      185

```

(2) INFORMATIONS POUR LA SEQ ID NO: 432:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 618 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 423226..425079

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 432:

```

Asn Ser Ser Ile Phe Tyr Arg Pro Gln Asp Trp Ser His Leu Ala Tyr
1      5      10      15
Arg Asn Cys Arg His Phe Leu Val Asn Gly Arg Met Leu Ile Asn Leu
20      25      30
Arg Gly Thr Asp Leu Ser Ser Gln Lys Phe Ala Thr Asp Ser Tyr Ile
35      40      45
Ala Asp Pro Tyr Ser Lys Asn Ile Tyr Ser Pro Gln Leu Phe Gly Ser
50      55      60
Pro Lys Gln Glu Lys Asp Tyr Ala Phe Ser Tyr Leu Lys Tyr Glu Asp
65      70      75      80
Phe Asp Trp Glu Gly Asp Thr Pro Leu His Leu Pro Lys Glu Asn Tyr
85      90      95
Phe Ile Tyr Glu Met His Val Arg Ser Phe Thr Arg Asp Pro Ser Ser
100      105      110
Gln Val Ser His Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys Ile Asp
115      120      125
His Leu Lys Gln Leu Gly Val His Ala Val Glu Leu Pro Ile Phe
130      135      140
Glu Phe Asp Glu Thr Val His Pro Phe Lys Asn Gln Asp Phe Pro His
145      150      155      160
Leu Cys Asn Tyr Trp Gly Tyr Ser Ser Val Asn Phe Phe Cys Pro Ser
165      170      175
Arg Arg Tyr Thr Tyr Gly Ala Asp Pro Cys Ala Pro Ala Arg Glu Phe
180      185      190
Lys Thr Leu Val Lys Ala Leu His Arg Ala Gly Ile Glu Val Ile Leu
195      200      205
Asp Val Val Phe Asn His Thr Gly Phe Glu Gly Thr Ser Cys Pro Leu
210      215      220
Pro Trp Ile Asp Leu Lys Ser Tyr Tyr Met Val Asn Asp His Gly Asp
225      230      235      240
Leu Met Asn Phe Ser Gly Cys Gly Asn Thr Val Asn Thr Asn Thr Pro
245      250      255
Thr Thr Leu Lys Trp Ile Leu Asp Ala Leu Arg Tyr Trp Val Gln Glu
260      265      270
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Val Phe Ser Arg
275      280      285
Asp Pro Gln Gly Val Pro Leu Pro Leu Thr Pro Ile Leu Gln Ala Ile
290      295      300
Ser Ser Asp Ser Ile Leu Ser Glu Thr Lys Leu Ile Ala Glu Pro Trp
305      310      315      320
Asp Ala Gly Gly Leu Tyr Gln Leu Gly His Phe Pro Ser Ile Ser Thr
325      330      335
Arg Trp Ser Glu Trp Asn Gly Cys Tyr Arg Asp His Val Lys Ala Phe
340      345      350
Leu Asn Gly Asp Ala His Gln Val Ser Ser Phe Ala Ser Arg Ile Ser
355      360      365
Gly Ser His Asp Ile Tyr Pro Asn Gly Lys Pro Thr Asn Ser Ile Asn
370      375      380
Tyr Ile Cys Ser His Asp Gly Phe Thr Leu Tyr Asp Thr Val Ala Tyr
385      390      395      400
Asn Asp Lys His Asn Glu Glu Asn Gly Glu Tyr Asn Arg Asp Gly Thr
405      410      415
Ser Ala Asn Tyr Ser Tyr Asn Phe Gly Cys Glu Gly Glu Thr Asp
420      425      430

```

```

Pro Thr Ile Cys Ala Leu Arg Glu Arg Gln Met Lys Asn Phe Phe Leu
    435                      440                      445
Ala Leu Phe Leu Ser Gln Gly Ile Pro Met Ile Gln Ser Gly Asp Glu
    450                      455                      460
Tyr Gly His Thr Ala Tyr Gly Asn Asn Asn His Trp Cys Leu Asp Thr
    465                      470                      475                      480
Lys Ile Asn Tyr Phe Leu Trp Asp Arg Leu Ala Glu Arg Lys Glu Leu
    485                      490                      495
Phe Ser Phe Leu Cys Gln Val Ile Ala Leu Arg Lys Ala Tyr Thr Glu
    500                      505                      510
Leu Phe Asn Thr Ser Phe Leu Ser Glu Asp Thr Ile Thr Trp Leu Asn
    515                      520                      525
Thr Lys Gly Ser Pro Arg Glu Trp Gly Ala Asp His Tyr Leu Ala Phe
    530                      535                      540
Xaa Leu Lys His Leu Asn Tyr Ser Leu Phe Val Xaa Phe Tyr Ser Gly
    545                      550                      555                      560
Asn Glu Arg Ile Glu Ile Ser Leu Pro Lys Pro Arg Lys Glu His Leu
    565                      570                      575
Ala Tyr Glu Lys Ile Val Asp Ser Thr Thr Gly Phe Phe Ser Gln Ile
    580                      585                      590
Leu Ser Pro Lys Leu Ser Leu Glu Pro Tyr Ser Ser Leu Val Ala Ile
    595                      600                      605
Ser Arg Arg Lys Thr Ser Leu Glu Ser Arg
    610                      615

```

(2) INFORMATIONS POUR LA SEQ ID NO: 433:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 303 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(425146..426054)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 433:

```

Arg Val Trp Phe Ser Glu Pro Gln Glu Asp Gly Leu Gln Pro Leu Trp
1                      5                      10                      15
His Met Asn Ile Leu Thr Gly Thr Leu Arg Thr Gly Gly Glu Lys Asn
    20                      25                      30
Lys Val Lys Lys Leu Asn Leu Leu Val Leu Leu Gly Val Phe Cys Gly
    35                      40                      45
Val Ser Gly Val Gly Asp Ala Asp Val Lys Val Ser Asp Ala Leu Ser
    50                      55                      60
Gln Ser Ile Leu Val Glu Pro Lys Ile Arg Val Leu Leu Leu Ser Glu
    65                      70                      75                      80
Ser Thr Thr Ala Leu Ile Glu Ala Lys Gly Ala Phe Ser Val Phe Gly
    85                      90                      95
Asp Gly Glu Leu Leu Arg Val Ser Ser Gln Gly Gln Arg Cys Ala Ala
    100                     105                     110
His Ala Leu Tyr Gly Gly Ile Arg Trp Gly Glu Asn Tyr Pro Asn Val
    115                     120                     125
Glu Cys Leu Lys Ile Glu Pro Leu Asp Gly Ala Ala Ser Leu Phe Val
    130                     135                     140
Asn Gly Ile Gln Tyr Lys Gly Ala Ile Tyr Ile His Arg Thr Asp Arg

```



```

Ile Leu Ser Arg Ser Ser Gln Leu Leu Ala Ile Glu Ala Asn Gln Glu
      195                200                205
Thr Leu Leu Glu Ile Ala Arg Arg Ala Arg Gly Thr Pro Arg Leu Ala
      210                215                220
Asn Asn Leu Leu Arg Trp Val Arg Asp Phe Ala Gln Met Arg Glu Gly
      225                230                235                240
Asn Cys Ile Asn Ser Arg Pro
                245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 435:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 427248..427817

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 435:

```

Met Gly Ile Lys Glu Asp Asn Trp Ile Arg Lys Met Ala Ile Glu Glu
1      5      10      15
Gly Met Ile Glu Pro Phe Ala Asp Ser Gln Val Lys Leu His Pro Glu
      20      25      30
Thr Gly Glu Lys Leu Ile Ser Tyr Gly Leu Ser Ser Tyr Gly Tyr Asp
      35      40      45
Leu Arg Ile Ser Arg Glu Phe Lys Val Phe Thr Asn Val Tyr Asn Ser
      50      55      60
Leu Val Asp Pro Lys Cys Phe Thr Glu Asp Ala Leu Ile Ser Ile Val
      65      70      75      80
Asp Asp Val Cys Ile Ile Pro Pro Asn Ser Phe Ala Leu Ala Arg Ser
      85      90      95
Val Glu Tyr Phe Arg Ile Pro Arg Asn Val Leu Thr Val Cys Ile Gly
      100     105     110
Lys Ser Thr Tyr Ala Arg Cys Gly Leu Ile Val Asn Val Thr Pro Phe
      115     120     125
Glu Pro Glu Trp Glu Gly Tyr Val Thr Ile Glu Ile Ser Asn Thr Thr
      130     135     140
Pro Leu Pro Ala Lys Val Tyr Ala Asn Glu Gly Ile Ala Gln Val Leu
      145     150     155     160
Phe Phe Glu Gly Asp Ala Ala Cys Asp Val Ser Tyr Ala Glu Arg Gln
      165     170     175
Gly Lys Tyr Gln Lys Gln Gln Gly Ile Thr Ile Pro Phe Val
      180     185     190

```

(2) INFORMATIONS POUR LA SEQ ID NO: 436:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 429560..429886

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 436:

```

Asn Ser Cys Val Asn Thr Lys Val Ala Asp Trp Arg Thr Lys Lys Leu
1      5      10      15
Ala Pro Ile Phe Pro Leu Asp Tyr Glu Asp Phe Phe Thr Val Phe Met
      20      25      30
Lys Lys Gln His Tyr Thr Leu Pro Gly Asn Val Ser Asn Met Arg Ile
      35      40      45
Leu Ser Pro Val Arg Pro Val Ser Glu Thr Ala Leu Thr Thr Ile Ile
      50      55      60
Ile Ser Gly Leu Glu Glu Glu Asp Lys Leu Gly Leu Leu Gly Gln Val
65      70      75      80
Gln Gln Phe Leu Phe Asp Ala Glu Glu Ala His Pro Gln Arg Gly Glu
      85      90      95
Ser Ile Leu Ile Gln Asn Val Leu Asp Asp Ile Thr Gln
      100      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 437:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 168 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(429857..430360)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 437:

```

Val Phe Cys Ala Gly Ala Tyr Phe Gly Cys Ala Arg Phe Glu Phe Leu
1      5      10      15
Glu Pro Thr Gly Ser Leu Phe Val Ala Lys Arg Asp Leu Gly Phe Phe
      20      25      30
Pro Gly Ala Ala Asn Gly Pro Ala Tyr Glu Ser Ala Phe Ser Tyr Thr
      35      40      45
Ser Ser Ser Gly Val Leu Ala Ala Pro Leu Val Phe Ala Asp Phe Pro
      50      55      60
Gly Glu Ser Phe Ser Leu Phe Asn Gly Gly Cys Phe Glu Asn Ala
65      70      75      80
Glu His Phe Pro Glu Ile Cys Ile Glu Ala Arg Tyr Asn Asn Leu Leu
      85      90      95
Gly Lys Pro Ala Ala Ile Leu Ser Arg Arg Leu Asp Lys Gly Leu Val
      100      105      110
Val Leu Ser Gly Pro His Ile Glu Tyr Leu Pro Glu Phe Cys Ser Leu
      115      120      125
Gln Glu Asp Asn Val Ile Gln Ala Arg Glu Gln Ile Ala Ala His Ser
      130      135      140
Ser Ser Leu Glu Glu Tyr Lys Gln Phe Leu Ile His Arg Leu Leu Ser
145      150      155      160
Asn Val Val Glu His Val Leu Tyr
      165

```

(2) INFORMATIONS POUR LA SEQ ID NO: 438:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(430323..430637)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 438:

Gly	Lys	Glu	Met	Lys	Arg	Ile	Leu	Val	Tyr	Ser	Asp	Lys	Gly	Val	Ser
1				5					10					15	
Pro	Tyr	Tyr	Leu	Arg	His	Thr	Val	Arg	Trp	Leu	Lys	Gln	Val	Ala	Ala
			20					25					30		
Pro	Phe	Gln	Met	Glu	Val	Cys	Arg	Val	Asn	Gly	Arg	Phe	Leu	Ile	His
		35				40						45			
Glu	Pro	Leu	Trp	Glu	Asp	Thr	Gln	Leu	Leu	Val	Ile	Pro	Gly	Gly	
	50					55				60					
Ala	Asp	Val	Pro	Tyr	His	Asn	Val	Leu	His	Gly	Leu	Gly	Thr	Ala	Arg
65					70					75					80
Ile	Asp	Asn	Tyr	Val	Arg	Glu	Gly	Gly	Cys	Tyr	Leu	Gly	Ile	Leu	Arg
			85					90					95		
Arg	Ser	Leu	Phe	Trp	Leu	Arg	Ala	Val							
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 439:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 285 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 430933..431787

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 439:

Ser	Ala	Val	Phe	Lys	Leu	Glu	Ser	Leu	Leu	Ser	Met	Met	Ser	Ser	Pro
1				5					10					15	
His	Pro	Met	Ser	Ser	Ser	Arg	Asn	Thr	Pro	Leu	Gly	Val	Phe	Tyr	Ser
			20					25					30		
Leu	Leu	Ala	Cys	Phe	Tyr	Trp	Gly	Met	Val	Phe	Val	Ile	Pro	Ser	Met
		35					40					45			
Leu	Gly	Asn	Phe	Ala	Asp	Leu	Asp	Ile	Val	Leu	Thr	Arg	Tyr	Ser	Val
	50					55				60					
Phe	Gly	Ile	Cys	Ser	Leu	Ile	Thr	Ile	Leu	Tyr	Lys	Arg	Ser	Asn	Ile
65					70					75					80
Phe	Lys	Thr	Val	Pro	Phe	Phe	Leu	Trp	Lys	Lys	Gly	Ile	Leu	Trp	Ala
			85					90					95		
Phe	Leu	Ile	Asn	Ile	Ala	Tyr	Tyr	Phe	Gly	Ile	Ala	Gln	Ala	Val	Arg
			100					105					110		
Tyr	Ser	Gly	Ser	Ala	Val	Thr	Val	Ile	Ile	Ala	Gly	Leu	Ala	Pro	Ile

(2) INFORMATION POUR LA SEQ ID NO: 440:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(i) CARACTERISTIQUES DE LA SÉRIE
(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 431658..431987

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 440:

(xi)	DESCRIPTION OF THE SEQUENCE																		
Phe	Ser	Ile	Ser	Tyr	Pro	Ser	Phe	Arg	Lys	Met	Pro	Xaa	Asp	Arg	Ser	15			
1				5					10										
Leu	Leu	Cys	Tyr	Gly	Asp	Phe	Ser	Ser	Ser	Arg	Ala	Ile	Ala	Ala	Trp	30			
			20						25										
Asn	Lys	Ala	Ser	Leu	His	Leu	Ser	Thr	Ala	Leu	Leu	Gly	Ala	Leu	Leu	45			
			35					40											
Ile	Phe	Glu	Pro	Ile	Phe	Gly	Trp	Ile	Leu	Ser	Tyr	Leu	Cys	Lys	Arg	60			
						55													
Glu	Met	Pro	Ser	Phe	Gln	Glu	Gly	Leu	Gly	Phe	Phe	Leu	Met	Leu	Gly	75			
65					70														
Ala	Ser	Leu	Cys	Leu	Leu	Leu	Ala	Gln	Lys	Lys	Ala	Ser	Glu	Gln	Glu	90			
				85					95										
Thr	Pro	Ser	Glu	Thr	Leu	Ile	Thr	Thr	Glu	Ser	Glu	Ala	Asn			105			
			100										110						

(2) INFORMATION POUR LA SEQ ID NO: 441:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 748 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 432232..434475

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 441:

Lys	Asp	Met	Gly	Cys	Glu	Glu	Lys	Leu	Ser	Gly	Ile	Leu	Glu	Leu	Ile
1				5					10					15	
Leu	Pro	Glu	Asp	Pro	Leu	Ser	Asp	Gln	Thr	Gly	Tyr	Ala	Phe	Leu	Arg
		20						25					30		
Val	Pro	Tyr	Lys	Asn	Ser	Leu	Val	Thr	Val	Cys	Gly	His	Leu	Pro	Leu
		35					40					45			
Ser	Leu	Phe	Lys	Ile	Gly	Ser	Ser	Val	Asp	Leu	Thr	Gly	His	Trp	Ser
	50					55					60				
Val	Asp	Ala	Ser	Gly	Ala	Leu	Val	Phe	Arg	Phe	Thr	Ser	Ala	Ala	Thr
	65				70					75					80
Tyr	Ser	Pro	Asp	Ser	Gly	Ile	Ile	Ala	Tyr	Leu	Asn	Ala	Gln	Ile	Lys
				85					90					95	
Gly	Val	Gly	Pro	Lys	Leu	Ala	Gln	Lys	Ile	Val	Ser	Thr	Phe	Gly	Glu
			100					105					110		
Asp	Thr	Leu	Thr	Val	Leu	Asp	Ser	Cys	Pro	Ser	Lys	Leu	Val	Glu	Val
		115					120					125			
Asp	Gly	Ile	Ser	Pro	Ala	Arg	Cys	Glu	Asp	Phe	Ser	Lys	Gln	Leu	Gln
	130					135					140				
Glu	Gln	Arg	Asp	Leu	Arg	His	Ala	Leu	Leu	Phe	Leu	Gln	Arg	His	Gly
	145				150					155					160
Ile	Ala	Ile	His	Tyr	Gly	Leu	Arg	Leu	Tyr	Lys	Lys	Tyr	Gln	Asn	Gln
				165					170					175	
Thr	Ile	Glu	Lys	Val	Cys	Gln	Asp	Pro	Phe	Leu	Leu	Ala	Lys	Glu	Met
		180						185					190		
Tyr	Gly	Ile	Gly	Phe	Lys	Thr	Ala	Asp	Leu	Ile	Ala	Thr	Cys	Leu	Gly
		195					200					205			
Val	Pro	Leu	Asn	Ser	Pro	Asn	Arg	Ile	Val	Ala	Gly	Ile	Gln	Tyr	Ser
	210					215					220				
Leu	Asp	Glu	Leu	Gln	Glu	Glu	Gly	His	Thr	Cys	Tyr	Pro	Leu	Asn	Asp
	225				230					235					240
Phe	Ile	Val	Leu	Val	Glu	Lys	Leu	Leu	Asn	Glu	Glu	Ala	Pro	Glu	Glu
			245						250					255	
Ile	Ile	Arg	Lys	Glu	Glu	Ile	Arg	Thr	Gln	Ile	His	Phe	Leu	Ser	Arg
			260					265					270		
Gln	Lys	Thr	Val	Tyr	Val	Lys	Glu	Leu	Glu	Gln	Asp	Thr	Tyr	Ile	Trp
		275					280					285			
Ser	Arg	Gln	Leu	Phe	Leu	Ala	Glu	Gln	Gln	Ile	Ala	Ile	Asp	Ile	Arg
	290					295					300				
Arg	Leu	Leu	Phe	Ser	Ser	Lys	Arg	Ile	Arg	Ser	Ile	Asn	Thr	Gln	Glu
	305				310					315					320
Ala	Ile	Leu	Glu	Val	Glu	Asn	Leu	Leu	Asp	Leu	Lys	Leu	Glu	Glu	Lys
			325						330					335	
Gln	Lys	Glu	Ala	Leu	His	Ala	Ser	Ser	Ser	Gln	Lys	Ile	His	Ile	Ile
			340				345					350			
Ser	Gly	Gly	Pro	Gly	Thr	Gly	Lys	Ser	Thr	Ile	Thr	Arg	Ala	Ile	Leu
		355				360						365			
Ser	Ile	Phe	Glu	Lys	Ile	Ser	Ser	Pro	Lys	Lys	Ile	Ile	Leu	Ala	Ala
	370					375					380				
Pro	Thr	Gly	Lys	Ala	Ala	Lys	Arg	Met	Thr	Glu	Ile	Thr	Gly	Lys	Arg
	385				390					395					400
Thr	Gln	Thr	Ile	His	Ser	Leu	Leu	Gln	Tyr	Asp	Phe	Lys	Thr	Leu	Ser

```

                                405                                410                                415
Phe Arg Lys Asn His Glu Asp Pro Ile Asp Cys Asp Leu Val Ile Val
                                420                                425                                430
Asp Glu Ser Gly Met Ile Asp Thr Ile Leu Leu Gln Arg Phe Leu Ala
                                435                                440                                445
Ala Leu Pro Asp His Ala Ile Leu Ile Leu Ile Gly Asp Val His Gln
                                450                                455                                460
Leu Pro Ser Val Gly Pro Gly Asn Val Leu Lys Asp Leu Ile Leu Ser
465                                470                                475                                480
His His Ile Glu Val Thr Tyr Leu Thr Lys Ile Phe Arg Gln Leu Gln
                                485                                490                                495
Asn Ser Asn Ile Thr Asn Ala His Lys Val Asn Gln Gly Glu Phe
                                500                                505                                510
Pro Val Leu Asn Ser Ser Ser Gly Lys Lys Asp Phe Leu Phe Phe Gln
                                515                                520                                525
Lys Glu Asp Pro Glu Glu Ala Ile Lys His Ile Ile His Leu Val Ser
                                530                                535                                540
Asp Phe Val Pro Lys Lys Phe Gly Ile Phe Thr Lys Asp Ile Gln Val
545                                550                                555                                560
Leu Ala Pro Xaa Arg Lys Gly Val Leu Gly Ile Leu Asn Leu Asn Arg
                                565                                570                                575
Glu Leu Lys Ala Ala Leu Asn Pro Asn Lys Leu Phe Ile Gln Gly Lys
                                580                                585                                590
Phe His Ser Phe Ser Thr Gly Asp Arg Val Met Gln Thr Arg Asn Asn
                                595                                600                                605
Tyr Asn Lys Glu Val Phe Asn Gly Asp Ile Gly Tyr Val Thr Ser Ile
                                610                                615                                620
Asp Leu Ser Thr Lys Ser Leu Ile Val Cys Val Asp Gly Arg Tyr Ile
625                                630                                635                                640
Ser Tyr Ser Gln Ala Glu Leu Asn Asp Leu Ile Pro Ala Tyr Ala Thr
                                645                                650                                655
Ser Ile His Lys Tyr Gln Gly Ser Glu Thr Ser Cys Ile Ile Leu Pro
                                660                                665                                670
Ile His Thr Ser His Tyr Val Met Leu Tyr Arg Asn Leu Leu Tyr Thr
                                675                                680                                685
Ala Ile Thr Arg Gly Lys Lys Leu Val Ile Leu Val Gly Thr Lys Lys
                                690                                695                                700
Ala Val Ala Ile Ala Val Arg Asn Asp Lys Val Gln His Arg Cys Thr
705                                710                                715                                720
Gly Leu Gln Gln Ala Met His Ser Leu Leu Asn Lys Pro Thr Pro Leu
                                725                                730                                735
Phe Ser Pro Tyr Thr Ile Cys Arg Pro Ser Leu Gly
                                740                                745

```

(2) INFORMATIONS POUR LA SEQ ID NO: 442:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 563 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(434620..436308)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 442:

Lys Arg Ser Phe Ser Val Gln Leu Glu Arg Arg Glu Ile Val Glu Ser
 1 5 10 15
 Ser Arg Ile Leu Ile Thr Ser Ala Leu Pro Tyr Ala Asn Gly Pro Leu
 20 25 30
 His Phe Gly His Ile Thr Gly Ala Tyr Leu Pro Ala Asp Val Tyr Ala
 35 40 45
 Arg Phe Gln Arg Leu Gln Gly Lys Glu Val Leu Tyr Ile Cys Gly Ser
 50 55 60
 Asp Glu Tyr Gly Ile Ala Ile Thr Leu Asn Ala Glu Leu Ala Gly Met
 65 70 75 80
 Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys Leu His Lys Asp Thr
 85 90 95
 Phe Lys Lys Leu Gly Ile Ser Val Asp Phe Phe Ser Arg Thr Thr Asn
 100 105 110
 Ala Tyr His Pro Ala Ile Val Gln Asp Phe Tyr Arg Asn Leu Gln Glu
 115 120 125
 Arg Gly Leu Val Glu Asn Gln Val Thr Glu Gln Leu Tyr Ser Glu Glu
 130 135 140
 Glu Gly Lys Phe Leu Ala Asp Arg Tyr Val Val Gly Thr Cys Pro Lys
 145 150 155 160
 Cys Gly Phe Asp Arg Ala Arg Gly Asp Glu Cys Gln Gln Cys Gly Ala
 165 170 175
 Asp Tyr Glu Ala Arg Asp Leu Lys Glu Pro Arg Ser Lys Leu Thr Gly
 180 185 190
 Ala Ala Leu Ser Leu Arg Asp Thr Glu His Ala Tyr Leu His Leu Glu
 195 200 205
 Arg Met Lys Glu Asp Leu Leu Ala Phe Val Gln Gly Ile Tyr Leu Arg
 210 215 220
 Pro His Met Arg Asn Phe Val Thr Asp Tyr Ile Glu His Leu Arg Pro
 225 230 235 240
 Arg Ala Val Thr Arg Asp Leu Ser Trp Gly Ile Pro Val Pro Asp Leu
 245 250 255
 Glu Asn Lys Val Phe Tyr Val Trp Phe Asp Ala Pro Ile Gly Tyr Ile
 260 265 270
 Ser Gly Thr Met Asp Trp Ala Ala Ser Ile Gly Asp Pro Glu Ala Trp
 275 280 285
 Lys Lys Phe Trp Leu Asp Asp Thr Val Thr Tyr Ala Gln Phe Ile Gly
 290 295 300
 Lys Asp Asn Thr Ser Phe His Ala Val Ile Phe Pro Ala Met Glu Ile
 305 310 315 320
 Gly Gln Ser Leu Pro Tyr Lys Lys Val Asp Ala Leu Val Thr Ser Glu
 325 330 335
 Phe Leu Leu Leu Glu Gly Phe Gln Phe Ser Lys Ser Asp Gly Asn Phe
 340 345 350
 Ile Asp Met Asp Ala Phe Leu Glu Thr Tyr Ser Leu Asp Lys Leu Arg
 355 360 365
 Tyr Val Leu Ala Ala Ile Ala Pro Glu Thr Ser Asp Ser Glu Phe Ser
 370 375 380
 Phe Gln Glu Phe Lys Thr Arg Cys Asn Ser Glu Leu Val Gly Lys Tyr
 385 390 395 400
 Gly Asn Phe Val Asn Arg Val Leu Ala Phe Ala Val Lys Asn Gly Cys
 405 410 415
 Thr Glu Leu Ser Ser Pro Gln Leu Glu Gln Lys Asp Leu Asp Phe Ile
 420 425 430
 Ser Lys Ser Gln Lys Leu Ala Lys Asp Ala Ala Glu His Tyr Ala Gln
 435 440 445
 Tyr Ser Leu Arg Lys Ala Cys Ser Thr Ile Met Glu Leu Ala Ala Leu
 450 455 460
 Gly Asn Gly Tyr Phe Asn Asp Glu Ala Pro Trp Lys Leu Ala Lys Glu

(2) INFORMATION POUR LA SEQ ID NO: 443:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(436272..436574)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 443:

(2) INFORMATION POUR LA SEQ ID NO: 444:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 373 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(436567..437685)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 444:

Ala	Cys	Ile	Leu	Pro	Arg	Gly	Lys	Val	Phe	Leu	Gly	Ile	Asp	Asp	Ser
1				5					10					15	
Lys	Lys	Leu	Thr	Pro	Lys	Gln	Arg	Arg	Tyr	Leu	Tyr	Glu	Leu	Leu	
		20						25					30		
Glu	Asp	Pro	Glu	Val	Asp	Cys	Gly	Val	Gly	Val	Ile	Ser	Val	Glu	Arg
		35					40					45			
Ile	Asp	Glu	Ile	Asn	Ile	Leu	Glu	Ala	Thr	Lys	Glu	Ala	Met	Val	Gln
	50					55					60				
Ala	Ile	Ala	Ser	Leu	Arg	Ser	Thr	Pro	Asp	Phe	Leu	Leu	Val	Asp	Gly
65					70				75						80
Leu	Phe	Leu	Pro	His	Lys	Ile	Pro	Ser	Leu	Lys	Ile	Ile	Lys	Gly	Asp
				85					90					95	
Ala	Arg	Ser	Val	Ser	Ile	Ala	Ala	Ala	Ser	Ile	Ile	Ala	Lys	Glu	Tyr
			100					105					110		
Arg	Asp	Glu	Leu	Met	Arg	Lys	Leu	His	Val	Glu	Tyr	Pro	Glu	Tyr	Gly
	115						120					125			
Phe	Asp	Lys	His	Lys	Gly	Tyr	Gly	Thr	Ala	Ala	His	Leu	Gln	Ala	Leu
	130					135					140				
Lys	His	Phe	Gly	Pro	Cys	Val	Tyr	His	Arg	Lys	Ser	Phe	Ser	Pro	Val
145					150					155					160
Lys	Glu	Ser	Ile	Xaa	Arg	Gly	Ser	Met	Ser	Val	Lys	Val	Ile	Ser	Pro
				165					170					175	
Phe	Ser	Gln	Asp	Gly	Val	Gln	Phe	Phe	Pro	Lys	Leu	Phe	Ile	Ile	Ser
		180						185					190		
Ala	Pro	Ala	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Thr	His	Met	Leu	Gln	Arg
	195						200					205			
Glu	Phe	Pro	Asp	Ala	Phe	Glu	Lys	Thr	Val	Ser	Ser	Thr	Thr	Arg	Ser
	210					215					220				
Ala	Arg	Pro	Gly	Glu	Val	His	Gly	Val	Asp	Tyr	Leu	Phe	Val	Ser	Glu
225					230					235					240
Asp	Asp	Phe	Lys	Gln	Ser	Leu	Asp	Arg	Glu	Asp	Phe	Leu	Glu	Trp	Val
				245					250					255	
Phe	Leu	Phe	Gly	Thr	Tyr	Tyr	Gly	Thr	Ser	Lys	Ala	Glu	Ile	Ser	Arg
		260						265					270		
Val	Leu	Gln	Lys	Gly	Lys	His	Cys	Ile	Ala	Val	Ile	Asp	Val	Gln	Gly
	275						280					285			
Ala	Leu	Ala	Leu	Lys	Lys	Gln	Met	Pro	Ala	Val	Thr	Ile	Phe	Ile	Gln
	290					295					300				
Ala	Pro	Ser	Gln	Glu	Glu	Leu	Glu	Arg	Arg	Leu	Asn	Ala	Arg	Asp	Ser
305					310					315					320
Glu	Lys	Asp	Phe	Gln	Lys	Lys	Glu	Arg	Leu	Glu	His	Ser	Ala	Val	Glu
				325					330					335	
Ile	Ala	Ala	Ala	Ser	Glu	Phe	Asp	Tyr	Val	Val	Val	Asn	Asp	Asp	Leu
			340					345					350		
Ile	Thr	Ala	Tyr	Gln	Val	Leu	Arg	Ser	Ile	Phe	Ile	Ala	Glu	Glu	His
	355						360					365			
Arg	Met	Ser	His	Gly											
	370														

(2) INFORMATIONS POUR LA SEQ ID NO: 445:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 123 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(437894..438262)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 445:

```

Asn Thr Met Gly Asn Leu Ile Lys Glu Leu Gln Asp Glu Gln Cys Arg
1      5      10
Thr Asp Leu Ala Asp Phe Cys Val Gly Asp Thr Ile Arg Val Ala Thr
      20      25      30
Asn Ile Ser Glu Gly Gly Lys Glu Arg Val Gln Val Phe Gln Gly Thr
      35      40      45
Val Met Ala Arg Lys Gly Gly Gly Ala Gly Glu Thr Val Ser Leu His
      50      55      60
Arg Val Ala Tyr Gly Glu Gly Met Glu Lys Ser Phe Leu Leu Asn Ser
65      70      75      80
Pro Lys Ile Val Ser Ile Glu Val Val Lys Arg Gly Lys Val Ser Arg
      85      90      95
Ala Arg Leu Phe Tyr Leu Arg Gly Lys Thr Gly Lys Ala Ala Lys Val
      100      105      110
Lys Glu Leu Ile Gly Ser Arg Ala Ala Lys Lys
      115      120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 446:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 281 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(438285..439127)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 446:

```

Lys His Lys Lys Lys Glu Val Gln Gly His Ile Leu Ile Ser Ala Gly
1      5      10
Gln Leu Leu Ser Ala Lys Lys Ser Arg Glu Leu Ala Ser Cys Ser His
      20      25      30
Leu Val Leu Leu Cys Gly His Tyr Glu Gly Ile Asp Glu Arg Ala Leu
      35      40      45
Thr Ala Glu Val Asp Glu Glu Ile Ser Ile Gly Asp Tyr Val Leu Thr
      50      55      60
Asn Gly Cys Ala Ala Ala Leu Val Leu Val Asp Ala Leu Ala Arg Phe
65      70      75      80
Ile Pro Gly Ile Leu Gly Asn Gln Glu Ser Ala Glu Tyr Asp Ser Leu
      85      90      95
Glu Asn Gly Leu Leu Glu Gly Pro Gln Tyr Thr Arg Pro Arg Val Phe
      100      105      110
Glu Gly Glu Ser Val Pro Glu Val Leu Leu Cys Gly Asp His Gln Lys
      115      120      125
Ile Ala Asp Trp Arg Lys Gln Val Ser Leu Glu Arg Thr Arg Glu Arg
      130      135      140
Arg Pro Asp Leu Tyr Leu Gln Tyr Phe Tyr Gly Asn Ser Ala Cys Leu
145      150      155      160
Ser Thr Gln Glu Asp Leu Pro Arg Ile Glu Val Val Ser Pro Lys Thr
      165      170      175

```

```

Phe Ser Val Val Leu Glu Val Gln Asp Leu Arg Lys Ala Lys Lys Phe
              180              185              190
Tyr Ser Arg Met Phe Gly Lys Glu Cys Trp Asp Gly Asp Lys Leu Phe
              195              200              205
Leu Leu Gly Lys Thr Ser Leu Tyr Leu Gln Gln Thr Lys Glu Thr Arg
              210              215              220
Gly Pro Thr Thr Val Phe Ile Glu Leu Glu Thr Asp His Asp Phe Val
225              230              235              240
Arg Phe Leu Lys Arg Trp Glu Met Leu Gly Gly Glu Leu Gly Glu Gln
              245              250              255
Gly Thr Gly Gly Phe Pro Leu Arg Gln Val Phe Asp Leu Asp Gly His
              260              265              270
Ile Trp Val Val Ser Cys Val Gln Lys
              275              280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 447:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 118 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(438986..439339)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 447:

```

Met Glu Ile Asp Ile Leu Ser Leu Phe Pro Asp Tyr Phe Ala Ser Pro
1              5              10              15
Leu Gln Ala Thr Ile Leu Gly Arg Ala Ile Lys Gln Gly Ala Leu Ser
              20              25              30
Val Arg Ser Arg Asp Ile Arg Glu Phe Gly Leu Gly Lys Trp Lys Gln
              35              40              45
Val Asp Asp Ser Pro Tyr Asn Gly Glu Gly Met Leu Leu Met Ala Glu
50              55              60
Pro Val Val Gln Ala Ile Arg Ser Ile Arg Arg Lys Lys Ser Lys Val
65              70              75              80
Ile Tyr Leu Ser Pro Gln Asp Asn Phe Phe Pro Gln Arg Lys Val Val
              85              90              95
Asn Trp Arg Arg Val Arg Ile Trp Tyr Cys Tyr Val Asp Thr Met Arg
              100              105              110
Glu Leu Met Lys Gly Arg
              115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 448:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 115 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(439358..439702)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 448:

```

Ala Leu Lys Ile Arg Leu Arg Gln Gln Gly Arg Lys Asn His Val Val
1      5      10      15
Tyr Arg Leu Val Leu Ala Asp Val Glu Ser Pro Arg Asp Gly Lys Tyr
20      25      30
Ile Glu Leu Leu Gly Trp Tyr Asp Pro His Ser Glu Gln Asn Tyr Gln
35      40      45
Leu Lys Ser Glu Arg Ile Phe Tyr Trp Leu Asn Gln Gly Ala Glu Leu
50      55      60
Thr Glu Lys Ala Gly Ala Leu Val Lys Gln Gly Ala Pro Gly Val Tyr
65      70      75      80
Ala Glu Leu Met Ala Lys Lys Val Ala Arg Arg Ala Val Val Arg Gln
85      90      95
Lys Arg Arg Ala Tyr Arg Gln Arg Leu Ala Ala Arg Lys Ala Glu Ala
100      105      110
Ala Ala Lys
115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 449:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 448 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(439699..441042)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 449:

```

Met Ile Ser Ser Leu Ser Gln Lys Leu Ser Asn Ile Phe Ser Ser Leu
1      5      10      15
Phe Thr Ala Lys Arg Val Thr Glu Glu Gly Ile Ser Asp Ser Ile Arg
20      25      30
Glu Val Arg Leu Ala Leu Leu Asp Ala Asp Val Asn Tyr Gln Ala Val
35      40      45
Lys Asp Phe Ile Ala Lys Val Lys Gln Lys Val Val Gly Glu Glu Val
50      55      60
Trp Lys His Val Ser Pro Gly Gln Gln Phe Ile Lys Cys Leu His Glu
65      70      75      80
Glu Leu Ser Ser Ser Leu Ala Ser Glu Gln Thr Ala Val Ser Leu Arg
85      90      95
Gly Cys Pro Ala Val Ile Leu Leu Cys Gly Leu Gln Gly Ala Gly Lys
100      105      110
Thr Thr Thr Cys Ala Lys Leu Ala Asp Tyr Phe Leu Arg Glu Lys Lys
115      120      125
Ala Lys Lys Val Leu Val Ala Ser Cys Asp Leu Lys Arg Phe Ser Ala
130      135      140
Val Glu Gln Leu Glu Gly Leu Val Lys Gln Thr Gly Ala Asp Phe Phe
145      150      155      160
Arg Arg Glu Gly Asn Asp Pro Val Asp Met Ala Ala Glu Ala Val Gln
165      170      175
His Ala Lys Ser Gln Gly Tyr Asp Leu Val Leu Val Asp Thr Ala Gly
180      185      190

```



```

Arg Leu His Val Asp Asp Ala Leu Met Asp Glu Leu Val Ala Ile Ala
195 200 205
Arg Val Thr Ser Pro Cys Glu Thr Leu Phe Val Met Asn Leu Ala Met
210 215 220
Gly Gln Asp Ala Val Val Thr Ala Lys Ala Phe Asp Glu Arg Leu Gly
225 230 235 240
Leu Thr Gly Val Val Val Ser Met Ala Asp Gly Asp Ala Arg Ala Gly
245 250 255
Ala Val Leu Ser Val Lys Ser Leu Leu Asn Lys Pro Ile Lys Phe Glu
260 265 270
Gly Cys Gly Glu Lys Ile Lys Asp Leu Arg Pro Phe Asn Ala Gln Ser
275 280 285
Met Ala Glu Arg Ile Leu Gly Met Gly Asp Thr Ile Ser Leu Val Asp
290 295 300
Lys Met Arg Glu Cys Ile Ser Glu Glu Glu Asn Lys Glu Leu Glu Glu
305 310 315 320
Lys Leu Thr Lys Ala Thr Phe Thr Tyr Glu Asp Phe His Lys Gln Ile
325 330 335
Leu Ala Phe Arg Arg Leu Gly Pro Leu Arg Lys Ile Met Asn Met Met
340 345 350
Pro Ser Phe Gly Gly Ala Lys Pro Ser Asp Lys Asp Leu Glu Glu Ser
355 360 365
Glu Lys Gln Met Lys Arg Asn Glu Ala Ile Ile Leu Ser Met Thr Pro
370 375 380
Glu Glu Arg Lys Glu Leu Val Glu Leu Ser Met Ser Arg Met Lys Arg
385 390 395 400
Ile Ala Ala Gly Cys Gly Leu Thr Leu Gly Asp Val Asn Gln Phe Arg
405 410 415
Lys Gln Met Met Gln Ser Lys Lys Phe Lys Gly Met Thr Arg Glu
420 425 430
Lys Met Glu Gln Met Gly Lys Lys Met Ser Gly Gly Asn Leu Trp Arg
435 440 445

```

(2) INFORMATIONS POUR LA SEQ ID NO: 450:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 290 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(441042..441911)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 450:

```

Met Lys Lys Leu Leu Arg Glu Ala Ser Glu Tyr Leu Leu Ser Arg Gly
1 5 10 15
Ile Arg Phe Pro Gln Arg Glu Ala Glu Asp Ile Leu Met Asp Leu Leu
20 25 30
Glu Ile Ser Ser Arg Ser Ala Leu His Gln Ala Lys Leu Ser Ser Glu
35 40 45
Glu Gln Ser Leu Tyr Trp Lys Arg Leu Arg Lys Arg Gly Asp Arg Cys
50 55 60
Pro Thr Ala Tyr Ile His Gly Lys Val His Phe Leu Gly Val Glu Leu
65 70 75 80
Gln Val Thr Pro Gln Val Leu Ile Pro Arg Gln Glu Thr Glu Ile Phe

```



```

Thr Cys Gln Asp Glu Arg Ser Gln His Lys Asn Lys Ala Lys Ala Met
 130      135      140
Arg Val Leu Lys Ala Arg Ile Arg Asp Ala Glu Val Gln Lys Arg Ala
145      150      155      160
Gln Glu Ala Ser Ala Met Arg Ser Ala Gln Val Gly Ser Gly Asp Arg
      165      170      175
Ser Glu Arg Ile Arg Thr Tyr Asn Phe Pro Gln Asn Arg Val Thr Asp
      180      185      190
His Arg Ile Gly Leu Thr Leu Tyr Asn Leu Asp Arg Val Met Glu Gly
      195      200      205
Glu Leu Asp Met Ile Thr Thr Ala Leu Val Thr His Val His Arg Gln
      210      215      220
Leu Phe Gly His Glu Glu Thr Ala
225      230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 452:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 567 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 444688..446388

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 452:

```

Leu Phe Ala Lys Gln Ala Gln Ala Ile Gln Lys Arg Phe Pro Lys Ser
1      5      10      15
Lys Leu Arg Ala Thr Phe Asp Leu Ile Tyr Ala Leu Thr Phe Ala Ala
      20      25      30
Ile Leu Ala Phe Leu Ile Arg Gln Phe Trp Phe Glu Leu Tyr Glu Val
      35      40      45
Pro Thr Gly Ser Met Arg Pro Thr Ile Leu Glu Gln Asp Arg Ile Leu
      50      55      60
Val Ser Lys Thr Thr Phe Gly Leu Arg Leu Pro Phe Ser Asn Arg Ser
      65      70      75      80
Ile Gly Tyr Thr Pro Glu Ala Ile Thr Arg Gly Glu Leu Val Val Phe
      85      90      95
Thr Val Gly Asp Leu Pro Ile Pro Asn Ala Asp Thr Lys Tyr Phe Gly
      100      105      110
Ile Ile Pro Gly Lys Lys Arg Tyr Ile Lys Arg Cys Met Gly Lys Pro
      115      120      125
Gly Asp Thr Val Tyr Phe Tyr Gly Gly Lys Ile Tyr Gly Ile Asp Cys
      130      135      140
Asp Gly Glu Pro Ile Phe Pro Gln Asn Thr Glu Asn Xaa Tyr His Val
      145      150      155      160
Pro Tyr Ile Ser Phe Asp Gly Thr Pro Glu Ile Leu Thr His Ser Glu
      165      170      175
Glu Gln Thr Asp Val Ile Phe Asn Gln Phe His Thr Pro Cys Gly Lys
      180      185      190
Ile Ser Leu Pro Gln Gln Ala Ser Tyr Gly Gln Phe Phe Tyr Lys Asn
      195      200      205
Ala Trp His Asn Asp Thr Pro Tyr Ala Leu Lys Asp Pro His Asn Glu
      210      215      220
Pro Val Ser Tyr Ala Asp Leu Phe Gly Ile Lys Asn Phe Ala Met Val

```

```

225          230          235          240
Arg Ile Leu Thr Lys Lys Gln Ala Ala Leu Thr His Val Leu Pro Ser
          245          250          255
Pro Leu Ser Asp Thr Tyr Leu Glu Ile Ala His Thr Pro Asn Val Ser
          260          265          270
Tyr Xaa His Pro His Leu Arg Pro Phe Glu Thr Gln Arg Ile Pro Thr
          275          280          285
Ile Glu Pro Met Lys Thr Leu Leu Pro Leu Arg Lys Glu His Ile His
          290          295          300
Leu Ile Arg Asn Asn Leu Thr Thr Ser Arg Phe Thr Val Val Asp Gly
305          310          315          320
Tyr Ala Tyr Lys Tyr Gln Pro Ala Pro Met Asn Thr Ser Gly Met Val
          325          330          335
Arg Met Phe Ala Leu Pro Met Pro Asn Ile Pro Asp Gly Cys Tyr Glu
          340          345          350
Phe Ser Lys Gly Asp Val Phe Lys Ile Asn Met Gly Gly Phe Arg Thr
          355          360          365
Lys Leu Lys Gln Pro His Pro Leu Thr Gln Leu Ser Asn Ser Gln Val
          370          375          380
Ile Asp Leu Phe Asn Cys Gly Ile Ser Phe His Thr Ile Tyr Ile Pro
385          390          395          400
Lys Asn Pro Gln Tyr Ala Pro Phe Pro Asn Arg Tyr Ala Phe Phe Asn
          405          410          415
Gln Gly Asn Leu Phe Val Met Asp Ser Pro Val Phe Ile Asp Ser Asp
          420          425          430
Pro Ala Leu Gln Lys Phe Ile Val Ser Glu Glu Glu Lys Glu Leu Gln
          435          440          445
Ser Ser Glu Asp Lys Pro Tyr Ile Ala Phe Ile Asp Arg Gly Pro Pro
          450          455          460
Pro Glu Ser Thr Glu Glu Phe Val Ser Phe Ile Thr Asn Phe Gly Leu
465          470          475          480
Lys Ile Pro Glu Gly His Val Leu Val Leu Gly Asp Asn Cys Pro Met
          485          490          495
Ser Ala Asp Ser Arg Asp Phe Gly Phe Val Pro Val Glu Asn Leu Leu
          500          505          510
Gly Ser Pro Val Gly Ile Phe Trp Pro Ile Asn Arg Leu Gly Leu Leu
          515          520          525
Ser Ser Asn Ile Thr Pro Leu Ser Leu Pro Gly Tyr Leu Val Asn Gly
          530          535          540
Leu Ala Leu Gly Ala Phe Leu Tyr Cys Ile Gly Leu Trp Tyr Tyr Arg
545          550          555          560
Lys Asn His Arg Leu Phe Pro
          565

```

(2) INFORMATIONS POUR LA SEQ ID NO: 453:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 539 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(446452..448068)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 453:

Lys Leu Thr Arg Thr Gly Asn Leu Ser Glu Glu Ser Leu Met Phe Ser
 1 5 10 15
 Ile Val Gly Leu Ile Leu Glu Leu Cys His Met Leu Arg Ile Ile Thr
 20 25 30
 Leu Leu Lys Glu Gln Lys Lys Arg Arg Leu Cys Phe Pro Ala Asp Phe
 35 40 45
 Ile Ala Glu Gly Leu Asp Gln Thr Arg Gly Trp Phe Tyr Thr Leu Thr
 50 55 60
 Val Ile Ala Ala Ala Leu Phe Asp Gln Pro Ala Phe Lys Asn Val Ile
 65 70 75 80
 Val Asn Gly Ile Ile Leu Ala Glu Asp Gly Asn Lys Met Ser Lys Arg
 85 90 95
 Leu Asn Asn Tyr Pro Ser Pro Lys Met Ile Met Asp Ala Tyr Gly Ala
 100 105 110
 Asp Ala Leu Arg Leu Tyr Leu Leu Asn Ser Val Val Val Lys Ala Glu
 115 120 125
 Asp Leu Arg Phe Ser Asp Lys Gly Val Glu Ser Val Leu Lys Gln Val
 130 135 140
 Leu Leu Pro Leu Ser Asn Ala Leu Ala Phe Tyr Asn Thr Tyr Ala Glu
 145 150 155 160
 Leu Tyr Gly Phe Asp Pro Lys Glu Thr Asp Asn Ile Glu Leu Ala Glu
 165 170 175
 Ile Asp Arg Trp Ile Leu Ser Ser Leu Tyr Ser Leu Leu Gly Lys Thr
 180 185 190
 Arg Glu Ser Met Ser Gln Tyr Asp Leu His Ala Ala Val Asn Pro Phe
 195 200 205
 Val Asp Phe Ile Glu Asp Leu Thr Asn Trp Tyr Ile Arg Arg Ser Arg
 210 215 220
 Arg Arg Phe Trp Asp Ala Glu Asp Ser Thr Asp Arg Arg Ala Ala Phe
 225 230 235 240
 Ser Thr Leu Tyr Glu Val Leu Val Val Phe Ser Lys Val Ile Ala Pro
 245 250 255
 Phe Ile Pro Phe Ile Ser Glu Asp Met Tyr Gln Gln Leu Arg Gly Glu
 260 265 270
 Thr Asp Pro Glu Ser Val His Leu Cys Asp Phe Pro His Val Val Leu
 275 280 285
 Glu Lys Ile Leu Pro Asn Leu Glu Arg Lys Met Gln Asp Ile Arg Glu
 290 295 300
 Ile Val Ala Leu Gly His Ser Leu Arg Lys Glu His Lys Leu Lys Val
 305 310 315 320
 Arg Gln Pro Leu Gln Asn Val Tyr Ile Val Gly Ser Gln Glu Arg Met
 325 330 335
 Glu Ala Leu Ser Gln Val Gly Ser Leu Ile Gly Glu Glu Leu Asn Val
 340 345 350
 Lys Asp Val His Phe Cys Ser Glu Thr Pro Glu Tyr Val Thr Thr Leu
 355 360 365
 Ile Lys Pro Asn Phe Arg Thr Leu Gly Lys Lys Val Gly Asn Arg Leu
 370 375 380
 Pro Glu Ile Gln Arg Ala Leu Ala Gly Leu Pro Gln Glu Gln Ile Gln
 385 390 395 400
 Ala Phe Met His Lys Gly Gln Met Val Val Ser Leu Gly Glu Glu Thr
 405 410 415
 Ile Ser Leu Asp Lys Glu Asp Ile Thr Val Ser Trp Ala Ser Ala Glu
 420 425 430
 Gly Phe Val Ala Arg Ser Ser Ala Ser Phe Val Ala Val Leu Asp Cys
 435 440 445
 Gln Leu Thr Glu Pro Leu Ile Met Glu Gly Ile Ala Arg Glu Leu Val
 450 455 460
 Asn Lys Ile Asn Thr Met Arg Arg Asn Gly Lys Leu His Val Ser Asp


```

Ile Gly Gln Leu Ser Gly Lys Ser Leu Val Gly Gln Ser Tyr Glu Pro
    275                280                285
Leu Phe Pro Tyr Phe Gln Asp Lys Lys Glu Leu Gly Ala Phe Arg Ile
    290                295                300
Leu Pro Ala Asp Phe Ile Glu Glu Ser Glu Gly Thr Gly Ile Val His
    305                310                315                320
Met Ala Pro Ala Phe Gly Glu Ala Asp Phe Phe Ala Cys Gln Glu His
                325                330                335
Asn Val Pro Leu Val Cys Pro Val Asp Asn Gln Gly Cys Tyr Thr Ala
                340                345                350
Glu Val Lys Asp Phe Val Gly Glu Tyr Ile Lys Ser Ala Asp Lys Gly
    355                360                365
Ile Ala Arg Arg Leu Lys Asn Glu Asn Lys Leu Phe Tyr Gln Gly Thr
    370                375                380
Val Arg His Arg Tyr Pro Phe Cys Trp Arg Thr Asp Ser Pro Leu Ile
    385                390                395                400
Tyr Lys Ala Val Asn Ser Trp Phe Val Ala Val Glu Lys Val Lys Ser
                405                410                415
Lys Met Leu Lys Ala Asn Glu Ser Ile His Trp Thr Pro Gly His Ile
                420                425                430
Lys Gln Gly Arg Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp Trp Ala
    435                440                445
Ile Ser Arg Asn Arg Tyr Trp Gly Thr Pro Ile Pro Ile Trp Arg Ser
    450                455                460
Asp Asp Gly Glu Leu Leu Val Ile Gly Ser Ile Gln Glu Leu Glu Ala
    465                470                475                480
Leu Ser Gly Gln Lys Ile Val Asp Leu His Arg His Phe Ile Asp Glu
                485                490                495
Ile Glu Ile Asn Gln Asn Gly Lys Ser Phe Arg Arg Ile Pro Tyr Val
    500                505                510
Phe Asp Cys Trp Phe Asp Ser Gly Ala Met Pro Tyr Ala Gln Asn His
    515                520                525
Tyr Pro Phe Glu Arg Ala Glu Glu Thr Glu Ala Leu Leu Pro Ser
    530                535                540

```

(2) INFORMATIONS POUR LA SEQ ID NO: 455:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 450546..451076

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 455:

```

Lys Leu Tyr Leu Phe Lys Gly Val Phe Phe Val Tyr Val Phe Ser Asn
1          5          10          15
Thr Phe Phe Phe Met Gln His Ala His Asn Ala Asp Ser Phe Pro Ala
    20          25          30
Trp Asp Cys Leu Gln His Asn Tyr Leu Arg Arg Asn Ala Leu Thr Ser
    35          40          45
Phe Cys Ser Tyr Val Pro Ile Leu Ser Thr Val Val Gly Ile Arg Thr
    50          55          60
Leu Tyr Asn Met Arg Lys Leu His Gln Ala Phe Val Arg Arg Thr Gly

```

65				70				75				80			
Gly	Phe	Leu	Cys	Gln	Asn	Asp	Pro	Asn	Ile	Pro	Cys	Asn	Lys	Phe	Pro
				85				90						95	
Cys	Ser	Ile	Ile	Arg	Lys	Glu	Trp	Pro	Gln	Val	His	Thr	Lys	Ala	Met
			100					105						110	
Gln	Glu	Val	Phe	Gly	Ile	Lys	Ala	Leu	Val	Cys	Leu	Gly	Ser	Leu	Ile
		115					120					125			
Leu	Lys	Ile	Phe	Arg	Ala	Val	Lys	Ala	Phe	Phe	His	Arg	Thr	Phe	Ser
	130					135					140				
Pro	Ser	Leu	Leu	Pro	Glu	Gln	Asp	Ala	Ser	Ile	Gln	Leu	Pro	Asp	Ser
145					150					155					160
Pro	Gln	Ser	Gly	Ile	Pro	Glu	Glu	Thr	Leu	Ser	Glu	Thr	Pro	Arg	Ser
				165					170					175	

Ser

(2) INFORMATIONS POUR LA SEQ ID NO: 456:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 160 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(451144..451623)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 456:

Lys	Asn	Lys	Arg	Leu	Gln	Arg	Phe	Leu	Phe	Leu	Leu	Pro	Ala	Val	Val
1				5				10						15	
Thr	Glu	Leu	Ala	Gln	Asp	Leu	Ser	Ser	Val	Lys	Gly	Ser	Leu	Leu	Ser
			20					25					30		
His	Tyr	Ile	Arg	Lys	Lys	Gly	Phe	Val	Lys	Ala	Ser	Pro	Val	Ile	Glu
		35					40					45			
Gly	Arg	Glu	Ser	Phe	Glu	Arg	Ser	Leu	Phe	Ala	Val	Trp	Val	Ser	Leu
	50					55					60				
Gln	Pro	Glu	Glu	Ile	Arg	His	Gln	Leu	Thr	Met	Glu	Ser	Phe	Tyr	Arg
65					70					75				80	
Asp	Glu	Gln	Lys	Lys	Lys	Arg	Val	Leu	Thr	Gly	Glu	Leu	Glu	Val	Tyr
			85						90					95	
Pro	His	Ile	Val	Lys	Asn	Asn	Pro	Gly	Asp	Tyr	Leu	Leu	Lys	Asn	Gly
			100					105					110		
Glu	Asp	Val	Val	Ala	Phe	Val	Tyr	Ala	Thr	Ser	Ile	Asp	Leu	Ser	Lys
		115						120				125			
Trp	Leu	Gly	Lys	Pro	Val	Val	Leu	Glu	Cys	Val	Ser	Arg	Pro	Asn	Asn
	130					135					140				
His	Phe	Ala	Phe	Pro	Ala	Tyr	Ile	Val	Leu	Ser	Val	Lys	Glu	Gly	Ala
145					150					155					160

(2) INFORMATIONS POUR LA SEQ ID NO: 457:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 359 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(451517..452593)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 457:

```

Lys Ile Glu Gln Ser Arg Leu Thr Phe Ser Phe Lys Ser Ile Ile Ile
1      5      10      15
Pro Ser Leu Glu Asp Glu Ser Ser Arg Ala Val Asn Ala Ser Leu Glu
20      25      30
Ala Gln Ile Leu Ala Asn Cys Arg Ser Phe Cys Val Arg Thr Leu Ser
35      40      45
Ile Ser Met Leu Ile Phe Ala Leu Ser Cys Gly Ala Asp Ala Cys Leu
50      55      60
Cys Ala Ala Asp Leu Ser Lys Ala Lys Val Glu Ala Ser Val Gly Asp
65      70      75      80
Arg Ala Ala Phe Ser Pro Phe Thr Gly Glu Ile Lys Gly Asn Arg Val
85      90      95
Arg Leu Arg Leu Ala Pro His Thr Asp Ser Phe Ile Ile Lys Glu Leu
100     105     110
Ser Lys Gly Asp Cys Leu Ala Val Leu Gly Glu Ser Lys Asp Tyr Tyr
115     120     125
Val Val Ala Ala Pro Glu Gly Val Arg Gly Tyr Val Phe Arg Thr Phe
130     135     140
Val Leu Asp Asn Val Ile Glu Gly Glu Lys Val Asn Val Arg Leu Glu
145     150     155     160
Pro Ser Thr Ser Ala Pro Ile Leu Ala Arg Leu Ser Lys Gly Thr Val
165     170     175
Val Lys Thr Leu Gly Ala Ala Gln Gly Lys Trp Ile Glu Ile Ala Leu
180     185     190
Pro Lys Gln Cys Val Phe Tyr Val Ala Lys Asn Phe Val Lys Asn Val
195     200     205
Gly Ala Leu Asp Leu Tyr Asn Gln Lys Glu Gly Gln Lys Lys Leu Ala
210     215     220
Leu Asp Leu Leu Ser Ser Ala Met Asp Phe Ala Asp Ala Glu Leu Gln
225     230     235     240
Lys Lys Ile Glu Asp Ile Asp Leu Asp Ala Ile Tyr Lys Lys Met Asn
245     250     255
Leu Ala Gln Ser Glu Glu Phe Lys Asp Val Pro Gly Leu Gln Ser Leu
260     265     270
Val Gln Lys Ala Leu Glu Arg Phe Gln Glu Ala Phe Leu Ala Lys Ser
275     280     285
Leu Glu Lys Ser Ala Val Lys Val Pro Gly Ile Gln His Lys Val Leu
290     295     300
Glu Xaa Ile Ala Val Val Ser Pro Ala Val Glu Glu Thr Pro Val Val
305     310     315     320
Thr Lys Ile Glu Glu Gln Lys Val Thr Thr Val Pro Val Pro Ala Pro
325     330     335
Ser Cys Cys Tyr Arg Ala Gly Ser Arg Phe Lys Leu Cys Gln Arg Phe
340     345     350
Phe Ile Ile Ala Leu Tyr Pro
355

```

(2) INFORMATIONS POUR LA SEQ ID NO: 458:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 188 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(452632..453195)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 458:

```

Gly Gln Ala Ile Val Asp Glu Val Phe Gln Glu His Leu Leu Tyr Leu
1          5          10          15
Glu Ser Thr Ala Pro Gln Lys Asn Lys Glu Glu Glu Lys Ile Ser Ser
20          25          30
Leu Leu Gly Ala Ile Gln Gln Met Ala Asn Gly Cys Glu Val Gln Val
35          40          45
Phe Ser Gln Lys Gly Leu Val Ser Met Leu Leu Gly Gly Ala Gly Ser
50          55          60
Ile Asn Met Leu Leu Gln His Ser Pro Glu His Lys Asp His Pro Asp
65          70          75          80
Leu Pro Thr Asp Leu Leu Glu Arg Ile Ala Gln Met Met Arg Ser Leu
85          90          95
Ser Ile Gly Pro Thr Ser Ile Leu Ala Lys Pro Glu Pro His Cys Asn
100         105         110
Cys Leu His Cys Gln Ile Gly Arg Ala Thr Val Glu Glu Glu Asp Ala
115         120         125
Gly Val Ser Asp Glu Asp Leu Thr Xaa Arg Ser Trp Asp Ile Ser Gln
130         135         140
Ser Gly Glu Lys Met Tyr Xaa Val Thr Asp Pro Leu Asn Pro Glu Glu
145         150         155         160
Gln Phe Asn Val Tyr Leu Xaa Thr Pro Ile Gly Cys Thr Cys Gly Gln
165         170         175
Pro Tyr Cys Glu His Val Lys Ala Val Leu Tyr Thr
180         185

```

(2) INFORMATIONS POUR LA SEQ ID NO: 459:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 434 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 453567..454868

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 459:

```

Met Lys Lys Thr Ser Val Ile Asp Thr Ser Val Leu Ile Tyr Asp Pro
1          5          10          15
Lys Ala Leu Ser Ser Phe Ser Asn Thr Arg Ile Ile Ile Pro Phe Thr
20          25          30
Val Ile Glu Glu Leu Glu Ser Cys Ala Lys Phe Arg Asp Glu Ser Gly
35          40          45
Lys Asn Ala Ser Arg Ala Leu Ser Asn Ile Arg Leu Leu Glu Gln
50          55          60

```

```

Ser Glu Arg Pro Ser Ser Gly Gln Ile Leu Leu Lys Asn Gly Ser Glu
65          70          75          80
Leu Cys Ile Glu Val Ser Pro Leu Val Asn Leu Ser Asn His Glu Lys
          85          90          95
Gln Lys Lys His Leu Thr Leu Glu Leu Leu Gln Ile Ile Ser Gln Arg
          100          105          110
Glu Pro Val Val Phe Val Thr Lys Ser Leu Gly Arg Arg Val His Ala
          115          120          125
Glu Ala Leu Gly Ile Glu Ala Lys Asp Tyr Glu Asn Lys Cys Val Ser
          130          135          140
Phe Arg Ser Leu Tyr Arg Gly His Arg Lys Leu Lys Val Ala Asn Ser
145          150          155          160
Thr Ile Glu Tyr Phe Tyr Lys Asp Gly Ser Ile Ala Phe Pro Ser Asp
          165          170          175
Leu Ser Pro Leu Pro Ser Pro Asn Glu Tyr Phe Phe Leu Ser Gly Asp
          180          185          190
Ser Asp Asn Tyr Ser Ala Val Gly Arg Tyr Ser Ser Lys Asp Asn Lys
          195          200          205
Ile Leu Ser Leu Lys Pro Ala Pro Glu Lys Ile Trp Gly Val Lys Pro
210          215          220
Leu Asn Ile Glu Gln Arg Cys Ala Leu Asp Leu Leu Arg Asp Asp
225          230          235          240
Ile Lys Leu Val Thr Leu Met Gly Gln Ala Gly Ser Gly Lys Thr Ile
          245          250          255
Leu Ala Leu Ala Ala Ala Met Tyr Gln Val Phe Glu Lys Pro Lys Tyr
          260          265          270
Asn Lys Leu Leu Val Ser Arg Pro Ile Ile Pro Met Gly Lys Asp Ile
          275          280          285
Gly Phe Leu Pro Gly Ile Lys Glu Ala Lys Leu Met His Trp Met Gln
290          295          300
Pro Ile Tyr Asp Asn Met Glu Phe Leu Phe Asp Val Asn Asn Met Gly
305          310          315          320
Asp Phe Ser Glu Thr Leu His Ser Leu Met Glu Thr Lys Lys Leu Glu
          325          330          335
Met Glu Ala Leu Thr Tyr Ile Arg Gly Arg Ser Leu Pro Lys Val Phe
          340          345          350
Met Ile Ile Asp Glu Ala Gln Asn Leu Thr Pro His Glu Ile Lys Thr
          355          360          365
Ile Ile Ser Arg Ala Gly Lys Gly Thr Lys Ile Val Leu Thr Gly Asp
          370          375          380
Pro Thr Gln Ile Asp Ser Leu Tyr Phe Asp Glu Asn Ser Asn Gly Leu
385          390          395          400
Thr Tyr Leu Val Gly Lys Phe His His Leu Pro Leu Tyr Gly His Met
          405          410          415
Phe Met Thr Arg Thr Glu Arg Ser Glu Leu Ala Ala Ala Ala Ala Thr
          420          425          430
Ile Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 460:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 153 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(454972..455430)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 460:

```

Ile Phe Leu Tyr Val Leu Ser Ser Tyr Leu Val Leu Tyr Leu Ser Leu
1      5      10      15
Leu Ile Ala Thr Ile Leu Gly Met Pro Gln Thr Leu Gly Val Cys Cys
      20      25      30
Arg Ile Glu Gly Ala Pro Gly Met Pro Ala Tyr Pro Leu Ile Ile Leu
      35      40      45
Leu Ser Val Val Thr Leu Ser Cys Cys Tyr Ala Glu Lys Arg Ala Val
      50      55      60
Ser Ile Gly Lys Tyr Gly Lys Ala Phe Val Leu Ser Cys Ile Asn Leu
      65      70      75      80
Leu Ser Pro Ile Leu Ala Tyr Asn Ile Leu Leu Phe Pro Asn Leu Leu
      85      90      95
Val Ser Thr Val Asp Asn Arg Tyr Thr Met Thr Val Phe Asn Ala Ala
      100      105      110
Ala Glu Thr Arg Thr Leu Gln His Leu Val Thr Ile Val Leu Ile Gly
      115      120      125
Leu Pro Phe Val Val Ala Tyr Ala Ile Tyr Ile Tyr Arg Val Phe Arg
      130      135      140
Gly Lys Thr Asp Phe Pro Ser Ile Tyr
      145      150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 461:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 222 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(455367..456032)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 461:

```

Met Glu Phe Ser Leu Ala Thr Ile Leu Pro Val Val Trp Tyr Val Ile
1      5      10      15
Leu Cys Ile Ala Val Phe Ala Tyr Ser Leu Gly Asp Gly Phe Asp Leu
      20      25      30
Gly Leu Ser Thr Ile Tyr Phe Leu Ser Lys Asp Glu Lys Glu Arg Arg
      35      40      45
Leu Leu Leu Asn Ser Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp
      50      55      60
Phe Val Ile Met Phe Ala Gly Leu Phe Ala Gly Phe Pro Thr Ala Tyr
      65      70      75      80
Gly Thr Leu Leu Ser Ile Phe Tyr Met Pro Ile Trp Xaa Met Val Met
      85      90      95
Leu Tyr Ile Phe Arg Gly Cys Ser Leu Glu Phe Arg Ser Lys Ala Glu
      100      105      110
Ser Asn Arg Trp Lys Leu Phe Trp Asp Val Leu Phe Ser Ile Ser Gly
      115      120      125
Met Ser Ile Ser Phe Phe Leu Gly Thr Leu Ala Gly Asn Leu Leu Val
      130      135      140

```

```

Gly Phe Pro Ile Ala Pro Asp Thr Ser Tyr Ser Ser Leu Ser Trp Lys
145          150          155          160
Leu Phe Phe Arg Pro Tyr Gln Val Leu Cys Gly Leu Phe Val Val Ala
          165          170          175
Ala Phe Ala Leu His Gly Ile Ser Phe Ala Leu Met Lys Thr Thr Glu
          180          185          190
Gly Leu His Glu Arg Leu Lys Asn Lys Phe Ser Phe Met Phe Cys Leu
          195          200          205
Val Thr Trp Phe Cys Ile Phe Pro Cys Ser Leu Arg Leu Phe
          210          215          220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 462:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 446 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(456047..457384)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 462:

```

Met Ser Ala Glu Ile Leu Ala Arg Val Gln Phe Ala Leu Phe Ile Gly
1          5          10          15
Phe His Tyr Leu Phe Val Pro Ile Ser Leu Gly Leu Ser Ile Met Ile
          20          25          30
Val Leu Met Glu Gly Leu Tyr Leu Phe Thr Lys Lys Ser Ile Tyr Lys
          35          40          45
Gln Leu Thr Trp Phe Trp Ile Lys Ile Phe Thr Leu Thr Phe Val Val
          50          55          60
Gly Val Val Thr Gly Leu Met Gln Ile Phe Ser Phe Gly Ala Asn Trp
65          70          75          80
Ser Arg Phe Ala Glu Tyr Thr Gly Asn Val Phe Gly Met Phe Leu Gly
          85          90          95
Ser Glu Gly Met Phe Ala Phe Phe Leu Glu Ser Gly Phe Leu Gly Val
          100          105          110
Leu Leu Phe Gly Arg Tyr Lys Val Ser Lys Lys Met His Phe Phe Ser
          115          120          125
Ala Cys Met Val Ala Leu Gly Ala His Met Ser Ala Phe Trp Ile Val
          130          135          140
Cys Ala Asn Ser Trp Met Gln Thr Pro Ser Gly Tyr Glu Met Val Met
145          150          155          160
Arg Asn Gly Met Leu Val Pro Gln Met Thr Ser Phe Trp Ala Ala Val
          165          170          175
Leu Ser Pro Ser Ala Leu Gln Arg Phe Thr His Val Val Leu Gly Ala
          180          185          190
Trp Leu Ser Gly Ile Phe Leu Val Leu Ser Val Ser Ala His Tyr Leu
          195          200          205
Arg Lys Glu Arg His Lys Asp Phe Ala Asn Gln Gly Leu Lys Ile Ser
          210          215          220
Met Phe Cys Ala Phe Leu Val Leu Ala Leu Gln Leu Trp Ser Ala Asp
225          230          235          240
Val Thr Ala Arg Gly Val Ala Lys His Gln Pro Ala Lys Leu Ala Ala
          245          250          255
Phe Glu Gly Val Phe Lys Thr Gln Glu His Thr Pro Ile Tyr Leu Leu

```

Gly Ile Val Asp Met Lys Lys Glu Arg Val Ile Gly Ile Pro Ile Pro
 260 265 270
 Ser Gly Leu Ser Leu Leu Val His Arg Asn Ala Lys Thr Pro Val Thr
 275 280 285
 Gly Leu Asp Gln Phe Pro Lys Asp Glu Trp Pro Asn Val Ala Phe Val
 290 295 300
 Phe Gln Thr Tyr His Leu Met Val Met Leu Trp Gly Val Met Val Leu
 305 310 315 320
 Leu Ala Leu Ile Ala Phe Ala Val Tyr Lys Lys Lys Ser Trp Ser Cys
 325 330 335
 Lys Lys Gly Ile Leu Trp Ile Leu Ser Leu Ser Val Leu Phe Pro Glu
 340 345 350
 Leu Cys Asn Glu Ile Gly Trp Ile Ser Thr Glu Val Gly Arg Gln Pro
 355 360 365
 Trp Val Val Tyr Gly Leu Lys Thr Lys Asp Ala Thr Ser Pro Ile
 370 375 380
 Val Asn Ala Gly Gln Ile Trp Gln Ser Leu Ile Leu Phe Ser Ile Ile
 385 390 395 400
 Phe Ile Cys Leu Leu Ser Val Phe Val Ser Leu Leu Leu Lys Lys Ile
 405 410 415
 Gly Glu Gly Pro Asp Glu Gln Asp Leu Ile Glu Val Asp Leu
 420 425 430
 435 440 445

(2) INFORMATIONS POUR LA SEQ ID NO: 463:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 457659..458450

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 463:

Met Phe Val Gly Ile Thr Tyr Tyr Thr Thr Pro Leu Leu Glu Ile Ala
 1 5 10 15
 Leu Ile Trp Val Val Leu Asn Tyr Leu Leu Lys Phe Phe Trp Gly Thr
 20 25 30
 Gly Ala Met Asp Leu Val Phe Gly Leu Leu Ser Phe Leu Cys Leu Phe
 35 40 45
 Val Leu Ala Glu Lys Leu His Leu Pro Val Ile Arg Asn Leu Met Leu
 50 55 60
 His Val Val Asn Ile Ala Ala Ile Val Val Phe Ile Ile Phe Gln Pro
 65 70 75 80
 Glu Ile Arg Leu Ala Leu Ser Arg Ile Arg Leu Arg Arg Gly Lys Phe
 85 90 95
 Val Ile Asn Met Gln Asp Glu Phe Ile Asp His Leu Thr Ala Cys Ile
 100 105 110
 Tyr Arg Met Ala Glu Arg Gln Ile Gly Ala Leu Ile Val Leu Glu Asn
 115 120 125
 Glu Arg Leu Leu Asn Asp Leu Leu Asn Leu Ser Ala Val Lys Ile Asn
 130 135 140
 Ala Asp Phe Ser Glu Glu Leu Leu Glu Ala Ile Phe Glu Pro Ser Ser
 145 150 155 160

```

His Leu His Asp Gly Ala Val Leu Met Arg Gly Glu Thr Ile Ser Tyr
      165      170      175
Ala Arg Val Ile Leu Pro Leu Ala His Asp Thr Thr Gln Leu Ser Arg
      180      185      190
Ser Met Gly Thr Arg His Arg Ala Ala Leu Gly Ala Ser Gln Arg Thr
      195      200      205
Asp Ala Leu Val Ile Val Val Ser Glu Glu Thr Gly Ala Val Ser Leu
      210      215      220
Ala Arg Asp Gly Ile Leu Thr Arg Gly Val Lys Met Asp Arg Phe Lys
      225      230      235      240
Ala Ile Leu Arg Ser Ile Leu Thr Arg Asn Glu Arg Lys Thr Asn Pro
      245      250      255
Ile Ile Ser Trp Met Arg Lys Lys
      260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 464:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 375 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 458508..459632

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 464:

```

Val Leu Pro Leu Leu Ser Gly Arg Leu Gln Ile Lys Ser Ile Thr Ile
1      5      10      15
Thr Arg Thr Phe His Asn Ile Pro Val Arg Val Ile Asp Leu Ala Pro
      20      25      30
Glu Gln Thr Val Ile Gly Leu Gln Ala Asn Gly Leu Leu Lys Lys Lys
      35      40      45
Val Ala Met Met Ile Thr Gly Asn Lys Ser Val Val Glu Lys Leu Arg
      50      55      60
Pro Ser Asn Leu Glu Ile Val Ile Ser Ala Lys Gly Arg Thr Glu Ser
      65      70      75      80
Trp Ile Glu Thr Ile Asp Pro Tyr Asn Leu Val Cys Leu Asp Thr Asp
      85      90      95
Ile His Leu Arg Lys Asn Ile Lys Ser Val Thr Ser Glu Asp Ile Phe
      100      105      110
Ile Arg Leu Thr Gln Phe Val Thr Glu Asp Val Ser Val Thr Ile Thr
      115      120      125
Lys Pro Ile Gly Arg Ala Pro Lys Gly Tyr Glu Tyr Leu Asp Thr Trp
      130      135      140
Pro Lys Tyr Leu Val Gln Lys Val Ser Gly Pro Lys Glu Tyr Val Ser
      145      150      155      160
Ser Leu Lys Asp His Gly Leu Glu Leu Thr Phe Asn Leu Asn Lys Val
      165      170      175
Ser Phe Glu Glu Leu Asp Arg Asn Arg Leu Ala Gln Gly Asn Leu Asp
      180      185      190
Glu Val Val Tyr Leu Val Pro Glu Asp Trp Lys Lys Val Tyr Ile Pro
      195      200      205
Phe Asp Asn Ser Tyr Met Glu Leu Asn Asp Pro Gln Ala Asp Phe Leu
      210      215      220
Arg Leu Leu Phe Leu Lys Gln Glu Phe Ile Pro Leu Asn Ile Asn Leu

```



```

Ile Val Pro Pro Gln Asn Ala Ile Asn Gln Ala Leu Arg Ala Leu His
      195      200      205
Arg Gly Glu Val Val Gly Ile Val Gly Asp Gln Val Leu Leu Ser Ser
      210      215      220
Glu Tyr Ser Tyr Pro Leu Phe Gly Ser Gln Ala Phe Thr Thr Thr Ser
225      230      235      240
Pro Ala Leu Leu Ala Tyr Lys Thr Lys Lys Thr Val Ile Ala Val Ala
      245      250      255
Ile Tyr Arg Lys Pro Asn Gly Asn Tyr Leu Val Val Pro Ser Lys Ala
      260      265      270
Phe His Ala Asn Thr Glu Leu Ser Ile Arg Glu Ser Thr Glu Gln Leu
      275      280      285
Met Asp Arg Leu Met Arg Phe Leu Glu Lys Gly Ile Thr Cys Lys Pro
      290      295      300
Glu Gln Trp Leu Trp Leu His Lys Arg Trp Lys Arg Lys Leu Arg His
305      310      315      320
Lys Phe Lys Arg Arg Tyr Ala Phe Ser His Ile Leu Ile Ile Val Lys
      325      330      335
Gly Thr Ser Leu Gln Ala Leu Gln Arg Phe Leu Ile Glu Phe Gly Glu
      340      345      350
Phe Tyr Ala Asp Ala Ser Leu Ser Leu Ala Ile Ile Gly Ala Thr Asp
      355      360      365
Thr Val Leu Ala Asn Ser Phe Ala Pro Tyr Ser Leu Gln Phe Phe Ser
      370      375      380
Ser Glu Glu Glu Leu Leu Ala Ala Pro Asn Phe Phe Pro Ala Ile Val
385      390      395      400
Asp Leu Phe Gly Leu Ser Arg Lys Thr Arg Leu His Tyr Lys Arg Thr
      405      410      415
Gly Ser Arg Lys Ile Phe Thr Arg Asn Glu Leu Lys Asp Ser Leu Leu
      420      425      430
Gln Lys Gln Ser Leu Ile Gln Ser Phe His Lys Leu Leu Arg Arg Val
      435      440      445
Asp Thr Arg Ser Arg Lys Gly
450      455

```

(2) INFORMATIONS POUR LA SEQ ID NO: 466:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 143 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(461196..461624)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 466:

```

Met Ser Glu His Val His Lys Glu Leu Leu His Leu Gly Glu Val Phe
1      5      10      15
Arg Ser Gln Arg Glu Glu Arg Ala Leu Ser Leu Lys Asp Val Glu Ala
      20      25      30
Ala Thr Ser Ile Arg Leu Ser Ala Leu Glu Ala Ile Glu Ala Gly His
      35      40      45
Leu Gly Lys Leu Ile Ser Pro Val Tyr Ala Gln Gly Phe Met Lys Lys
50      55      60
Tyr Ala Ala Phe Leu Asp Met Asp Gly Asp Arg Leu Leu Lys Glu His

```

(2) INFORMATION POUR LA SEQ ID NO: 467:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(A) LONGUEUR: 245 cm
(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 461887..462621

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 467:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 468:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 288 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(462895..463758)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 468:

Trp	Ser	Gly	Met	Leu	Lys	Val	Leu	Phe	His	Thr	Met	Thr	Leu	Phe	Gly	1	5	10	15
His	Leu	Leu	Ser	Thr	Pro	Ile	Tyr	Ile	Val	Gly	Asp	Ala	Cys	Gly	Lys	20	25	30	
Asp	Arg	Asp	Glu	Tyr	Lys	Asn	Pro	Leu	Arg	Ala	Phe	Ser	Phe	Glu		35	40	45	
Ser	Gln	Phe	Leu	Gln	Ile	Glu	Asn	Ala	Lys	Phe	Lys	Thr	Leu	Pro	Asp	50	55	60	
Gln	Ser	Leu	Gly	Tyr	Arg	Gln	Ala	Asp	Thr	Ser	Leu	Phe	Ala	Thr	Ile	65	70	75	80
Pro	Val	Thr	Glu	Met	Ser	Gly	Phe	Leu	Leu	Ser	Ser	Arg	Tyr	Leu	Gly	85	90	95	
Ala	Glu	Val	Ser	Trp	Lys	Ser	Ser	Lys	Glu	Leu	Gln	Asp	Thr	Asp	Pro	100	105	110	
Gln	Ala	Val	Gly	Tyr	Phe	Ala	Phe	Gln	Asp	Lys	Ser	Phe	Tyr	Gln	Tyr	115	120	125	
Ile	Thr	Leu	Ser	Val	Gly	Ala	Tyr	Thr	Leu	Ala	Leu	Thr	Asn	Trp	Gln	130	135	140	
Trp	Ser	Val	Leu	Phe	Ser	Gly	Met	Val	Asp	Pro	Glu	Asn	Ile	Glu	Ile	145	150	155	160
Gly	Ser	Gly	Leu	Tyr	Gln	Val	Val	Leu	Ser	Ser	Lys	Tyr	His	Ala	Ser	165	170	175	
Lys	Ser	Leu	Ser	Val	Ile	Met	Gly	Val	Ile	Asn	Glu	Val	Gly	Leu	His	180	185	190	
Asp	Lys	Gln	Ala	Trp	Pro	Leu	Leu	Gly	Phe	Ser	Tyr	Lys	Pro	Glu	Asp	195	200	205	
Arg	Leu	Thr	Leu	Asn	Cys	Ile	Tyr	Pro	Val	Asn	Phe	Ser	Ala	Glu	Tyr	210	215	220	
Gln	Cys	Thr	Pro	Val	Cys	Asp	Leu	Gly	Val	Ala	Tyr	Arg	Leu	Thr	Arg	225	230	235	240
Leu	Arg	Lys	Lys	Phe	Pro	Lys	Asn	Ser	Leu	Ala	Thr	Ser	Glu	Gly	Ile	245	250	255	
Phe	Glu	Tyr	Ser	Gly	Arg	Glu	Ile	Glu	Gly	Asn	Ile	Lys	Leu	Ile	Phe	260	265	270	
Trp	Pro	Gly	Gln	Asn	Leu	Lys	Met	Phe	Gly	Gly	Tyr	Phe	Arg	Arg	Glu	275	280	285	

(2) INFORMATIONS POUR LA SEQ ID NO: 469:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 464048..464629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 469:

His	Leu	Val	Gly	Lys	Met	Pro	Ser	Thr	Val	Ala	Pro	Ile	Lys	Gly	Gln
1				5					10					15	
Asp	His	Phe	Leu	Asn	Leu	Val	Phe	Pro	Glu	Arg	Val	Ala	Ala	Ala	Tyr
			20					25					30		
Met	Ser	Pro	Leu	Ala	Gln	Lys	Tyr	Pro	Lys	Ala	Ala	Leu	Ser	Ile	Ala
		35					40					45			
Ser	Leu	Ala	Gly	Phe	Leu	Leu	Gly	Ile	Leu	Lys	Leu	Ile	Thr	Phe	Pro
	50				55						60				
Val	Leu	Cys	Ala	Ala	Gly	Leu	Phe	Val	Phe	Pro	Ile	Arg	Gly	Leu	Ile
65					70					75				80	
Ser	Cys	Leu	Phe	His	Lys	Ser	Phe	Gln	Gly	Cys	Ser	Gly	Tyr	Val	Leu
				85				90					95		
Ala	Thr	Phe	Leu	Ser	Leu	Phe	Ser	Leu	Ala	Leu	Thr	Ile	Val	Gly	Ile
			100				105					110			
Val	Ser	Cys	Ile	Thr	Trp	Ala	Pro	Gly	Phe	Ile	Phe	Pro	Met	Ile	Ser
		115				120						125			
Val	Ser	Ile	Ala	Phe	Ala	Thr	Val	Glu	Thr	Cys	Phe	Gln	Ile	Tyr	Thr
		130				135					140				
His	Leu	Phe	Pro	Ala	Leu	Glu	His	Lys	Pro	Ser	Ser	Ser	Leu	Lys	Ile
145					150				155					160	
Glu	Ile	Ala	Ala	Ala	Lys	Leu	Pro	Arg	Ser	Ser	Ser	Ala	Pro	Asp	Leu
				165				170					175		
Asn	Cys	Pro	Ser	Leu	Pro	Thr	Gln	Ser	Ala	Ser	Pro	Ser	Gln	Arg	Phe
				180			185						190		
Ser	Ala														

(2) INFORMATIONS POUR LA SEQ ID NO: 470:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 376 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 464721..465848

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 470:

Ile	Leu	Val	Leu	Ser	Val	Phe	Cys	Phe	Trp	Asp	Asn	Phe	Met	Thr	Pro
1				5					10					15	
Val	Thr	Pro	Val	Pro	Pro	Gln	Ser	Pro	Gln	Gln	Val	Lys	Gly	Leu	Leu
			20					25					30		
Ser	Arg	Phe	Leu	Thr	Ala	Pro	Asp	Arg	His	Pro	Lys	Leu	Arg	Tyr	Val
		35				40						45			
Tyr	Asp	Ile	Ala	Leu	Ile	Ala	Ile	Ser	Ile	Leu	Cys	Ile	Val	Ser	Ile
	50				55					60					
Ile	Leu	Trp	Thr	Gln	Gly	Ser	Gly	Leu	Ala	Leu	Phe	Ala	Ile	Ala	Pro
65				70				75						80	

```

Ala Leu Ala Ile Gly Ala Leu Gly Val Thr Leu Leu Val Ser Asp Leu
      85                      90                      95
Ala Glu Ser Gln Lys Ser Lys Glu Ile Ala Asp Thr Val Ala Ala Val
      100                    105                    110
Ser Leu Pro Phe Ile Leu Thr Gly Thr Ala Ala Gly Leu Met Phe Ser
      115                    120                    125
Ala Ile Ala Val Gly Lys Gly Ala Val Ile Leu Ala Asn Pro Leu Phe
      130                    135                    140
Leu Met Gly Ser Met Thr Leu Gly Phe Ala Leu Met Ser Leu His Arg
      145                    150                    155
Val Thr Tyr Gln Tyr Leu Ser Asn Arg Glu Gln Trp Lys Gln Gln Lys
      165                    170                    175
Lys Leu Glu Gln Val Glu Leu Ala Ala Trp Glu Ser His Leu Pro Lys
      180                    185                    190
Glu Ser Lys Ser Ser Ala Leu Glu Glu Val Arg Tyr Ser Pro Arg Leu
      195                    200                    205
Met Lys Arg Gly Lys Thr Trp Arg Lys Arg Ala Ile Arg Arg Lys Asn
      210                    215                    220
Tyr Ile Pro Ile Pro Leu Val Asp Lys Thr Leu Gln Thr Met Gln Pro
      225                    230                    235
Asp Ala Leu Phe Ser Ser Thr Thr Thr His Ser Thr Asp Ser Glu Gln
      245                    250                    255
Ile Leu Thr Ser Val Ser Pro Gln Ser Ser Asp Thr Glu Ser Ser Ser
      260                    265                    270
Ser Ser Ser Phe His Thr Pro Pro Asn Ser Asp Lys Glu Leu Ser Asp
      275                    280                    285
Ser Asn Ser Ser Asp Ser Ser Ser Ser Ser Glu Tyr Met Asp Ala Leu
      290                    295                    300
Glu Thr Val Ala Ala Gly Asp Val Ser Gly Ile Thr Pro Pro Ser Lys
      305                    310                    315
Pro Ser Ser Ser Pro Lys Thr Thr Arg Arg Val Val Lys Leu Ser Arg
      325                    330                    335
Ser Glu Arg Asn Ala Gln His His Arg Asn Lys Asp Gln Glu Gln Arg
      340                    345                    350
Gln Asp Ser Ser Glu Ser Ser Asp Glu Glu Ser Ser Ser Asp Ser Ser
      355                    360                    365
Gln Lys Lys Lys Pro Ser Arg Lys
      370                    375

```

(2) INFORMATIONS POUR LA SEQ ID NO: 471:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 436 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(466113..467420)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 471:

```

Asn Asn Met Gly Ile Ala His Thr Glu Trp Glu Ser Val Ile Gly Leu
1      5      10      15
Glu Val His Val Glu Leu Asn Thr Glu Ser Lys Leu Phe Ser Pro Ala
      20      25      30
Arg Asn His Phe Gly Asp Glu Pro Asn Thr Asn Ile Ser Pro Val Cys

```

35 40 45
 Thr Gly Met Pro Gly Ser Leu Pro Val Leu Asn Lys Asp Ala Val Arg
 50 55 60
 Lys Ala Val Leu Phe Gly Cys Ala Val Glu Gly Asp Val Ala Leu Phe
 65 70 75 80
 Ser Arg Phe Asp Arg Lys Ser Tyr Phe Tyr Pro Asp Ser Pro Arg Asn
 85 90 95
 Phe Gln Ile Thr Gln Tyr Glu His Pro Ile Val Arg Gly Gly Cys Ile
 100 105 110
 Arg Ala Val Val Glu Gly Glu Glu Lys Thr Phe Xaa Leu Ala Gln Thr
 115 120 125
 His Leu Glu Asp Asp Ala Gly Met Leu Lys His Phe Gly Asp Phe Ala
 130 135 140
 Gly Val Asp Tyr Asn Arg Ala Gly Val Pro Leu Ile Glu Ile Val Ser
 145 150 155 160
 Lys Pro Cys Met Phe Ser Ala Glu Asp Ala Val Ala Tyr Ala Asn Ala
 165 170 175
 Leu Val Ser Ile Leu Gly Tyr Ile Gly Ile Ser Asp Cys Asn Met Glu
 180 185 190
 Glu Gly Ser Ile Arg Phe Asp Val Asn Ile Ser Val Arg Pro Arg Gly
 195 200 205
 Ser Arg Glu Leu Arg Asn Lys Val Glu Ile Lys Asn Met Asn Ser Phe
 210 215 220
 Thr Phe Met Ala Gln Ala Leu Glu Ala Glu Lys Arg Arg Gln Ile Glu
 225 230 235 240
 Glu Tyr Leu Ser His Pro Asn Glu Asp Pro Lys Lys Val Val Pro Ala
 245 250 255
 Ala Thr Tyr Arg Trp Asp Pro Glu Lys Lys Lys Thr Val Leu Met Arg
 260 265 270
 Leu Lys Glu Arg Ala Glu Asp Tyr Met Tyr Phe Val Glu Pro Asp Leu
 275 280 285
 Pro Val Leu Gln Ile Thr Glu Thr Tyr Ile Asp Glu Val Arg Gln Thr
 290 295 300
 Leu Pro Glu Leu Pro His Ser Lys Tyr Met Arg Tyr Ile Thr Asp Phe
 305 310 315 320
 Asp Ile Ala Glu Asp Leu Ala Met Ile Leu Val Gly Asp Arg His Thr
 325 330 335
 Ala His Phe Phe Glu Thr Ala Thr Met Ser Cys Lys Asn Tyr Arg Ala
 340 345 350
 Leu Ser Asn Trp Ile Thr Val Glu Phe Ala Gly Arg Cys Lys Ala Lys
 355 360 365
 Gly Lys Thr Leu Leu Phe Thr Gly Ile Leu Pro Glu Trp Val Ala Gln
 370 375 380
 Leu Val Asn Phe Ile Val Arg Gly Val Ile Thr Gly Lys Ile Ala Lys
 385 390 395 400
 Glu Ile Ala Asp Arg Met Val Ser Ser Phe Gly Glu Ser Pro Glu Asp
 405 410 415
 Ile Leu Arg Arg His Pro Ser Leu Leu Pro Met Thr Asp Asp His Ala
 420 425 430
 Leu Arg Tyr Arg
 435

(2) INFORMATIONS POUR LA SEQ ID NO: 472:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 491 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(467419..468891)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 472:

Met	Tyr	Arg	Lys	Ser	Ala	Leu	Glu	Leu	Arg	Asp	Ala	Val	Val	Asn	Arg
1				5					10					15	
Glu	Leu	Ser	Val	Thr	Ala	Ile	Thr	Glu	Tyr	Phe	Tyr	His	Arg	Ile	Glu
			20					25					30		
Ser	His	Asp	Glu	Gln	Ile	Gly	Ala	Phe	Leu	Ser	Leu	Cys	Lys	Glu	Arg
		35					40					45			
Ala	Leu	Leu	Arg	Ala	Ser	Arg	Ile	Asp	Asp	Lys	Leu	Ala	Lys	Gly	Asp
	50					55					60				
Pro	Ile	Gly	Leu	Leu	Ala	Gly	Ile	Pro	Ile	Gly	Val	Lys	Asp	Asn	Ile
65					70					75				80	
His	Ile	Thr	Gly	Val	Lys	Thr	Thr	Cys	Ala	Ser	Lys	Met	Leu	Glu	Asn
				85				90						95	
Phe	Val	Ala	Pro	Phe	Asp	Ser	Thr	Val	Val	Arg	Arg	Ile	Glu	Met	Glu
			100					105					110		
Asp	Gly	Ile	Leu	Leu	Gly	Lys	Leu	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly
		115					120					125			
Ser	Thr	Thr	Arg	Tyr	Ser	Ala	Phe	His	Pro	Thr	Asn	Asn	Pro	Trp	Asp
	130					135					140				
Leu	Glu	Arg	Val	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	Ala	Ala	Val
145					150					155				160	
Ser	Ala	Arg	Phe	Cys	Pro	Ile	Ala	Leu	Gly	Ser	Asp	Thr	Gly	Gly	Ser
				165				170						175	
Ile	Arg	Gln	Pro	Ala	Ala	Phe	Cys	Gly	Val	Val	Gly	Phe	Lys	Pro	Ser
		180						185					190		
Tyr	Gly	Ala	Val	Ser	Arg	Tyr	Gly	Leu	Val	Ala	Phe	Gly	Ser	Ser	Leu
		195					200					205			
Asp	Gln	Ile	Gly	Pro	Leu	Thr	Thr	Val	Val	Glu	Asp	Val	Ala	Leu	Ala
	210					215					220				
Met	Asp	Ala	Phe	Ala	Gly	Arg	Asp	Pro	Lys	Asp	Ser	Thr	Thr	Arg	Asp
225					230					235				240	
Phe	Phe	Lys	Gly	Thr	Phe	Ser	Gln	Ala	Leu	Ser	Leu	Glu	Val	Pro	Lys
				245					250					255	
Leu	Ile	Gly	Val	Pro	Arg	Gly	Phe	Leu	Asp	Gly	Leu	Gln	Glu	Asp	Cys
		260						265					270		
Lys	Glu	Asn	Phe	Phe	Glu	Ala	Leu	Ala	Val	Met	Glu	Arg	Glu	Gly	Ser
		275					280					285			
Arg	Ile	Ile	Asp	Val	Asp	Leu	Ser	Val	Leu	Lys	His	Ala	Val	Pro	Val
	290					295					300				
Tyr	Tyr	Ile	Val	Ala	Ser	Ala	Glu	Ala	Ala	Thr	Asn	Leu	Ala	Arg	Phe
305					310					315				320	
Asp	Gly	Val	Arg	Tyr	Gly	His	Arg	Cys	Ala	Gln	Ala	Asp	Asn	Met	His
				325					330					335	
Glu	Met	Tyr	Ala	Arg	Ser	Arg	Lys	Glu	Gly	Phe	Gly	Lys	Glu	Val	Thr
			340					345					350		
Arg	Arg	Ile	Leu	Leu	Gly	Asn	Tyr	Val	Leu	Ser	Ala	Glu	Arg	Gln	Asn
		355					360					365			
Ile	Phe	Tyr	Lys	Lys	Gly	Met	Ala	Val	Arg	Ala	Arg	Leu	Ile	Asp	Ala
	370					375					380				
Phe	Gln	Ala	Ala	Phe	Glu	Arg	Cys	Asp	Val	Ile	Ala	Met	Pro	Val	Cys
385					390					395					400
Ala	Thr	Pro	Ala	Ile	Arg	Asp	Gln	Asp	Val	Leu	Asp	Pro	Val	Ser	Leu

```

              405              410              415
Tyr Leu Gln Asp Ile Tyr Thr Val Ala Val Asn Leu Ala Tyr Leu Pro
              420              425              430
Ala Ile Ser Val Pro Ser Gly Leu Ser Lys Glu Gly Leu Pro Leu Gly
              435              440              445
Val Gln Phe Ile Gly Glu Arg Gly Ser Asp Gln Gln Ile Cys Gln Val
              450              455              460
Gly Tyr Ser Phe Gln Glu His Ser Gln Ile Lys Gln Leu Tyr Pro Lys
465              470              475              480
Ala Val Asn Gly Leu Phe Asp Gly Gly Ile Glu
              485              490

```

(2) INFORMATIONS POUR LA SEQ ID NO: 473:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(468906..469280)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 473:

```

Gly Phe Phe Cys Phe Lys Lys Phe Gly Gly Phe Phe Phe Phe Leu Gly
1          5          10          15
Ser Cys Leu Pro Phe Phe Gly Leu Glu Val Ala Gly Phe Phe Asn
          20          25          30
Gln Gly Gly Ile Leu Phe Phe Ala Lys Asn Ala Ala Leu Glu Leu Glu
          35          40          45
Asp Ala His Val Glu Glu Phe Val Thr Ser Met Asn Asp Val Ile Ala
          50          55          60
Leu Met Gln Glu Val Ile Ala Ile Asp Ile Ser Asp Ile Ile Leu Glu
65          70          75          80
Ala Thr Val His His Phe Val Gly Pro Glu Asp Leu Arg Glu Asp Met
          85          90          95
Val Thr Ser Asp Phe Thr Gln Glu Glu Phe Leu Ser Asn Val Pro Val
          100         105         110
Ser Leu Gly Gly Leu Val Lys Val Pro Thr Val Ile Lys
          115         120         125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 474:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 469349..469675

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 474:


```

Ile Val Lys Lys Ile Thr Lys Ser Glu Leu Ser Ile His Leu Arg Trp
1          5          10          15
Arg Asp Val Met Leu Cys Lys Val Cys Arg Gly Leu Ser Ser Leu Ile
          20          25          30
Val Val Leu Gly Ala Ile Asn Thr Gly Ile Leu Gly Val Thr Gly Tyr
          35          40          45
Lys Val Asn Leu Leu Thr His Leu Leu Gly Glu Gly Thr Met Trp Thr
          50          55          60
Gln Ala Ala Tyr Val Val Thr Gly Ile Ala Gly Val Met Val Cys Leu
65          70          75          80
Asn Phe Leu Lys Cys Cys Phe Lys Lys Arg His Glu Asp Cys Cys Ser
          85          90          95
Ser Lys Gly Gly Cys His His His His Met Asp Arg Glu
          100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 475:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 467 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(469826..471226)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 475:

```

Ser Tyr Cys Ser Trp Cys Lys Phe Trp Glu Glu Tyr Ser Pro Ser Ala
1          5          10          15
Ala Arg Gly Leu Arg Leu Met Phe Thr Asp Phe Trp Arg Thr Arg Val
          20          25          30
Leu Arg Gln Thr Ser Pro Met Asp Val Val Phe Gly Asn Leu Asp Val
          35          40          45
Asn Glu Ala Arg Leu Met Ala Ala Tyr Thr Ser Glu Cys Ala Asp Tyr
          50          55          60
Leu Glu Ala His Asp Leu Ala Gly Pro Asp Gly Val Ala Ala Ala Arg
65          70          75          80
Glu Ile Ala Gln Arg Trp Asp Lys Arg Val Arg Asp Leu Gln Asp Lys
          85          90          95
Gly Ala Ala Gln Lys Leu Leu Asn Asp Pro Leu Gly Arg Arg Thr Pro
          100          105          110
Asn Tyr Gln Ser Lys Asn Pro Gly Glu Tyr Thr Val Gly Asn Ser Met
          115          120          125
Phe Tyr Asp Gly Pro Gln Val Ala Asn Leu Gln Asn Val Asp Thr Gly
          130          135          140
Phe Trp Leu Asp Met Ser Asn Phe Ser Asp Val Val Leu Ser Arg Glu
145          150          155          160
Ile Gln Thr Gly Leu Arg Ala Arg Ala Thr Leu Glu Glu Ser Met Pro
          165          170          175
Met Leu Glu Asn Leu Glu Glu Arg Phe Arg Arg Leu Gln Glu Thr Cys
          180          185          190
Asp Ala Ala Arg Thr Glu Ile Glu Glu Ser Gly Trp Thr Arg Glu Ser
          195          200          205
Ala Ser Arg Met Gly Gly Asp Glu Thr Gln Gly Pro Ser Arg Ala Gln
210          215          220
Gln Ala Phe Gln Ser Phe Val Asn Glu Cys Asn Ser Ile Glu Phe Ser

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225          230          235          240
Phe Gly Ser Phe Gly Glu His Val Arg Val Leu Cys Ala Arg Val Ser
          245          250          255
Arg Gly Leu Val Ala Ala Gly Glu Ala Ile Arg Arg Cys Phe Ser Cys
          260          265          270
Cys Lys Gly Ser Thr His Arg Tyr Ala Pro Arg Asp Asp Leu Ser Pro
          275          280          285
Glu Gly Ala Ser Leu Ala Glu Thr Leu Ala Arg Phe Ala Asp Asp Met
          290          295          300
Gly Ile Glu Gln Gly Ala Asp Gly Thr Tyr Asp Ile Pro Trp Val Asp
305          310          315          320
Asp Trp Arg Arg Gly Val Pro Ser Ile Glu Gly Glu Gly Ser Ala Ser
          325          330          335
Ile Tyr Glu Ile Met Met Pro Ile Tyr Glu Val Met Asn Met Asp Leu
          340          345          350
Glu Thr Arg Arg Ser Phe Ala Val Gln Gln Gly His Tyr Gln Asp Pro
          355          360          365
Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ala Ser Asp Tyr Asp Leu Pro
          370          375          380
Arg Ser Pro Tyr Pro Thr Pro Pro Leu Pro Ser Arg Tyr Gln Leu Gln
385          390          395          400
Asn Met Asp Val Glu Ala Gly Phe Arg Glu Ala Val Tyr Ala Ser Phe
          405          410          415
Val Ala Gly Met Tyr Asn Tyr Val Val Thr Gln Pro Gln Glu Arg Ile
          420          425          430
Pro Asn Ser Gln Gln Val Glu Gly Ile Leu Arg Asp Met Leu Thr Asn
          435          440          445
Gly Ser Gln Thr Phe Ser Asn Leu Met Gln Arg Trp Asp Arg Glu Val
          450          455          460
Asp Arg Glu
465

```

(2) INFORMATIONS POUR LA SEQ ID NO: 476:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 173 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(471106..471624)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 476:

```

Val Phe Ile Leu Val Leu Gly Trp Phe Val Met Ser Ile Gly Gly Val
1          5          10          15
Gly Gly Asn Gly Asn Ser Arg Ile Pro Ser His Asn Gly Asp Gly Ser
          20          25          30
Asn Arg Arg Ser Gln Asn Thr Lys Gly Asn Asn Lys Val Glu Asp Arg
          35          40          45
Val His Ser Leu Tyr Ser Ser Leu Ser Asn Glu Asn Arg Glu Ser Pro
          50          55          60
Tyr Pro Val Val Asp Val Ser Ser Met Ile Glu Ser Thr Pro Thr Ser
65          70          75          80
Gly Glu Thr Pro Arg Ala Ser Arg Gly Val Phe Ser Arg Phe Gln Arg
          85          90          95

```

Gly Leu Gly Arg Val Ala Asp Lys Val Arg Arg Ala Val Gln Cys Ala
 100 105 110
 Trp Gly Ser Val Ser Thr Arg Arg Ser Ser Ala Thr Arg Ala Val Glu
 115 120 125
 Ser Gly Ser Ser Ser Arg Thr Ala Arg Gly Ala Ser Ser Gly Arg Ser
 130 135 140
 Ile Leu Leu Gln Gln Leu Glu Gly Cys Val Leu Cys Ser Gln Ile Ser
 145 150 155 160
 Gly Glu Leu Gly Phe Tyr Ala Arg Pro Leu Trp Met
 165 170

(2) INFORMATIONS POUR LA SEQ ID NO: 477:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 471954..473267

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 477:

Val Lys Pro Pro Ser Ser Leu Lys Ile Leu Ile Met Ser Ser Val His
 1 5 10 15
 Phe Leu Arg Thr Val Pro Trp Arg Ala Ser Phe Leu Leu Phe Val Leu
 20 25 30
 Met His His Lys Thr Ile Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys
 35 40 45
 Trp Phe Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe
 50 55 60
 Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe
 65 70 75 80
 Thr Asp Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys
 85 90 95
 Asn Gly Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg
 100 105 110
 Asn His Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser
 115 120 125
 Leu Gln His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys
 130 135 140
 Gly Asn Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn
 145 150 155 160
 Val Ser Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly
 165 170 175
 Ala Ile Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu
 180 185 190
 Phe Phe Thr Gly Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile
 195 200 205
 Ser Asp Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn
 210 215 220
 Gln Glu Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala
 225 230 235 240
 Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe
 245 250 255
 Ile Asn Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly

Gly Ser Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn
 260 275 280 285
 Asn Ser Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr
 290 295 300
 Leu Glu Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp
 305 310 315 320
 Ile Leu Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser
 325 330 335
 Pro Leu Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala
 340 345 350
 Thr Ala Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile
 355 360 365
 Phe Ser Ser Glu Arg Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu
 370 375 380
 Thr Ser Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val
 385 390 395 400
 Leu Lys Asp Arg Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro
 405 410 415
 Gln Ala Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser
 420 425 430
 Asp Leu Lys Leu Leu Arg
 435

(2) INFORMATIONS POUR LA SEQ ID NO: 478:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 148 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 473252..473695

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 478:

Phe Glu Val Thr Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu
 1 5 10 15
 Lys Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe
 20 25 30
 Leu Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Leu
 35 40 45
 Ser Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu Gln
 50 55 60
 Ser His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr
 65 70 75 80
 Gln Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser
 85 90 95
 Leu Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg
 100 105 110
 Gln Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met
 115 120 125
 Gln Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala Tyr
 130 135 140
 Leu Phe Gly Thr
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 479:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 182 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 473982..474527

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 479:

Lys	Gln	Asn	Ile	Gly	Ser	Phe	Ser	Lys	Glu	Gly	Phe	Gly	Ser	Trp	His
1				5					10					15	
Ser	Val	Ala	Val	Ser	Gly	Glu	Val	Cys	Ala	Ser	Ile	Pro	Ile	Val	Ser
			20					25					30		
Asn	Gly	Ser	Gly	Leu	Phe	Ser	Ser	Phe	Ser	Ile	Phe	Ser	Lys	Leu	Gln
		35					40					45			
Gly	Phe	Ser	Gly	Thr	Gln	Asp	Gly	Phe	Glu	Glu	Ser	Ser	Gly	Glu	Ile
	50					55					60				
Arg	Ser	Phe	Ser	Ala	Ser	Ser	Phe	Arg	Asn	Ile	Ser	Leu	Pro	Ile	Gly
65					70					75				80	
Ile	Thr	Phe	Glu	Lys	Lys	Ser	Gln	Lys	Thr	Arg	Thr	Tyr	Tyr	Tyr	Phe
				85					90					95	
Leu	Gly	Ala	Tyr	Ile	Gln	Asp	Leu	Lys	Arg	Asp	Val	Glu	Ser	Gly	Pro
			100					105					110		
Val	Val	Leu	Leu	Lys	Asn	Ala	Val	Ser	Trp	Asp	Ala	Pro	Met	Ala	Asn
		115					120					125			
Leu	Asp	Ser	Arg	Ala	Tyr	Met	Phe	Arg	Leu	Thr	Asn	Gln	Arg	Ala	Leu
	130					135					140				
His	Arg	Leu	Gln	Thr	Leu	Leu	Asn	Val	Ser	Cys	Val	Leu	Arg	Gly	Gln
145					150					155				160	
Ser	Ile	Val	Thr	Pro	Trp	Ile	Trp	Gly	His	Leu	Gln	Val	Leu	Val	Pro
				165					170					175	
Leu	Pro	Ser	Ile	Ala	Phe										
				180											

(2) INFORMATIONS POUR LA SEQ ID NO: 480:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 199 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(474602..475198)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 480:

Ile	Met	Val	Cys	Pro	Leu	Arg	Asn	Cys	Cys	Thr	Ser	His	Thr	Ser	Thr
1					5					10				15	
Glu	Asn	Leu	Pro	Met	Glu	Glu	Thr	Ser	Pro	Leu	Val	Glu	Ala	Ile	Val

20 25 30
 Gln Ala Val Gln Thr Cys Leu Thr Val Ala Lys His Thr Glu Asn Ala
 35 40 45
 Lys Val Tyr Asn Gln Lys Arg Lys Arg Tyr His Gln Thr Gly Cys Trp
 50 55 60
 Arg Gln Leu Lys Lys Leu Leu Cys Cys Cys Cys Pro Lys Glu Lys Pro
 65 70 75 80
 Val Ser Gly Ser Ile Thr Ala Leu Ser Leu Trp Met Gln Ser His Ile
 85 90 95
 Pro Thr Arg Gly Leu Leu Val Val Gly Tyr Ala Val Tyr Ser Ser Gly
 100 105 110
 Val Arg Trp Glu Ala Ile Leu Glu Gly Glu Thr Leu Ser Pro Gly Asp
 115 120 125
 Arg Ala Gln Leu Asp Ala Cys Leu Glu Ser Ala Gln Val Arg Leu Ala
 130 135 140
 Gly Leu Met Leu Asn Tyr Trp Asp Gly Asp Phe Pro Gly Tyr Gly Thr
 145 150 155 160
 Ser Gly Gly Arg Phe Ser Pro Arg Met Gln Glu Asp Ile Ile Ala Arg
 165 170 175
 Phe Arg Asp Lys Val Gly Ile Cys Glu Leu Thr Asp Ala Val Ala Leu
 180 185 190
 Lys His Phe Cys Arg Arg Thr
 195

(2) INFORMATIONS POUR LA SEQ ID NO: 481:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 305 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(475613..476527)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 481:

Glu Thr Phe Thr Asn Gly Leu Lys Glu His Tyr Val Ser Arg Asp Val
 1 5 10 15
 Gly Phe Val Ala Ser Leu His Ala Leu Gly Asp Tyr Ile Leu Asn Tyr
 20 25 30
 Thr Gln Asp Asp Arg Asp Gly Phe Leu Ala Arg Tyr Gly Gly Phe Gln
 35 40 45
 Ala Thr Ala Ala Cys His Tyr Glu Asn Gly Ser Ile Phe Gly Val Ala
 50 55 60
 Phe Gly Gln Leu Tyr Gly Gln Thr Lys Ser Arg Met Tyr Tyr Ser Lys
 65 70 75 80
 Asp Ala Gly Asn Met Thr Met Leu Ser Cys Phe Gly Arg Ser Tyr Val
 85 90 95
 Asp Ile Lys Gly Thr Glu Thr Val Val Tyr Trp Glu Thr Ala Tyr Gly
 100 105 110
 Tyr Ser Val His Arg Met His Thr Gln Tyr Phe Asn Asp Lys Thr Gln
 115 120 125
 Lys Phe Asp His Ser Lys Cys His Trp His Asn Asn Asn Tyr Tyr Ala
 130 135 140
 Phe Val Gly Ala Glu His Asn Phe Leu Glu Tyr Cys Ile Pro Thr Arg
 145 150 155 160

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(2)  INFORMATIONS POUR LA SEQ ID NO: 482:

(i)  CARACTERISTIQUES DE LA SEQUENCE:
(A)  LONGUEUR: 708 acides aminés
(B)  TYPE: acide aminé
(D)  CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(476517..478640)

(xi)  DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 482:

Val Leu Ala Met Pro Phe Ser Leu Arg Ser Thr Ser Phe Cys Phe Leu
1          5          10          15
Ala Cys Leu Cys Ser Tyr Ser Tyr Gly Phe Ala Ser Ser Pro Gln Val
          20          25          30
Leu Thr Pro Asn Val Thr Thr Pro Phe Lys Gly Asp Asp Val Tyr Leu
          35          40          45
Asn Gly Asp Cys Ala Phe Val Asn Val Tyr Ala Gly Ala Glu Glu Gly
          50          55          60
Ser Ile Ile Ser Ala Asn Gly Asp Asn Leu Thr Ile Thr Gly Gln Asn
65          70          75          80
His Thr Leu Ser Phe Thr Asp Ser Gln Gly Pro Val Leu Gln Asn Tyr
          85          90          95
Ala Phe Ile Ser Ala Gly Glu Thr Leu Thr Leu Arg Asp Phe Ser Ser
          100          105          110
Leu Met Phe Ser Lys Asn Val Ser Cys Gly Glu Lys Gly Met Ile Ser
          115          120          125
Gly Lys Thr Val Ser Ile Ser Gly Ala Gly Glu Val Ile Phe Trp Asp
          130          135          140
Asn Ser Val Gly Tyr Ser Pro Leu Ser Thr Val Pro Thr Ser Ser Ser
145          150          155          160
Thr Pro Pro Ala Pro Thr Val Ser Asp Ala Arg Lys Gly Ser Ile Phe
          165          170          175
Ser Val Glu Thr Ser Leu Glu Ile Ser Gly Val Lys Lys Gly Val Met

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Val 1	Leu	Ala	Met	Pro 5	Phe	Ser	Leu	Arg	Ser 10	Thr	Ser	Phe	Cys	Phe 15	Leu
Ala	Cys	Leu	Cys 20	Ser	Tyr	Ser	Tyr	Gly 25	Phe	Ala	Ser	Ser	Pro 30	Gln	Val
Leu	Thr	Pro 35	Asn	Val	Thr	Thr	Pro 40	Phe	Lys	Gly	Asp	Asp 45	Val	Tyr	Leu
Asn	Gly 50	Asp	Cys	Ala	Phe	Val 55	Asn	Val	Tyr	Ala	Gly 60	Ala	Glu	Glu	Gly
Ser 65	Ile	Ile	Ser	Ala	Asn 70	Gly	Asp	Asn	Leu	Thr 75	Ile	Thr	Gly	Gln	Asn 80
His	Thr	Leu	Ser	Phe 85	Thr	Asp	Ser	Gln	Gly 90	Pro	Val	Leu	Gln	Asn 95	Tyr
Ala	Phe	Ile	Ser 100	Ala	Gly	Glu	Thr	Leu 105	Thr	Leu	Arg	Asp	Phe 110	Ser	Ser
Leu	Met	Phe 115	Ser	Lys	Asn	Val	Ser 120	Cys	Gly	Glu	Lys	Gly 125	Met	Ile	Ser
Gly	Lys 130	Thr	Val	Ser	Ile	Ser 135	Gly	Ala	Gly	Glu	Val 140	Ile	Phe	Trp	Asp
Asn 145	Ser	Val	Gly	Tyr	Ser 150	Pro	Leu	Ser	Thr	Val 155	Pro	Thr	Ser	Ser	Ser
Thr	Pro	Pro	Ala	Pro 165	Thr	Val	Ser	Asp	Ala 170	Arg	Lys	Gly	Ser	Ile	Phe
Ser	Val	Glu	Thr	Ser	Leu	Glu	Ile	Ser	Gly	Val	Lys	Lys	Gly	Val	Met

180 185 190
 Phe Asp Asn Asn Ala Gly Asn Phe Gly Thr Val Phe Arg Gly Lys Asn
 195 200 205
 Asn Asn Asn Ala Gly Gly Gly Gly Ser Gly Ser Ala Thr Pro Ser Ser
 210 215 220
 Thr Thr Phe Thr Val Lys Asn Cys Lys Gly Lys Val Ser Phe Thr Asp
 225 230 235 240
 Asn Val Ala Ser Cys Gly Gly Gly Val Val Tyr Lys Gly Ile Val Leu
 245 250 255
 Phe Lys Asp Asn Glu Gly Gly Ile Phe Phe Arg Gly Asn Thr Ala Tyr
 260 265 270
 Asp Asp Leu Arg Ile Leu Ala Ala Thr Asn Gln Asp Gln Asn Thr Glu
 275 280 285
 Thr Gly Gly Gly Gly Gly Val Ile Cys Ser Pro Asp Asp Ser Val Lys
 290 295 300
 Phe Glu Gly Asn Lys Gly Ser Ile Val Phe Asp Tyr Asn Phe Ala Lys
 305 310 315 320
 Gly Arg Gly Gly Ser Ile Leu Thr Lys Glu Phe Ser Leu Val Ala Asp
 325 330 335
 Asp Ser Val Val Phe Ser Asn Asn Thr Ala Glu Lys Gly Gly Ala
 340 345 350
 Ile Tyr Ala Pro Thr Ile Asn Met Ser Thr Asn Gly Gly Ser Ile Leu
 355 360 365
 Phe Glu Arg Asn Arg Ala Ala Glu Gly Gly Ala Ile Cys Val Ser Ala
 370 375 380
 Ala Ser Ser Gly Ser Thr Gly Lys Leu Thr Leu Ser Ala Ser Asp Gly
 385 390 395 400
 Asp Ile Val Phe Ser Gly Asn Met Thr Ser Asp Arg Pro Gly Glu Arg
 405 410 415
 Ser Ala Val Arg Ile Leu Ser Ser Gly Thr Thr Val Ala Leu Asn Ala
 420 425 430
 Ser Gly Leu Ser Lys Leu Ile Phe His Asp Pro Val Val Gln Ile Asn
 435 440 445
 Ser Ala Ala Ala Ala Ser Thr Pro Ser Pro Ser Ser Ser Ser Thr Pro
 450 455 460
 Ala Ala Val Thr Ile Asn Gln Ser Gly Asn Gly Ser Val Ile Phe Thr
 465 470 475 480
 Ala Glu Ser Leu Thr Pro Ser Glu Lys Leu Gln Val Leu Asn Ser Thr
 485 490 495
 Ser Asn Phe Pro Gly Thr Leu Thr Val Ser Gly Gly Glu Leu Val Val
 500 505 510
 Thr Glu Gly Ala Thr Leu Thr Thr Gly Thr Ile Thr Ala Thr Ser Gly
 515 520 525
 Arg Val Ser Leu Gly Ser Gly Ala Ser Leu Ser Ala Val Ala Gly Ala
 530 535 540
 Ala Asn Asn Asn Tyr Thr Cys Thr Val Ser Lys Leu Gly Ile Asp Leu
 545 550 555 560
 Glu Ser Phe Leu Thr Pro Asn Tyr Lys Thr Ala Ile Leu Gly Ala Tyr
 565 570 575
 Gly Thr Val Thr Val Lys Arg Gly Ser Thr Leu Asp Leu Val Met Glu
 580 585 590
 Asn Glu Ala Glu Val Tyr Asp Asn Pro Leu Phe Val Gly Ser Leu Thr
 595 600 605
 Ile Pro Phe Val Thr Leu Ser Ser Ser Ser Thr Arg Ser Gly Val Met
 610 615 620
 Val Ala Gly Val Cys Asp Val Asp Ala Asp Ala Ala His Tyr Gly Tyr
 625 630 635 640
 Gln Gly Ser Trp Ser Ala Asp Trp Thr Lys Pro Pro Leu Ala Pro Asp
 645 650 655

Ala Lys Gly Met Val Pro Pro Asn Thr Ser Asn Thr Leu Tyr Leu Thr
 660 665 670
 Trp Arg Pro Ala Ser Asn Tyr Gly Glu Tyr Arg Leu Asp Pro Gln Arg
 675 680 685
 Lys Gly Glu Leu Val Pro Asn Ser Leu Trp Val Ala Gly Ser Ala Leu
 690 695 700
 Arg Asn Leu Tyr
 705

(2) INFORMATIONS POUR LA SEQ ID NO: 483:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(478665..479084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 483:

Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr
 1 5 10 15
 Ala Asp His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe
 20 25 30
 Lys Ser Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe
 35 40 45
 Asp Arg Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala
 50 55 60
 Tyr Ile Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu
 65 70 75 80
 Leu Ser His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg
 85 90 95
 His Gly Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn
 100 105 110
 Ile Glu Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg
 115 120 125
 Gly Tyr Gly Leu Ser Ala Gly Ser Arg Val Arg Phe
 130 135 140

(2) INFORMATIONS POUR LA SEQ ID NO: 484:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 212 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479088..479723)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 484:

Gly Met Arg Cys Leu Ser Met Ala Ile Lys Glu Ala Gly Ser Leu Arg

```

1          5          10          15
Gly Ile Leu Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr
20          25          30
Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu
35          40          45
Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His
50          55          60
Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu
65          70          75          80
Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu
85          90          95
Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn
100          105          110
Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe
115          120          125
Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys
130          135          140
Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr
145          150          155          160
Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln
165          170          175
His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp
180          185          190
Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val
195          200          205
Ile Thr Pro Ser
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 485:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 115 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479668..480012)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 485:

```

Ser Val Asp His Ala Phe Gln Ser Ala Phe Val Ser Phe Phe Phe Val
1          5          10          15
Ser Lys Gln Cys Ser Tyr Glu Ser Ser Tyr Gln Ser Ser Ser Ala Arg
20          25          30
Phe Ser Ile Leu Gln Ser Leu Val Ala Gln Leu Leu Val Leu Leu Gln
35          40          45
Leu Val Gly Leu Ser Phe Leu Arg Ile Trp Met Ile Gln Leu Asn Asp
50          55          60
Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu
65          70          75          80
Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu
85          90          95
Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala
100          105          110
Trp Asp Ser
115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 486:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 524 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(479895..481466)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 486:

Val	Val	Phe	Gly	Asn	Leu	Leu	Gly	Ser	Phe	Thr	Val	Leu	Gly	Arg	Gly	1	5	10	15
His	Ser	Leu	Thr	Phe	Glu	Asn	Ile	Arg	Thr	Ser	Thr	Asn	Gly	Ala	Ala	20	25	30	
Leu	Ser	Asn	Ser	Ala	Ala	Asp	Gly	Leu	Phe	Thr	Ile	Glu	Gly	Phe	Lys	35	40	45	
Glu	Leu	Ser	Phe	Ser	Asn	Cys	Asn	Ser	Leu	Leu	Ala	Val	Leu	Pro	Ala	50	55	60	
Ala	Thr	Thr	Asn	Lys	Gly	Ser	Gln	Thr	Pro	Thr	Thr	Thr	Ser	Thr	Pro	65	70	75	80
Ser	Asn	Gly	Thr	Ile	Tyr	Ser	Lys	Thr	Asp	Leu	Leu	Leu	Leu	Asn	Asn	85	90	95	
Glu	Lys	Phe	Ser	Phe	Tyr	Ser	Asn	Leu	Val	Ser	Gly	Asp	Gly	Gly	Ala	100	105	110	
Ile	Asp	Ala	Lys	Ser	Leu	Thr	Val	Gln	Gly	Ile	Ser	Lys	Leu	Cys	Val	115	120	125	
Phe	Gln	Glu	Asn	Thr	Ala	Gln	Ala	Asp	Gly	Gly	Ala	Cys	Gln	Val	Val	130	135	140	
Thr	Ser	Phe	Ser	Ala	Met	Ala	Asn	Glu	Ala	Pro	Ile	Ala	Phe	Val	Ala	145	150	155	160
Asn	Val	Ala	Gly	Val	Arg	Gly	Gly	Gly	Ile	Ala	Ala	Val	Gln	Asp	Gly	165	170	175	
Gln	Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	180	185	190	
Phe	Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	195	200	205	
Gly	Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	210	215	220	
Lys	Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Phe	Pro	Val	Tyr	Ile	Ala	Ala	225	230	235	240
Lys	Gln	Pro	Thr	Ser	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asn	Asn	Tyr	Gly	245	250	255	
Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Val	Gly	Ser	Asn	260	265	270	
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser	275	280	285	
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	290	295	300	
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn	Ile	Ala	Asn	305	310	315	320
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser	325	330	335	
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala				

340 345 350
 Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala
 355 360 365
 Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala
 370 375 380
 Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn
 385 390 395 400
 Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly Glu
 405 410 415
 Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu Tyr
 420 425 430
 Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala
 435 440 445
 Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met
 450 455 460
 Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln
 465 470 475 480
 Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser
 485 490 495
 Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn
 500 505 510
 Pro Pro Ala Gln Asp Ser Gln Ser Cys Ser His Trp
 515 520

(2) INFORMATIONS POUR LA SEQ ID NO: 487:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 79 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(481496..481732)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 487:

Leu Ile Leu Ser Leu Ser Phe Cys Val Met Gln Thr Ser Phe His Lys
 1 5 10 15
 Phe Phe Leu Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly
 20 25 30
 Gly Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly
 35 40 45
 Glu Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser
 50 55 60
 Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Pro
 65 70 75

(2) INFORMATIONS POUR LA SEQ ID NO: 488:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 522 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 481864..483429

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 488:

Pro	Ala	Met	Ile	Lys	Arg	Thr	Ser	Leu	Ser	Phe	Ala	Cys	Leu	Ser	Phe	1	5	10	15
Phe	Tyr	Leu	Ser	Thr	Ile	Ser	Ile	Leu	Gln	Ala	Asn	Glu	Thr	Asp	Thr	20	25	30	
Leu	Gln	Phe	Arg	Arg	Phe	Thr	Phe	Ser	Asp	Arg	Glu	Ile	Gln	Phe	Val	35	40	45	
Leu	Asp	Pro	Val	Ser	Leu	Ile	Thr	Ala	Gln	Asn	Val	Thr	Phe	Ser	Asn	50	55	60	
Ile	Asn	Ser	Trp	Gly	Arg	Gly	Val	Cys	Thr	Ile	Ala	Asp	Asn	Thr	Gln	65	70	75	80
Thr	Gln	Ile	Phe	Ser	Asn	Ser	Ile	Asn	Thr	Thr	Ser	Ala	Ala	Gly	Gly	85	90	95	
Val	Phe	Asp	Met	Val	Thr	Ile	Ser	Phe	Thr	Ala	Ser	Asn	Asn	Ala	Asn	100	105	110	
Leu	Leu	Phe	Cys	Asn	Asn	Tyr	Cys	Thr	His	Asn	Lys	Gly	Gly	Gly	Ala	115	120	125	
Ile	Arg	Ser	Lys	Gly	Pro	Ile	Arg	Phe	Ser	Asn	Asn	Gln	Asp	Val	Leu	130	135	140	
Phe	Tyr	Asn	Asn	Thr	Thr	Ala	Gly	Ala	Gln	Tyr	Thr	Gly	Thr	Gly	Asn	145	150	155	160
Lys	Ser	Glu	Lys	Asn	Arg	Gly	Gly	Ala	Leu	Tyr	Ala	Lys	Asn	Ile	Thr	165	170	175	
Leu	Thr	Gly	Asn	Arg	Thr	Leu	Ala	Phe	Ile	Asn	Asn	Met	Ser	Gly	Asp	180	185	190	
Cys	Gly	Gly	Ala	Ile	Ala	Ala	Asn	Thr	Gln	Ile	Ser	Ile	Thr	Asp	Thr	195	200	205	
Ala	Lys	Gly	Val	Leu	Phe	Glu	Asn	Asn	His	Thr	Leu	Asn	His	Ile	Pro	210	215	220	
Asp	Thr	Arg	Ala	Glu	Asn	Met	Ala	Arg	Gly	Gly	Ala	Ile	Cys	Ser	Arg	225	230	235	240
Lys	Ser	Ser	Cys	Ser	Ile	Ser	Asn	Asn	Leu	Gly	Pro	Ile	Ile	Phe	Asn	245	250	255	
Tyr	Asn	Gln	Gly	Gly	Lys	Gly	Gly	Ala	Ile	Ser	Ala	Thr	Gln	Cys	Val	260	265	270	
Ile	Ser	Asn	Glu	Glu	Arg	Ile	Val	Phe	Ser	Asn	Asn	Ser	Ser	Ile		275	280	285	
Gly	Trp	Asn	Lys	Ser	Thr	His	Ala	Ser	Asn	Gly	Gly	Ala	Ile	Gln	Thr	290	295	300	
Ala	Gln	Gly	Phe	Thr	Leu	Gln	Asn	Asn	Lys	Gly	Pro	Ile	Tyr	Phe	Asp	305	310	315	320
Ser	Asn	Thr	Ala	Ala	His	Ala	Gly	Gly	Ala	Ile	Asp	Cys	Gly	Tyr	Ile	325	330	335	
Asp	Ile	Arg	Asn	Asn	Gly	Pro	Ile	Tyr	Phe	Leu	Asn	Asn	Ser	Ala	Ala	340	345	350	
Trp	Gly	Ala	Ala	Phe	Asn	Leu	Ser	Lys	Leu	Arg	Pro	Ala	Thr	Asn	Tyr	355	360	365	
Ile	His	Thr	Gly	Thr	Gly	Asp	Ile	Val	Phe	Asn	Asn	Asn	Val	Val	Phe	370	375	380	
Lys	Phe	Asp	Ala	Asn	Leu	Leu	Gly	Met	Arg	Lys	Leu	Phe	His	Ile	Asn	385	390	395	400
Asn	Asn	Thr	Gln	Thr	Pro	Tyr	Thr	Leu	Ser	Leu	Gly	Ala	Lys	Glu	Asp	405	410	415	
Thr	Arg	Ile	Tyr	Phe	Tyr	Asp	Leu	Phe	Gln	Trp	Glu	Arg	Val	Arg	Glu				

```

          420          425          430
Pro Asn Asn Ala Gln Val Ser Pro Ser Ser Arg Asn Val Ile Thr Ile
          435          440          445
Asn Pro Ile Glu Glu Phe Ser Gly Ala Val Val Phe Ser Tyr Lys Gln
          450          455          460
Met Ser Ser Asp Ile Lys Thr Leu Met Gly Thr Glu His Asn Tyr Ile
465          470          475
Arg Glu Ala Pro Thr Thr Leu Lys Phe Gly Thr Leu Ala Ile Glu Asp
          485          490          495
Gly Ala Glu Leu Glu Phe Phe Asp Ile Pro Phe Thr Gln Asn Pro Thr
          500          505          510
Ser Leu Leu Ala Leu Gly Ser Asp Leu Arg
          515          520

```

(2) INFORMATIONS POUR LA SEQ ID NO: 489:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 521 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 483402..484964

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 489:

```

Ser Thr Cys Phe Arg Lys Arg Pro Thr Leu Thr Val Gly Lys His Gly
1          5          10          15
Lys Leu Asn Ile Thr Asn Leu Gly Val Ile Leu Pro Ile Ile Leu Lys
          20          25          30
Glu Gly Lys Ser Pro Pro Cys Ile Arg Val Asn Pro Gln Asp Met Thr
          35          40          45
Gln Asn Thr Asp Thr Gly Gln Thr Pro Ser Ser Thr Ser Ser Ile Ser
          50          55          60
Thr Pro Met Ile Ile Phe Asn Gly Arg Leu Ser Ile Val Asp Glu Asn
65          70          75          80
Tyr Glu Ser Val Tyr Asp Ser Met Asp Leu Ser Arg Gly Lys Ala Glu
          85          90          95
Gln Pro Ile Leu Ser Ile Glu Thr Thr Asn Asp Gly Gln Leu Gly Pro
          100          105          110
Asn Trp Gln Asn Ser Leu Asn Thr Ser Leu Leu Ser Pro Pro His Tyr
          115          120          125
Gly Tyr Gln Gly Leu Trp Thr Pro Asn Trp Ile Thr Thr Thr Tyr Thr
          130          135          140
Ile Thr Leu Asn Asn Asn Ser Ser Ala Pro Thr Ser Ala Asn Ser Ile
145          150          155          160
Ala Glu Gln Lys Lys Thr Ser Glu Thr Phe Thr Pro Asn Ser Thr Thr
          165          170          175
Thr Ala Gly Ile Pro Ser Ile Lys Ala Ser Ala Gly Ser Gly Ser Gly
          180          185          190
Ser Ser Thr Thr Thr Asp Val Gln Val Thr Arg His Thr Leu Thr Val
          195          200          205
Asn Trp Thr Pro Val Gly Tyr Ile Val Asp Pro Ile Arg Arg Gly Asp
210          215          220
Leu Ile Ala Asn Ser Leu Val His Ser Gly Arg Asn Met Thr Met Gly
225          230          235          240

```

```

Leu Arg Ser Leu Leu Pro Asp Asn Ser Trp Phe Ala Leu Gln Gly Ala
      245      250      255
Ala Thr Thr Leu Phe Thr Lys Gln Gln Lys Arg Leu Ser Tyr His Gly
      260      265      270
Tyr Ser Ser Ala Ser Lys Gly Tyr Thr Val Ser Ser Gln Ala Ser Gly
      275      280      285
Ala His Gly His Lys Phe Leu Leu Ser Phe Ser Gln Ser Ser Asp Lys
      290      295      300
Met Lys Glu Lys Glu Thr Asn Asn Arg Leu Ser Ser Arg Tyr Tyr Leu
305      310      315
Ser Ala Leu Cys Phe Glu His Pro Met Phe Asp Arg Ile Ala Leu Ile
      325      330      335
Gly Ala Ala Ala Cys Asn Tyr Gly Thr His Asn Met Arg Ser Phe Tyr
      340      345      350
Gly Thr Lys Arg Ser Ser Lys Gly Lys Phe His Ser Thr Thr Leu Gly
      355      360      365
Ala Ser Leu Arg Cys Glu Leu Arg Asp Ser Met Pro Leu Arg Ser Ile
      370      375      380
Met Leu Thr Pro Phe Ala Gln Ala Leu Phe Ser Arg Thr Lys Pro Gly
385      390      395
Ala Ile Arg Glu Ser Gly Asp Leu Ala Arg Leu Phe Thr Leu Glu Gln
      405      410      415
Ala His Thr Ala Ile Val Ser Pro Ile Gly Ile Lys Gly Ala Tyr Ser
      420      425      430
Ser Asp Thr Trp Pro Thr Leu Ser Trp Glu Met Glu Leu Ala Tyr Gln
      435      440      445
Pro Thr Leu Tyr Trp Lys Arg Pro Leu Leu Asn Thr Leu Leu Ile Gln
      450      455      460
Asn Asn Gly Ser Trp Val Thr Thr Asn Thr Pro Leu Ala Lys His Ser
465      470      475
Phe Tyr Gly Arg Gly Ser His Ser Leu Lys Phe Ser His Leu Lys Leu
      485      490      495
Phe Ala Asn Tyr Gln Ala Glu Val Ala Thr Ser Thr Val Ser His Tyr
      500      505      510
Ile Asn Ala Gly Gly Ala Leu Val Phe
      515      520

```

(2) INFORMATIONS POUR LA SEQ ID NO: 490:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 989 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 484898..487864

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 490:

```

Leu Ser Ser Arg Ser Gly Tyr Phe His Cys Leu Thr Leu His Gln Cys
1      5      10      15
Arg Arg Ser Ser Gly Leu Leu Thr Met Lys Lys Ala Phe Phe Phe
      20      25      30
Leu Ile Gly Ser Ser Leu Ser Gly Leu Ala Arg Glu Val Pro Ser Arg
      35      40      45
Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro Thr Lys Glu Ser Leu

```

50 55 60
 Ser Asn Lys Ile Ser Leu Thr Gly Asp Thr His Asn Leu Thr Asn Cys
 65 70 75 80
 Tyr Leu Asp Asn Leu Arg Tyr Ile Leu Ala Ile Leu Gln Lys Thr Pro
 85 90 95
 Asn Glu Gly Ala Ala Val Thr Ile Thr Asp Tyr Leu Ser Phe Phe Asp
 100 105 110
 Thr Gln Lys Glu Gly Ile Tyr Phe Ala Lys Asn Leu Thr Pro Glu Ser
 115 120 125
 Gly Gly Ala Ile Gly Tyr Ala Ser Pro Asn Ser Pro Thr Val Glu Ile
 130 135 140
 Arg Asp Thr Ile Gly Pro Val Ile Phe Glu Asn Asn Thr Cys Cys Arg
 145 150 155 160
 Pro Phe Thr Ser Ser Asn Pro Asn Ala Ala Val Asn Lys Ile Arg Glu
 165 170 175
 Gly Gly Ala Ile His Ala Gln Asn Leu Tyr Ile Asn His Asn His Asp
 180 185 190
 Val Val Gly Phe Met Lys Asn Phe Ser Tyr Val Arg Gly Gly Ala Ile
 195 200 205
 Ser Thr Ala Asn Thr Phe Val Val Ser Glu Asn Gln Ser Cys Phe Leu
 210 215 220
 Phe Met Asp Asn Ile Cys Ile Gln Thr Asn Thr Ala Gly Lys Gly Gly
 225 230 235 240
 Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe Glu Ser Asn Asn Cys Asp
 245 250 255
 Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala Gly Gly Ala Ile Phe Ser
 260 265 270
 Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly Asn Ile Val Phe Tyr Asn
 275 280 285
 Asn Arg Cys Phe Lys Asn Val Glu Thr Ala Ser Ser Glu Ser Ser Asp
 290 295 300
 Gly Gly Ala Ile Lys Val Thr Thr Arg Leu Asp Val Thr Gly Asn Arg
 305 310 315 320
 Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn Tyr Gly Gly Ala
 325 330 335
 Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly Pro Thr Tyr Phe
 340 345 350
 Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile Tyr Ile Asp Gly
 355 360 365
 Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala Ile Ile Phe Asn
 370 375 380
 Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly Thr Ser Thr Ser
 385 390 395 400
 Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala Ser Ser Ser Gly
 405 410 415
 Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu Ile Phe Tyr Asp
 420 425 430
 Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser Phe Asn Lys Glu
 435 440 445
 Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala Thr Val Asn Ser
 450 455 460
 Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr Pro Ala Pro Leu
 465 470 475 480
 Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His Ala Gln Leu Thr
 485 490 495
 Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser Leu Gly Asn Gly
 500 505 510
 Ala Val Leu Ser Cys Tyr Lys Asn Gly Ala Gly Asn Ser Ala Ser Asn
 515 520 525

Ala	Ser	Ile	Thr	Leu	Lys	His	Ile	Gly	Leu	Asn	Leu	Ser	Ser	Ile	Leu
530						535				540					
Lys	Ser	Gly	Ala	Glu	Ile	Pro	Leu	Leu	Trp	Val	Glu	Pro	Thr	Asn	Asn
545					550					555					560
Ser	Asn	Asn	Tyr	Thr	Ala	Asp	Thr	Ala	Ala	Thr	Phe	Ser	Leu	Ser	Asp
				565					570						575
Val	Lys	Leu	Ser	Leu	Ile	Asp	Asp	Tyr	Gly	Asn	Ser	Pro	Tyr	Glu	Ser
			580					585					590		
Thr	Asp	Leu	Thr	His	Ala	Leu	Ser	Ser	Gln	Pro	Met	Leu	Ser	Ile	Ser
	595						600					605			
Glu	Ala	Ser	Asp	Asn	Gln	Leu	Arg	Ser	Asp	Asp	Met	Asp	Phe	Ser	Gly
610					615						620				
Leu	Asn	Val	Pro	His	Tyr	Gly	Trp	Gln	Gly	Leu	Trp	Ser	Trp	Gly	Trp
625					630					635					640
Ala	Lys	Thr	Gln	Asp	Pro	Glu	Pro	Ala	Ser	Ser	Ala	Thr	Ile	Thr	Asp
				645					650						655
Pro	Lys	Lys	Ala	Asn	Arg	Phe	His	Arg	Thr	Leu	Leu	Leu	Thr	Trp	Leu
			660					665						670	
Pro	Ala	Gly	Tyr	Val	Pro	Ser	Pro	Lys	His	Arg	Ser	Pro	Leu	Ile	Ala
	675						680					685			
Asn	Thr	Leu	Trp	Gly	Asn	Met	Leu	Leu	Ala	Thr	Glu	Ser	Leu	Lys	Asn
690						695					700				
Ser	Ala	Glu	Leu	Thr	Pro	Ser	Asp	His	Pro	Phe	Trp	Gly	Ile	Thr	Gly
705					710					715					720
Gly	Gly	Leu	Gly	Met	Met	Val	Tyr	Gln	Asp	Pro	Arg	Glu	Asn	His	Pro
				725					730					735	
Gly	Phe	His	Met	Arg	Ser	Ser	Gly	Tyr	Ser	Ala	Gly	Met	Ile	Ala	Gly
			740					745					750		
Gln	Thr	His	Thr	Phe	Ser	Leu	Lys	Phe	Ser	Gln	Thr	Tyr	Thr	Lys	Leu
	755						760						765		
Asn	Glu	Arg	Tyr	Ala	Lys	Asn	Asn	Val	Ser	Ser	Lys	Asn	Tyr	Ser	Cys
770						775					780				
Gln	Gly	Glu	Met	Leu	Phe	Ser	Leu	Gln	Glu	Gly	Phe	Leu	Leu	Ala	Lys
785					790					795					800
Leu	Val	Gly	Leu	Tyr	Ser	Tyr	Gly	Asp	His	Asn	Cys	His	His	Phe	Tyr
				805					810					815	
Thr	Gln	Gly	Glu	Asn	Leu	Thr	Ser	Gln	Gly	Thr	Phe	Arg	Ser	Gln	Thr
			820					825					830		
Met	Gly	Gly	Ala	Val	Phe	Phe	Asp	Leu	Pro	Met	Lys	Pro	Phe	Gly	Ser
			835				840					845			
Thr	His	Ile	Leu	Thr	Ala	Pro	Phe	Leu	Gly	Ala	Leu	Gly	Ile	Tyr	Ser
	850					855					860				
Ser	Leu	Ser	His	Phe	Thr	Glu	Val	Gly	Ala	Tyr	Pro	Arg	Ser	Phe	Ser
865					870					875					880
Thr	Lys	Thr	Pro	Leu	Ile	Asn	Val	Leu	Val	Pro	Ile	Gly	Val	Lys	Gly
				885					890					895	
Ser	Phe	Met	Asn	Ala	Thr	Gln	Arg	Pro	Gln	Ala	Trp	Thr	Val	Glu	Leu
			900					905					910		
Ala	Tyr	Gln	Pro	Val	Leu	Tyr	Arg	Gln	Glu	Leu	Glu	Ile	Ala	Thr	Gln
	915						920					925			
Leu	Leu	Ala	Ser	Lys	Gly	Ile	Trp	Phe	Gly	Ser	Gly	Ser	Pro	Ser	Ser
930						935					940				
Arg	His	Ala	Met	Ser	Tyr	Lys	Ile	Ser	Gln	Gln	Thr	Gln	Pro	Leu	Ser
945					950					955					960
Trp	Leu	Thr	Leu	His	Phe	Gln	Tyr	His	Gly	Phe	Tyr	Ser	Ser	Ser	Thr
				965					970						975
Phe	Cys	Asn	Tyr	Leu	Asn	Gly	Glu	Ile	Ala	Leu	Arg	Phe			
			980					985							

(2) INFORMATIONS POUR LA SEQ ID NO: 491:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 168 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(485222..485725)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 491:

```

Arg Thr Asp Arg Gly Glu Asp Arg Ser Ser Cys Thr Thr Gly Val Ile
1      5      10      15
Asp Lys Glu Glu Ile Ala Val Ile Thr Leu Lys Arg Ile Ala Arg Ser
20      25      30
Ser Ile Asp Ser Ala Thr Phe Ser Cys Cys Ile Ser Leu Asn Thr Asp
35      40      45
Val Val His Lys Glu Lys Thr Arg Leu Ile Leu Ala His Asn Lys Gly
50      55      60
Ile Ser Gly Thr Asn Gly Ser Ser Ser Asp Ile Arg Lys Val Leu His
65      70      75      80
Lys Ser Asp His Ile Met Ile Val Ile Tyr Val Lys Ile Leu Ser Met
85      90      95
Asn Cys Ser Ala Phe Ser Tyr Phe Ile Asn Ser Cys Ile Arg Ile Thr
100     105     110
Arg Cys Lys Trp Ser Ala Thr Ser Ile Ile Phe Lys Asp Tyr Arg Thr
115     120     125
Tyr Cys Ile Thr Asn Leu His Gly Arg Arg Ile Gly Thr Arg Ile Thr
130     135     140
Asn Arg Thr Thr Thr Phe Arg Gly Glu Ile Phe Cys Lys Ile Asn Thr
145     150     155     160
Phe Phe Leu Cys Ile Lys Lys Ala
165

```

(2) INFORMATIONS POUR LA SEQ ID NO: 492:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 348 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 488204..489247

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 492:

```

Phe Ser Ser Phe Thr Pro Phe Leu Ile Tyr Asn Pro Ser Leu Gly Ala
1      5      10      15
Ala Lys His Thr Leu Leu Leu Arg Ser Asn Leu Pro Ser Leu Phe Gln
20      25      30
Tyr Leu Phe Arg Leu Leu Leu Leu Pro Tyr Arg Val Leu Ser Thr Pro
35      40      45

```

```

Pro Pro Pro Val Ile Ser Arg Pro Ser Thr Pro Ser Ala Pro Lys Pro
50      55      60
Ser Thr Pro Pro Pro Leu Pro Lys Ala Pro Lys Pro Val Lys Thr
65      70      75      80
Gln Glu Asp Leu Leu Pro Leu Val Pro Glu Gln Val Phe Val Glu Met
      85      90      95
Tyr Glu Asp Met Ala Arg Arg Gln Thr Ile Glu Ala Leu Val Pro Ala
      100      105      110
Trp Asp Ser Asp Ile Ile Phe Lys Cys Leu Cys Tyr Phe His Thr Leu
      115      120      125
Tyr Pro Gly Leu Ile Pro Leu Glu Thr Phe Pro Pro Ala Thr Ile Phe
      130      135      140
Asn Phe Lys Gln Lys Ile Ile Ser Ile Leu Glu Asp Lys Lys Ala Val
145      150      155      160
Leu Arg Gly Glu Pro Ile Lys Gly Pro Leu Pro Ile Trp Cys Ser Lys
      165      170      175
Glu Asn Tyr Arg Arg His Leu Gln Arg Thr Thr Leu Leu Pro Val Phe
      180      185      190
Met Trp Tyr His Pro Thr Pro Lys Thr Xaa Ser Asp Thr Met Gln Thr
      195      200      205
Met Lys Gln Leu Ala Ile Lys Gly Ser Val Gly Ala Ser His Trp Leu
      210      215      220
Leu Val Ile Val Asp Ile Gln Ala Arg Arg Leu Val Tyr Xaa Asp Ser
225      230      235      240
Leu Tyr Asn Tyr Val Met Pro Pro Glu Asn Met Lys Lys Glu Leu Gln
      245      250      255
Ser Phe Ala Gln Gln Leu Asp Gln Val Tyr Pro Ala Tyr Asp Ser Lys
      260      265      270
Lys Phe Ser Val Lys Ile Ala Ala Lys Glu Val Ile Gln Arg Gly Ser
      275      280      285
Gly Ser Ser Cys Gly Ala Trp Cys Cys Gln Phe Leu His Trp Tyr Leu
      290      295      300
Lys Asp Pro Leu Thr Asp Ala Leu Asn Asp Leu Pro Val Asp Ser Val
305      310      315      320
Glu Arg His Glu Asn Leu Ala Ser Phe Val Gln Ala Cys Glu Ala Ala
      325      330      335
Val Gln Asp Leu Pro Glu Leu Ser Trp Pro Glu Ala
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 493:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 113 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(488233..488571)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 493:

```

His Arg His Leu Lys Ile Met Ser Glu Ser Gln Ala Gly Thr Asn Ala
1      5      10      15
Ser Met Val Cys Arg Arg Ala Ile Ser Ser Tyr Ile Ser Thr Asn Thr
      20      25      30
Cys Ser Gly Thr Lys Gly Arg Arg Ser Ser Cys Val Leu Thr Gly Leu

```

Gly Ala Leu Gly Arg Arg Gly Gly Gly Val Glu Gly Phe Gly Ala Glu
 35 40 45
 50 55 60
 Gly Val Leu Gly Arg Asp Met Thr Gly Gly Gly Gly Val Leu Arg Thr
 65 70 75 80
 Arg Tyr Gly Lys Arg Arg Arg Arg Lys Arg Tyr Trp Asn Arg Asp Gly
 85 90 95
 Arg Leu Leu Leu Ser Arg Arg Val Cys Leu Ala Ala Pro Arg Glu Gly
 100 105 110
 Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 494:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 489440..490456

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 494:

Leu Phe Val Cys Leu Ile Asn Glu Gln Phe Ile Met Glu Pro Ile His
 1 5 10 15
 Asn Pro Pro Pro Gln Thr Cys Ser Tyr Ser Arg Pro Ser Thr Thr Tyr
 20 25 30
 Thr Ser Phe Lys Asp Ala Ser Cys Asp Thr Lys Val Thr Arg Ile Ile
 35 40 45
 Ile Ala Leu Phe Leu Ile Val Ile Ser Cys Gly Leu Ile Leu Cys Ala
 50 55 60
 Tyr Thr Phe Arg Asp Leu Leu Asp Ala Asp Tyr Leu Ala Gln Glu Gly
 65 70 75 80
 Pro Gln Gln Ala Thr Lys Leu Leu Gln Gln Leu Asp Asp Val Leu Thr
 85 90 95
 Gly Pro Pro Leu Pro Ile Trp Asp Asn Glu His Leu Phe Gln Phe Ser
 100 105 110
 Cys Leu Met Gln Asn Lys His Arg Arg Val Leu Pro Ile Asp Ile Cys
 115 120 125
 Asn Pro Leu Thr Lys Phe Asn Phe Leu Glu Cys Ile Cys Asn Cys Leu
 130 135 140
 Met Thr Lys Gln Ser Val Asn Val Asn Glu Thr Asp Met Cys Glu Leu
 145 150 155 160
 Phe Cys Pro Pro Thr Cys Thr Pro Glu Asn Tyr Arg Arg Leu Leu Cys
 165 170 175
 Thr Ser Ser Val Phe Pro Phe Val Met Trp His Asp Pro Ser Ala Asp
 180 185 190
 Thr Gln Glu Ala Met Leu Thr Lys Met Asp Gln Thr Met Ser Ser Gly
 195 200 205
 Arg Val Gly Asn Ser His Trp Val Leu Val Ile Val Asp Ile Glu Tyr
 210 215 220
 Arg Cys Val Thr Phe Phe Asp Ser Leu Cys Asp Tyr Val Ala Ser Pro
 225 230 235 240
 Gln Gln Met Arg Glu Gln Leu Glu Gly Leu Ala Val Ser Leu Gly Ala
 245 250 255

Ile Tyr Pro Lys Glu Gly Gly Ala Asp Ser Asp Gln Glu Glu Leu Leu
 260 265 270
 Ser Pro Phe Gln Val Arg Ile Gly Ser Thr Val Lys Val Gln Ser Pro
 275 280 285
 Gly Glu Phe Thr Cys Gly Ala Trp Cys Cys Gln Phe Leu Ala Trp Tyr
 290 295 300
 Leu Glu Asn Pro Asp Phe Asp Leu Glu Glu Lys Val Pro Thr Asn Pro
 305 310 315 320
 Ser Glu Arg Arg Ala Leu Leu Ala Asp Phe Ile Ser Thr Thr Glu Gln
 325 330 335
 Ala Met Ser

(2) INFORMATIONS POUR LA SEQ ID NO: 495:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 753 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(490507..492765)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 495:

Pro Arg Ile Tyr Gly Thr Val Phe Val Asn Lys Cys Arg Lys Tyr Cys
 1 5 10 15
 Gly Pro Phe Phe Leu Asn Thr Gln His Val Glu Leu Leu Val Ser Gly
 20 25 30
 Lys Gln Ser Ser Pro Gln Asp Leu Leu Gly Ile Val Ser Glu Ser Leu
 35 40 45
 Asn Gln Asp Arg Ile Val Leu Phe Arg Pro Gly Ala Glu Thr Val Phe
 50 55 60
 Val Glu Leu Arg Gly Lys Ile Gln Gln Ala Glu Ser His His Ser Gly
 65 70 75 80
 Ile Phe Ser Leu Pro Val Met Lys Gly Ile Ser Pro Gln Asp Tyr Arg
 85 90 95
 Val Tyr His Gln Asn Gly Leu Leu Ala His Asp Pro Tyr Ala Phe Pro
 100 105 110
 Leu Leu Trp Gly Glu Ile Asp Ser Phe Leu Phe His Glu Gly Thr His
 115 120 125
 Gln Arg Ile Tyr Glu Arg Met Gly Ala Ile Pro Cys Glu Ile Asp Gly
 130 135 140
 Val Pro Gly Val Arg Phe Ile Val Trp Ala Pro His Ala Gln Arg Val
 145 150 155 160
 Ser Val Ile Gly Asp Phe Asn Gly Trp His Gly Leu Val Asn Pro Leu
 165 170 175
 His Lys Val Ser Asp Gln Gly Val Trp Glu Leu Phe Val Pro Gly Leu
 180 185 190
 Thr Ala Gly Ala Cys Tyr Lys Trp Glu Met Val Thr Glu Ser Gly Gln
 195 200 205
 Val Leu Ile Lys Ser Asp Pro Tyr Gly Lys Phe Phe Gly Pro Pro Pro
 210 215 220
 Arg Ser Val Ser Val Val Ile Asp Asp Ser Tyr Glu Trp Asn Asp Ser
 225 230 235 240
 Glu Trp Leu Glu Glu Arg Ile Lys Lys Thr Glu Gly Pro Met Asn Leu

Tyr Glu Val His Val Gly Ser Trp Gln Trp Gln Glu Gly Gln Pro Leu
 245 250 255
 260 265 270
 Asn Tyr Lys Glu Leu Ala Asp Gln Leu Ala Leu Tyr Cys Lys Gln Met
 275 280 285
 His Tyr Thr His Val Glu Leu Leu Pro Val Thr Glu His Pro Leu Asn
 290 295 300
 Glu Ser Trp Gly Tyr Gln Thr Thr Gly Tyr Tyr Ala Pro Thr Ser Arg
 305 310 315 320
 Tyr Gly Ser Phe Glu Asp Leu Gln Tyr Phe Ile Asp Thr Met His Gln
 325 330 335
 His Gly Ile Gly Val Ile Leu Asp Trp Val Pro Gly His Phe Pro Ile
 340 345 350
 Asp Ser Phe Ala Met Ser Gly Phe Asp Gly Thr Pro Leu Tyr Glu Tyr
 355 360 365
 Thr Arg Asn Pro Ser Pro Leu His Pro His Trp His Thr Tyr Thr Phe
 370 375 380
 Asp Tyr Ala Lys Pro Glu Val Cys Asn Phe Leu Leu Gly Ser Ala Leu
 385 390 395 400
 Phe Trp Ile Asp Lys Met His Val Asp Gly Ile Arg Val Asp Ala Val
 405 410 415
 Ser Ser Met Leu Tyr Leu Asp Tyr Gly Arg Tyr Ala Gly Glu Trp Val
 420 425 430
 Pro Asn Arg Tyr Gly Gly Arg Glu Asn Leu Asp Ala Ile Arg Phe Leu
 435 440 445
 Gln Gln Phe Asn Thr Val Ile His Glu Lys Tyr Pro Gly Val Leu Thr
 450 455 460
 Phe Ala Glu Glu Ser Thr Thr Phe Pro Lys Ile Thr Val Ser Val Glu
 465 470 475 480
 Glu Gly Gly Leu Gly Phe Asp Tyr Lys Trp Asn Met Gly Trp Met His
 485 490 495
 Asp Thr Leu His Tyr Phe Glu Lys Asp Phe Pro Tyr Arg Pro Tyr His
 500 505 510
 Gln Ser Asp Leu Thr Phe Pro Gln Trp Tyr Ala Phe Ser Glu Arg Phe
 515 520 525
 Leu Leu Pro Phe Ser His Asp Glu Val Val His Gly Lys Arg Ser Leu
 530 535 540
 Ile Gly Lys Met Pro Gly Asp Ala Trp Arg Gln Phe Ala Gln Leu Arg
 545 550 555 560
 Leu Leu Leu Gly Tyr Gln Ile Cys Gln Pro Gly Lys Lys Leu Leu Phe
 565 570 575
 Met Gly Gly Glu Phe Gly Gln Gly Arg Glu Trp Ser Pro Gly Arg Glu
 580 585 590
 Leu Asp Trp Glu Leu Leu Asp Ile Ser Tyr His Gln Gly Val His Leu
 595 600 605
 Cys Ser Gln Glu Leu Asn Ala Leu Tyr Val Gln Ser Pro Gln Leu Trp
 610 615 620
 Gln Ala Asp His Leu Pro Ser Ser Phe Arg Trp Val Asp Phe Ser Asp
 625 630 635 640
 Val Arg Asn Gly Val Val Ala Tyr Leu Arg Phe Ala Asp Ala Asp Ala
 645 650 655
 Lys Lys Ala Leu Leu Cys Val His His Phe Gly Val Gly Tyr Phe Pro
 660 665 670
 His Tyr Leu Leu Pro Ile Leu Pro Leu Glu Ser Cys Asp Leu Leu Met
 675 680 685
 Asn Thr Asp Asn Thr Arg Phe Gly Gly Ser Gly Lys Gly Phe Arg Glu
 690 695 700
 Pro Glu Ile Leu Thr Pro Glu Ile Ala Arg Gln Glu Arg Glu Ala Ala
 705 710 715 720

Gly Leu Ile Glu Ala Asp Asp Glu Ser Gly Pro Asp Cys Trp Gly Leu
 725 730 735
 Asp Ile Glu Leu Pro Pro Ser Ala Thr Leu Ile Phe Ser Val Thr Leu
 740 745 750
 Gln

(2) INFORMATIONS POUR LA SEQ ID NO: 496:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 179 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 492357..492893

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 496:

His Pro Cys Val His Arg Tyr Ala Asp Glu Ser Leu His Gly Ile Lys
 1 5 10 15
 Lys Asn Arg Phe Pro Pro Lys Val Lys Gly Arg His Lys Asp His Glu
 20 25 30
 Pro Ile Asn His Phe Asp Asp Arg Leu Asp Asn Leu Gly Glu Lys Phe
 35 40 45
 Leu Ser Leu Gln Glu Glu Lys Ser Leu Asn Gly Ala Thr Leu Pro
 50 55 60
 Val Glu Ser Tyr Leu Ala Thr Gln Gln Lys Arg Ser Leu Pro Gln Gly
 65 70 75 80
 Gly Lys Glu Leu Ser Asp Leu Asp Ser Asn Phe Gln Lys Gln Phe Pro
 85 90 95
 Lys Asp Leu Val Asp Cys Ser Val Tyr Gln Lys Arg Glu Val Pro Arg
 100 105 110
 Val Glu Tyr Leu Arg Lys Lys Asp His Asn Ile Phe Cys Ile Tyr Leu
 115 120 125
 Gln Lys Arg Ser His Arg Tyr Val Val Pro Ala Phe Ile Ser Thr Phe
 130 135 140
 Ser Lys Arg Phe Phe Ile Leu Gln Glu Ile Ile Leu Pro Cys Ser Ser
 145 150 155 160
 Thr Arg Lys Arg Asp Glu Tyr Thr Pro Gly Leu Met Ile Ala Ser Ser
 165 170 175
 Leu Glu Thr

(2) INFORMATIONS POUR LA SEQ ID NO: 497:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 336 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(492737..493744)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 497:

Tyr Lys Gly Ala Gly Ser Phe Met Ile Lys Ile Ala Gln Ser Phe Lys
 1 5 10 15
 Pro Tyr Ile Met Glu Pro Gly Ala Lys Ile Pro Ile Pro Gly Ser Thr
 20 25 30
 Leu Tyr Ala Gln Val Phe Pro Ser Leu Trp Arg Ile Phe Ser Ser Ser
 35 40 45
 His Glu Leu Val Asn Glu Gly Arg Val Pro Ile Gln Gly Pro Leu Gln
 50 55 60
 Arg Phe Ala Val Phe Gln Asn Leu Asn Arg Gly Gly Val Ala Val Met
 65 70 75 80
 Thr Glu Gln Tyr Lys Tyr Tyr Leu Ser Pro Asn Gly Cys Tyr Thr Arg
 85 90 95
 Ser Ile Ala Asp Leu Pro Ser Ala Ser Phe Tyr Ser Gly Glu Tyr Val
 100 105 110
 Ser Phe Gly Val His Lys His Ala Asp Xaa Glu Lys Ile Arg Arg Arg
 115 120 125
 Lys Asp Leu Lys Glu Ile Leu Pro Phe Leu Phe Arg His Gly Ala Leu
 130 135 140
 Leu Gln Asn Gln Pro Asn Leu Ser Met Glu Lys Thr Glu Val Ala Leu
 145 150 155 160
 Leu Leu Asp Thr Leu Asp Ala Ala Ile Ala Glu Pro Asn Lys Glu Arg
 165 170 175
 Val Phe Ser Leu Leu Glu Arg Phe Val Tyr Ala Gly Leu Ser Lys Thr
 180 185 190
 Leu Leu Pro Arg Leu Tyr Asp Glu Glu Tyr Gln Gly Ile Val Ser Glu
 195 200 205
 Asp Pro Arg Pro Gly Asn Glu Ala Val Pro Phe Ser Leu Leu Arg Ala
 210 215 220
 Ala Ala Leu Ser Met Arg Arg Ile Phe Ile Gln Glu Ser Asp Gly Val
 225 230 235 240
 Val Thr Leu Leu Pro Ala Leu Pro Pro Glu Phe Pro Cys Gly Arg Trp
 245 250 255
 Ile Gly Leu Tyr Phe Glu Asn Ile Gly Glu Ile Ser Phe Glu Trp Ser
 260 265 270
 Lys Lys Thr Ile Arg Arg Val Ile Leu Lys Ala His Val Ser Arg Glu
 275 280 285
 Leu Ala Ile Ile Ser Pro Gly Val Tyr Ser Ser Arg Phe Arg Val Glu
 290 295 300
 Glu Gln Gly Arg Ile Ile Ser Cys Lys Ile Lys Asn Leu Leu Glu Lys
 305 310 315 320
 Val Glu Ile Lys Ala Gly Thr Thr Tyr Leu Trp Asp Arg Phe Cys Lys
 325 330 335

(2) INFORMATIONS POUR LA SEQ ID NO: 498:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 235 acides aminés
 - (B) TYPE: acide aminé
 - (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 493971..494675

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 498:

Met	Thr	Pro	Ser	Ala	Leu	Phe	His	Lys	Arg	Leu	Ile	Glu	Gln	Phe	Thr
1				5					10					15	
Ile	Phe	Leu	Ser	Val	Asp	Arg	Gly	Ile	Ser	Pro	Leu	Ser	Val	Gln	Ala
			20					25					30		
Tyr	Cys	Gln	Asp	Val	Leu	Leu	Phe	Leu	Gln	Arg	Ala	Ser	Ile	Glu	Ala
		35					40					45			
Thr	Asp	Arg	Ile	Asn	Gln	Glu	Ser	Val	Phe	Leu	Phe	Val	Glu	Lys	Cys
	50					55					60				
His	Lys	Ala	Lys	Glu	Ser	Glu	Thr	Thr	Leu	Ala	Arg	Arg	Leu	Ile	Ala
65				70					75						80
Leu	Lys	Val	Phe	Phe	His	Phe	Leu	Lys	Asp	Val	Lys	Met	Leu	Asp	Gln
			85					90					95		
Gln	Pro	Phe	Ile	Glu	His	Pro	Lys	Ile	Trp	Lys	Arg	Leu	Pro	Ser	Ile
			100				105						110		
Leu	Ser	Thr	Glu	Glu	Val	Asn	Ser	Leu	Leu	Asp	Gln	Pro	Leu	Asn	Ile
	115						120					125			
Pro	Asn	Leu	Asp	Thr	His	Ile	Ala	Ser	Arg	Asp	Ala	Ala	Ile	Leu	Tyr
	130					135					140				
Thr	Phe	Tyr	Ala	Thr	Gly	Ile	Arg	Val	Ser	Glu	Leu	Cys	Asp	Leu	Cys
145					150					155					160
Ile	Gly	Asp	Ile	Ser	Asp	Asp	Phe	Ile	Arg	Val	Thr	Gly	Lys	Gly	Arg
			165					170					175		
Lys	Thr	Arg	Leu	Val	Pro	Ile	Ser	Ile	Lys	Ala	Lys	Gln	Ala	Ile	Asp
			180				185						190		
Ala	Tyr	Leu	Ser	Ser	Phe	Arg	Asp	Glu	Leu	Gln	Lys	Lys	Ile	Pro	Leu
	195						200					205			
Lys	Asn	Met	Tyr	Phe	Cys	Leu	Ser	Glu	Gly	Lys	Asn	Ser	Ile	Val	Pro
	210					215					220				
Val	Tyr	Gly	Asn	Ala	Leu	Phe	Met	Gln	Asn						
225					230				235						

(2) INFORMATIONS POUR LA SEQ ID NO: 499:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 494573..494869

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 499:

Thr	Thr	Lys	Lys	Asn	Pro	Ser	Glu	Glu	His	Val	Phe	Leu	Ser	Ile	Arg
1				5					10					15	
Gly	Lys	Lys	Leu	Asp	Arg	Ser	Cys	Val	Trp	Lys	Arg	Ile	Thr	Phe	Tyr
			20					25					30		
Ala	Lys	Leu	Val	Thr	Thr	Lys	Arg	Ile	Ser	Pro	His	Ser	Leu	Arg	His
		35					40					45			
Pro	Phe	Ala	Thr	His	Leu	Leu	Asn	Asn	His	Ala	Asp	Leu	Arg	Ile	Ile
	50					55					60				
Gln	Glu	Met	Leu	Gly	His	Ser	Arg	Ile	Ser	Ser	Thr	Glu	Ile	Tyr	Thr
65					70				75						80
His	Val	Ala	Ser	Glu	Ser	Leu	Ile	Glu	Lys	Phe	His	Thr	Tyr	His	Pro

Arg Asp Ile

(2) INFORMATIONS POUR LA SEQ ID NO: 500:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 494835..495365

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 500:

Ser	Lys	Asn	Ser	Thr	Pro	Thr	Ile	Leu	Glu	Ile	Ser	Lys	Ile	Cys	Asp	15
1				5					10							
Glu	Val	Phe	Ser	Ser	Phe	Ser	Leu	Glu	Gln	Val	Ser	Tyr	Lys	Gly	Thr	30
			20					25								
Arg	Ala	Ser	Leu	Glu	Asn	Ser	Leu	Val	Tyr	Pro	Arg	Leu	His	Leu	Tyr	45
			35				40									
Trp	Asp	Asn	Asn	Ser	His	Thr	Gly	Arg	Asp	Ser	Lys	Asn	Tyr	Lys	Glu	60
			50			55										
Ser	Ala	Pro	Leu	Pro	Val	Leu	Gln	Ile	Leu	Leu	Leu	Gln	Gln	Glu	Arg	80
					70					75						
65	Phe	Pro	Lys	Val	Glu	Leu	Glu	Ile	Pro	Asn	Thr	Pro	His	Gln	Pro	95
					85					90						
Lys	Gln	Gln	Asn	Ser	Thr	Lys	Pro	Ser	Pro	Lys	Gly	Leu	Thr	Ala	Val	110
			100					105								
Ser	Phe	Thr	Phe	Pro	His	Leu	Phe	Ser	Asp	Ala	Ala	Glu	Lys	Thr	Thr	125
			115				120									
Asp	Ser	Gly	Tyr	Pro	Asn	Lys	His	Thr	Arg	Tyr	Leu	Asn	Lys	Lys	Ile	140
			130			135					140					
Phe	Arg	Arg	Lys	Ala	Met	Pro	Arg	Ile	Gly	Leu	Glu	Pro	Thr	Cys	Arg	160
					150					155						
145	Glu	Ala	Leu	Asp	Pro	Lys	Ser	Ser	Val	Ser	Thr	Asn	Phe	Thr	Thr	175
					165					170						
Ala																

(2) INFORMATIONS POUR LA SEQ ID NO: 501:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(494872..495174)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 501:

```

Met Lys Gln Leu Ser Ile Leu Leu Gly Met Val Ser Leu Ser Ser Ala
1      5      10      15
Val Phe Gly Ala Asp Ala Val Tyr Ser Gly Ser Leu Val Gln Pro Ser
      20      25      30
Glu Ser Val Leu Val Ala Gly Val Glu Phe Glu Glu Gln Glu Gly Glu
      35      40      45
Arg Ile Pro Tyr Ser Phe Tyr Tyr Pro Tyr Gln Tyr Asp Tyr Tyr Tyr
      50      55      60
Pro Asn Thr Gly Val Asp Glu Asp Thr Pro Glu Ser Phe Gln Glu Lys
      65      70      75      80
His Glu Cys Pro Cys Lys Lys Pro Val Pro Glu Lys Lys Lys Lys Lys
      85      90      95
Pro Arg Arg Arg Ser
      100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 502:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 316 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 495687..496634

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 502:

```

Val Pro Ser Phe Leu Lys Gly Leu Asp Thr Leu Thr Ser Val Thr Met
1      5      10      15
Asp Thr Pro Thr Pro Leu Ser Ser Val Pro Thr Asn Ala Ser Leu Lys
      20      25      30
Gly Glu Pro Gly Ser Ser Ser Gln Phe Ser Ser Ala Glu Lys Gly Val
      35      40      45
Leu Lys Thr Ser Ile Gly Asp Val Val Leu Ser Gln Ser Ile Glu Asp
      50      55      60
Gly Gly Asn Glu Thr Gln Ile Ser Leu Val Gly Val Val Asn Ile Asn
      65      70      75      80
Met Ala Gln Glu Glu Leu Pro Ala Leu Val Ser Pro Arg Thr Phe Ile
      85      90      95
Phe Leu Pro Pro Glu Thr Val Glu Leu Glu Ile Gln Ile Ala Glu Met
      100      105      110
Phe Gln Ala Leu Glu Glu Thr Pro Ser Ser Asp Ser Arg Ser Leu Gln
      115      120      125
Gln Lys Glu Thr Ser Ala Gln Thr Pro Pro Ala Pro Ser Gly Lys Val
      130      135      140
Ser Ile Phe Ser Leu Gln Ala Gln Gly Ser Ser Gln Thr Arg Ser Leu
      145      150      155      160
Pro Ser Ser Gln Glu Ser Leu Ser Pro Gln Gln Pro Ala Arg Ala Ile
      165      170      175
Gln Gly Leu Asn Thr Pro Phe Ser Pro Ala Ala Arg Cys Thr Ile Arg
      180      185      190
Ala Val Pro Leu Ser Ile Val Pro His Arg Arg Ala Asn Pro Lys Pro
      195      200      205
Ser Gln Ser Val Leu Ile Ile Ala Leu Val Leu Thr Arg Gln Ala Ile
      210      215      220
Gln Gln Glu Arg Leu Asn Phe Leu Pro Arg Asn Gly Asn Phe Leu Leu

```

(2) INFORMATION POUR LA SEQ ID NO: 503:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 294 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 496295..497176

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 503:

(X1)	DESCRIP	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995	1000	1005	1010	1015	1020	1025	1030	1035	1040	1045	1050	1055	1060	1065	1070	1075	1080	1085	1090	1095	1100	1105	1110	1115	1120	1125	1130	1135	1140	1145	1150	1155	1160	1165	1170	1175	1180	1185	1190	1195	1200	1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1260	1265	1270	1275	1280	1285	1290	1295	1300	1305	1310	1315	1320	1325	1330	1335	1340	1345	1350	1355	1360	1365	1370	1375	1380	1385	1390	1395	1400	1405	1410	1415	1420	1425	1430	1435	1440	1445	1450	1455	1460	1465	1470	1475	1480	1485	1490	1495	1500	1505	1510	1515	1520	1525	1530	1535	1540	1545	1550	1555	1560	1565	1570	1575	1580	1585	1590	1595	1600	1605	1610	1615	1620	1625	1630	1635	1640	1645	1650	1655	1660	1665	1670	1675	1680	1685	1690	1695	1700	1705	1710	1715	1720	1725	1730	1735	1740	1745	1750	1755	1760	1765	1770	1775	1780	1785	1790	1795	1800	1805	1810	1815	1820	1825	1830	1835	1840	1845	1850	1855	1860	1865	1870	1875	1880	1885	1890	1895	1900	1905	1910	1915	1920	1925	1930	1935	1940	1945	1950	1955	1960	1965	1970	1975	1980	1985	1990	1995	2000	2005	2010	2015	2020	2025	2030	2035	2040	2045	2050	2055	2060	2065	2070	2075	2080	2085	2090	2095	2100	2105	2110	2115	2120	2125	2130	2135	2140	2145	2150	2155	2160	2165	2170	2175	2180	2185	2190	2195	2200	2205	2210	2215	2220	2225	2230	2235	2240	2245	2250	2255	2260	2265	2270	2275	2280	2285	2290	2295	2300	2305	2310	2315	2320	2325	2330	2335	2340	2345	2350	2355	2360	2365	2370	2375	2380	2385	2390	2395	2400	2405	2410	2415	2420	2425	2430	2435	2440	2445	2450	2455	2460	2465
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Arg Thr Asp Met Gln Arg His Leu Gln Glu Val Ser Gln Cys His Gln
 260 265 270
 Ala Arg Ser Asn Val Leu Lys Leu Leu Lys Glu Leu Met Asp Thr Phe
 275 280 285
 Ile Tyr Asn Met Arg Pro
 290

(2) INFORMATION POUR LA SEQ ID NO: 504:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 271 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 497703..498515

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 504:

Ile Thr Lys Asp Ser Tyr Tyr Tyr Val Ile Leu Val Cys Ser Arg Thr
 1 5 10 15
 Asp Val Ala Leu Ser Gln Thr Leu Asp Leu Pro Asp Ala Ser Leu Ala
 20 25 30
 Val Gln Thr Glu Lys Phe Pro Tyr Ser Cys Ser Ile Ser Lys Glu Ser
 35 40 45
 Ala Pro Ser Cys Ile Arg Lys Ile Phe Ala His Leu Ala Ser Gln Lys
 50 55 60
 Glu Ser Ala Pro Leu Ser Phe Ser Arg Leu Gln Pro Thr Thr Pro Lys
 65 70 75 80
 Glu Arg Ile Leu Phe Phe Gly Ser Ser Pro Ser Ser Gln Leu Ser Ser
 85 90 95
 Thr Val Arg Thr Thr Thr Ser Ser Pro Trp Asn Leu Phe Ser Asn Ser
 100 105 110
 Gln Ala Arg Asn Ser Thr Arg Lys Leu Ser Glu Lys Leu His Leu Ser
 115 120 125
 Ser Glu Leu Ser Ala Arg Asp Ser Thr Lys Pro Ser Ser Ser Glu Pro
 130 135 140
 Val Lys Pro Ser Glu Asn Leu Leu His Thr Pro Glu His His Lys Glu
 145 150 155 160
 Ser Phe Ser Ser Leu Lys Lys Asp Asn Leu Ser Pro Ile Met Glu Glu
 165 170 175
 Ile Asp Ser Phe Ser Ala Glu Thr Glu Ser Leu Glu Glu Arg Leu Val
 180 185 190
 Thr Gln Lys Lys Glu Glu Thr Val Ala Gln Glu Gln Lys His Pro Leu
 195 200 205
 Leu Arg Thr Ser Thr Pro Pro Ser Lys Ala Ser Gly Glu Ser Gln Asp
 210 215 220
 Ser Ser Glu His Ser Ser Lys Glu Asp Pro Tyr Ser Gln Gln Pro Ser
 225 230 235 240
 His Lys Ile Gln Arg Arg Gly Thr Ser Gln Lys Ser Cys Ser Tyr His
 245 250 255
 His Thr Thr Tyr Cys Arg Asp Leu Leu Phe Lys Leu Pro Ser His
 260 265 270

(2) INFORMATION POUR LA SEQ ID NO: 505:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 320 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 498280..499239

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 505:

His	Lys	Lys	Lys	Lys	Lys	Pro	Leu	His	Lys	Asn	Lys	Asn	Ile	Leu	Tyr
1				5					10					15	
Leu	Glu	Pro	Pro	Pro	Leu	Leu	Pro	Lys	His	Gln	Glu	Lys	Val	Lys	Thr
			20					25					30		
Arg	Pro	Ser	Thr	Leu	Arg	Lys	Lys	Thr	Leu	Ile	Leu	Ser	Asn	Leu	Leu
			35				40					45			
Thr	Lys	Tyr	Lys	Glu	Glu	Glu	Arg	Ala	Lys	Arg	Val	Val	Pro	Ile	Ile
	50					55					60				
Thr	Pro	Pro	Thr	Val	Gly	Ile	Phe	Ser	Leu	Ser	Tyr	Leu	Leu	Thr	Lys
65					70					75				80	
Gln	Gly	Ile	Leu	Ala	Asp	Phe	Ser	Ala	Tyr	Ser	Ala	Tyr	Lys	Asp	Asn
				85					90				95		
Leu	Glu	Thr	Thr	Gln	Gln	Glu	Leu	Thr	Met	Leu	His	Gln	Glu	Arg	Ile
			100					105					110		
Glu	Gln	Val	Gln	Lys	Ile	Val	Asp	Lys	Ser	Lys	Thr	Met	Arg	Phe	Trp
		115					120					125			
Asp	Ser	Leu	Ala	Ser	Ile	Val	Ala	Thr	Ile	Ile	Pro	Trp	Ile	Glu	Met
		130				135					140				
Gly	Val	Ala	Val	Thr	Ile	Ile	Ala	Leu	Gly	Gly	Gly	Ile	Leu	Ser	Trp
145					150					155				160	
Cys	Ser	Leu	Phe	Ala	Ala	Leu	Ile	Met	Ile	Val	Ile	Ser	Leu	Leu	Glu
			165					170						175	
Ala	Phe	Asp	Gly	Trp	Arg	Ala	Ile	Ala	Lys	His	Leu	Pro	Gly	Asn	Asp
		180					185					190			
Leu	Glu	Lys	Lys	Met	Arg	Tyr	Leu	Gly	Tyr	Val	Lys	Leu	Ala	Leu	Thr
		195				200						205			
Val	Phe	Ser	Cys	Leu	Leu	Ser	Leu	Ser	Ala	Leu	Tyr	Val	Ala	Lys	Leu
	210					215					220				
Gly	Met	Ser	Pro	Leu	Leu	Gly	Val	Val	Lys	Ser	Ile	Ala	Pro	Ala	
225					230					235				240	
Leu	Ser	Gly	Met	Leu	Gly	Leu	Thr	Gln	Gly	Val	Ala	Leu	Tyr	Leu	Gln
			245					250						255	
Ser	Ser	Ser	Gln	Lys	Ile	Arg	Ala	Arg	Cys	Thr	Gln	Ile	Asp	Ala	Arg
			260				265						270		
Ile	Glu	Leu	Ile	Asn	Trp	Glu	Arg	Asp	Glu	Tyr	Phe	Leu	Arg	Ala	Glu
		275					280					285			
Gln	Leu	Leu	Asp	Ser	Met	Gln	Thr	Ser	Phe	Glu	Gln	Leu	Thr	Glu	Thr
	290					295					300				
Leu	Gln	Leu	Gln	Arg	Glu	Ile	Asp	Gln	Thr	Phe	Thr	Asp	Ala	Leu	Arg
305					310					315					320

(2) INFORMATIONS POUR LA SEQ ID NO: 506:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 506 acides aminés

(B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 499215..500732

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 506:

```

Pro Asn Val Tyr Arg Arg Leu Thr Ile Ala Ile Leu Pro Met Thr Ile
1      5      10      15
Thr Val Pro Gln Glu Thr Leu Pro Ser Leu Gln Thr Ile Ala Thr Gly
20      25      30
Glu Gln Thr Glu Thr Ser Cys Glu Glu Ala Ser Ala Leu Ser Asn Glu
35      40      45
Ile Gln Leu Leu Glu Pro Gly Gln Ala Ala Ile Leu Arg Ser Leu Ser
50      55      60
Asp Leu Cys Leu Ser Val Ile Glu Gln Thr Glu Lys Thr Leu Pro His
65      70      75      80
Ser Lys His Ser Pro Ser Phe Arg Glu Ser Cys Pro Leu Lys Tyr Leu
85      90      95
Ser Gln Gln Thr Ser Ala Ser Ser Arg Thr Gln Glu Ser Ala Thr Ala
100     105     110
Glu Gln Gln Ser Leu Thr Pro Thr Pro Thr Pro Gln Lys Thr Pro Thr
115     120     125
Gln Thr Leu His Asn Lys Pro Ser Thr Pro Ile Ser His Lys Ser Ser
130     135     140
Val Gln Gly Arg Ile Gln Thr Ser Pro Gln His Ser Thr Pro Leu Arg
145     150     155     160
Ser Ile Pro Val Ile Ile Ser Leu Pro Asn Thr Gln Gln Ala Leu Thr
165     170     175
Asp Arg Glu Pro Ile Gln Asn Ser Asn Cys Ser Pro Thr Leu Ser Val
180     185     190
Thr Ile Phe Asn Lys Glu Ser Ser Ser Ser Ser Lys Lys Asp Ser Ala
195     200     205
Ala Ser Arg Glu Gln Ser Ser Ser His Ser Ser Ser Leu Gln Lys Asn
210     215     220
Leu Ser Ser Pro Arg Ala Leu Leu Ser Pro Met Ala Leu Phe Glu
225     230     235     240
Thr Thr Ala Gln Lys Glu Thr Leu Ala Arg Glu Gly Leu Leu His Glu
245     250     255
Arg Glu Asp Leu Ser Gln Glu Gly Asp Arg Asp His His Gln Ser Asp
260     265     270
Gln Gln Gln Glu Glu Lys Glu Asp Leu Ala Ile Ser Ala Ser Phe Leu
275     280     285
Ser His Ser Lys Lys Arg Arg Glu His His Phe Asp Pro Glu Tyr Leu
290     295     300
Pro Glu Glu Ile Arg Glu Phe Ala Leu Ser Glu Ala Gln Leu Ser Gln
305     310     315     320
Leu Leu His Ile Arg Leu Asn His Leu Asp Ile Leu Arg Ile Cys Ala
325     330     335
Glu Ile Met Lys Leu Met Leu Asn Ser Arg Glu Gln Asp Leu Leu Glu
340     345     350
Arg Arg Ser Thr Arg Thr His Phe Met Gln Glu Ala Lys Lys Ile Ala
355     360     365
Asp Ser Phe Ala Lys Gln Ala Arg Ile Thr Lys Trp Leu Gly Ile Ala
370     375     380
Thr Ala Thr Leu Gly Ile Phe Gly Gly Ile Ser Pro Ile Ile Gly Glu

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385                               390                               395                               400
Val Gly Gly Glu Gly Leu Leu Asn Val Ile Arg Lys Ala Thr Gly Gly
                               405                               410                               415
Trp Gln Gln Ala Ser Ser Lys Thr Phe Phe Glu Gly Trp Gly Lys Cys
                               420                               425                               430
Val Leu Ser Leu Ser Glu Leu Ala Lys Val Ser Ser Thr Val Tyr Asp
                               435                               440                               445
Leu Arg Pro Lys Pro Val Arg Thr Ile Ala Glu Ser Tyr Lys Glu Leu
                               450                               455                               460
Phe Arg Leu Glu His Asp Glu Met Leu Arg Ser Ile Glu Glu Leu Lys
465                               470                               475                               480
Asp His Gly Arg Asn Met Asp Ser Phe Leu Leu Gln Ile Leu Gln Thr
                               485                               490                               495
Gln His Asp Ala Val Arg Ser Leu Tyr Gln
                               500                               505

```

(2) INFORMATIONS POUR LA SEQ ID NO: 507:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 307 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(500790..501710)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 507:

```

Met Arg Lys Ile Ile Leu Cys Ser Pro Arg Gly Phe Cys Ala Gly Val
1                               5                               10                               15
Ile Arg Ala Ile Gln Thr Val Glu Val Ala Leu Glu Lys Trp Gly Arg
20                               25                               30
Pro Ile Tyr Val Lys His Glu Ile Val His Asn Arg His Val Val Asp
35                               40                               45
Lys Leu Arg Glu Lys Gly Ala Ile Phe Ile Glu Asp Leu Gln Glu Val
50                               55                               60
Pro Arg Asn Ser Arg Val Ile Phe Ser Ala His Gly Val Pro Pro Ser
65                               70                               75                               80
Leu Arg Glu Glu Ala Thr Glu Arg Gly Leu Ile Ala Ile Asp Ala Thr
85                               90                               95
Cys Gly Leu Val Thr Lys Val His Ser Ala Val Lys Met Tyr Ala Lys
100                               105                               110
Lys Gly Tyr His Ile Ile Leu Ile Gly Lys Arg Lys His Val Glu Ile
115                               120                               125
Ile Gly Ile Arg Gly Glu Ala Pro Asp Gln Ile Thr Val Val Glu Asn
130                               135                               140
Ile Ala Glu Val Glu Ala Leu Pro Phe Ser Ala Gln Asp Pro Leu Phe
145                               150                               155                               160
Tyr Val Thr Gln Thr Thr Leu Ser Met Asp Asp Ala Ala Asp Ile Val
165                               170                               175
Ala Ala Leu Lys Ala Arg Tyr Pro Arg Ile Phe Thr Leu Pro Ser Ser
180                               185                               190
Ser Ile Cys Tyr Ala Thr Gln Asn Arg Gln Gly Ala Leu Arg Asn Ile
195                               200                               205
Leu Pro Gln Val Asp Phe Val Tyr Val Ile Gly Asp Arg Gln Ser Ser
210                               215                               220

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Asn Ser Asn Arg Leu Arg Glu Val Ala Glu Arg Arg Gly Val Thr Ala
225                230                235                240
Arg Leu Val Asn His Pro Asp Glu Val Thr Glu Glu Ile Leu Gln Tyr
                245                250                255
Ser Gly Asn Ile Gly Ile Thr Ala Gly Ala Ser Thr Pro Glu Asp Val
                260                265                270
Val Gln Ala Cys Leu Met Lys Leu Gln Glu Leu Ile Pro Asp Leu Ser
                275                280                285
Ile Glu Met Asp Leu Phe Val Glu Glu Asp Thr Val Phe Gln Leu Pro
                290                295                300
Lys Glu Leu
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 508:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(501808..502863)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 508:

```

Phe Ala Ile Leu Leu Ser Asn Gly Ser Ala Phe Leu Gly Arg Ala Ser
1                5                10                15
Gln Ser Leu Cys Asn Glu Trp Phe Glu Lys Arg Val Gln Tyr Trp Glu
                20                25                30
Tyr Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu
                35                40                45
Gly Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys
                50                55                60
Ser His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp
65                70                75                80
Met Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe Ala
                85                90                95
Lys Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp
                100                105                110
Gln Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu
                115                120                125
Ser Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile
130                135                140
Leu Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu
145                150                155                160
Glu Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn
                165                170                175
Met Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser
                180                185                190
Phe Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu
                195                200                205
Ser Thr Pro Ile Pro Leu Phe Gly Phe Glu Lys Ile His Pro His Pro
210                215                220
Arg Val Gln Tyr Ser Lys Pro Ile Cys Val Leu Ile Asn Glu Gln Asp
225                230                235                240
Phe Ser Cys Ala Asp Phe Phe Pro Val Val Leu Lys Asp Asn Asp Arg

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(2) INFORMATION POUR LA SEQ ID NO: 509:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(502692..503675)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 509:

(X1)	(X2)	(X3)	(X4)	(X5)	(X6)	(X7)	(X8)	(X9)	(X10)	(X11)	(X12)	(X13)	(X14)	(X15)	(X16)	(X17)	(X18)	(X19)	(X20)	(X21)	(X22)	(X23)	(X24)	(X25)	(X26)	(X27)	(X28)	(X29)	(X30)	(X31)	(X32)	(X33)	(X34)	(X35)	(X36)	(X37)	(X38)	(X39)	(X40)	(X41)	(X42)	(X43)	(X44)	(X45)	(X46)	(X47)	(X48)	(X49)	(X50)	(X51)	(X52)	(X53)	(X54)	(X55)	(X56)	(X57)	(X58)	(X59)	(X60)	(X61)	(X62)	(X63)	(X64)	(X65)	(X66)	(X67)	(X68)	(X69)	(X70)	(X71)	(X72)	(X73)	(X74)	(X75)	(X76)	(X77)	(X78)	(X79)	(X80)	(X81)	(X82)	(X83)	(X84)	(X85)	(X86)	(X87)	(X88)	(X89)	(X90)	(X91)	(X92)	(X93)	(X94)	(X95)	(X96)	(X97)	(X98)	(X99)	(X100)	(X101)	(X102)	(X103)	(X104)	(X105)	(X106)	(X107)	(X108)	(X109)	(X110)	(X111)	(X112)	(X113)	(X114)	(X115)	(X116)	(X117)	(X118)	(X119)	(X120)	(X121)	(X122)	(X123)	(X124)	(X125)	(X126)	(X127)	(X128)	(X129)	(X130)	(X131)	(X132)	(X133)	(X134)	(X135)	(X136)	(X137)	(X138)	(X139)	(X140)	(X141)	(X142)	(X143)	(X144)	(X145)	(X146)	(X147)	(X148)	(X149)	(X150)	(X151)	(X152)	(X153)	(X154)	(X155)	(X156)	(X157)	(X158)	(X159)	(X160)	(X161)	(X162)	(X163)	(X164)	(X165)	(X166)	(X167)	(X168)	(X169)	(X170)	(X171)	(X172)	(X173)	(X174)	(X175)	(X176)	(X177)	(X178)	(X179)	(X180)	(X181)	(X182)	(X183)	(X184)	(X185)	(X186)	(X187)	(X188)	(X189)	(X190)	(X191)	(X192)	(X193)	(X194)	(X195)	(X196)	(X197)	(X198)	(X199)	(X200)	(X201)	(X202)	(X203)	(X204)	(X205)	(X206)	(X207)	(X208)	(X209)	(X210)	(X211)	(X212)	(X213)	(X214)	(X215)	(X216)	(X217)	(X218)	(X219)	(X220)	(X221)	(X222)	(X223)	(X224)	(X225)	(X226)	(X227)	(X228)	(X229)	(X230)	(X231)	(X232)	(X233)	(X234)	(X235)	(X236)	(X237)	(X238)	(X239)	(X240)	(X241)	(X242)	(X243)	(X244)	(X245)	(X246)	(X247)	(X248)	(X249)	(X250)	(X251)	(X252)	(X253)	(X254)	(X255)	(X256)	(X257)	(X258)	(X259)	(X260)	(X261)	(X262)	(X263)	(X264)	(X265)	(X266)	(X267)	(X268)	(X269)	(X270)	(X271)	(X272)	(X273)	(X274)	(X275)	(X276)	(X277)	(X278)	(X279)	(X280)	(X281)	(X282)	(X283)	(X284)	(X285)	(X286)	(X287)	(X288)	(X289)	(X290)	(X291)	(X292)	(X293)	(X294)	(X295)	(X296)	(X297)	(X298)	(X299)	(X300)	(X301)	(X302)	(X303)	(X304)	(X305)	(X306)	(X307)	(X308)	(X309)	(X310)	(X311)	(X312)	(X313)	(X314)	(X315)	(X316)	(X317)	(X318)	(X319)	(X320)	(X321)	(X322)	(X323)	(X324)	(X325)	(X326)	(X327)	(X328)	(X329)	(X330)	(X331)	(X332)	(X333)	(X334)	(X335)	(X336)	(X337)	(X338)	(X339)	(X340)	(X341)	(X342)	(X343)	(X344)	(X345)	(X346)	(X347)	(X348)	(X349)	(X350)	(X351)	(X352)	(X353)	(X354)	(X355)	(X356)	(X357)	(X358)	(X359)	(X360)	(X361)	(X362)	(X363)	(X364)	(X365)	(X366)	(X367)	(X368)	(X369)	(X370)	(X371)	(X372)	(X373)	(X374)	(X375)	(X376)	(X377)	(X378)	(X379)	(X380)	(X381)	(X382)	(X383)	(X384)	(X385)	(X386)	(X387)	(X388)	(X389)	(X390)	(X391)	(X392)	(X393)	(X394)	(X395)	(X396)	(X397)	(X398)	(X399)	(X400)	(X401)	(X402)	(X403)	(X404)	(X405)	(X406)	(X407)	(X408)	(X409)	(X410)	(X411)	(X412)	(X413)	(X414)	(X415)	(X416)	(X417)	(X418)	(X419)	(X420)	(X421)	(X422)	(X423)	(X424)	(X425)	(X426)	(X427)	(X428)	(X429)	(X430)	(X431)	(X432)	(X433)	(X434)	(X435)	(X436)	(X437)	(X438)	(X439)	(X440)	(X441)	(X442)	(X443)	(X444)	(X445)	(X446)	(X447)	(X448)	(X449)	(X450)	(X451)	(X452)	(X453)	(X454)	(X455)	(X456)	(X457)	(X458)	(X459)	(X460)	(X461)	(X462)	(X463)	(X464)	(X465)	(X466)</
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Ala	Thr	Ile	Ala	Pro	Ser	Ile	Arg	Ala	Pro	Gln	Leu	Gln	Lys	Ser	Met
				245					250					255	
Arg	Ser	Phe	Phe	Pro	Lys	Lys	Asp	Asp	Ala	Phe	His	Arg	Ser	Ser	Ser
			260					265					270		
Leu	Phe	Tyr	Ser	Pro	Met	Val	Pro	His	Phe	Trp	Ala	Glu	Leu	Arg	Asn
		275					280					285			
His	Tyr	Ala	Thr	Ser	Gly	Leu	Lys	Ser	Gly	Tyr	Asn	Ile	Gly	Ser	Thr
	290					295					300				
Met	Gly	Phe	Ser	Leu	Ser	Leu	Gly	Leu	Leu	Tyr	Gly	Ser	Arg	Arg	Val
305					310					315					320
Phe	Ser	Ala	Leu	Ile	Phe	Leu	Arg								
				325											

(2) INFORMATIONS POUR LA SEQ ID NO: 510:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 421 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(503722..504984)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 510:

Met	Leu	Lys	Phe	Gln	Leu	Cys	Leu	Leu	Phe	Leu	Phe	Gly	Tyr	Leu	Ala
1				5					10					15	
Ile	Val	Phe	Glu	His	Ile	Val	Arg	Val	Asn	Lys	Ser	Ala	Val	Ser	Leu
			20					25					30		
Ala	Met	Gly	Gly	Leu	Met	Trp	Leu	Val	Cys	Phe	Ser	His	Ile	Pro	His
		35					40					45			
Ile	Asp	His	Val	Met	Met	Val	Glu	Glu	Ile	Ala	Asp	Met	Ala	Gln	Val
	50				55					60					
Ile	Phe	Phe	Leu	Phe	Ala	Met	Ala	Ile	Val	Glu	Leu	Ile	Asp	Ala	
65				70					75					80	
His	Arg	Gly	Phe	Ser	Ile	Val	Val	Arg	Cys	Cys	Asn	Val	Glu	Ser	Arg
				85					90				95		
Ser	Val	Leu	Leu	Trp	Val	Leu	Leu	Ile	Leu	Ser	Phe	Phe	Leu	Ser	Ala
			100				105						110		
Ala	Leu	Asp	Asn	Leu	Thr	Ser	Ile	Ile	Ile	Ile	Ile	Ser	Ile	Leu	Lys
		115				120						125			
Arg	Leu	Val	Lys	Ala	Arg	Glu	Asp	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Cys
	130					135					140				
Val	Ile	Gly	Val	Asn	Ala	Gly	Gly	Ala	Trp	Thr	Pro	Leu	Gly	Asp	Val
145				150					155					160	
Thr	Thr	Thr	Met	Leu	Trp	Ile	Asn	Asp	Lys	Ile	Ser	Thr	Ser	Gly	Ile
			165					170					175		
Ile	Thr	Thr	Leu	Phe	Leu	Pro	Ser	Val	Val	Cys	Val	Val	Ile	Ala	Gly
			180				185						190		
Ile	Cys	Gly	Gln	Leu	Leu	Leu	Lys	Lys	Arg	Arg	Cys	Ser	Gly	Leu	Ser
	195					200						205			
Glu	Asp	Leu	Asp	Arg	Glu	Pro	Ala	Leu	Pro	Lys	Ser	Asn	Leu	Ile	Ala
	210				215					220					
Cys	Val	Gly	Phe	Gly	Ser	Leu	Leu	Met	Val	Pro	Met	Trp	Lys	Ala	Val
225				230					235					240	
Leu	Gly	Val	Pro	Pro	Phe	Met	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Val

(2) INFORMATION POUR LA SEQ ID NO: 511:

(i) CARACTERISTIQUES DE LA SEQUE
(A) LONGUEUR: 408 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 505763..506986

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 511:

(xi)	DESCRIPTION OF THE SEQUENCE														
Lys	His	Leu	Ile	Pro	Lys	Leu	Val	Thr	Cys	Leu	Lys	Glu	Gly	Tyr	Ser
1				5					10					15	
Phe	Asn	Thr	Leu	Lys	Lys	Asp	Phe	Thr	Ala	Gly	Ile	Thr	Ala	Gly	Ile
			20					25					30		
Leu	Ala	Phe	Pro	Leu	Ala	Ile	Ala	Ile	Ala	Ile	Gly	Ile	Gly	Val	Ser
		35					40					45			
Pro	Leu	Gln	Gly	Leu	Leu	Ala	Ser	Ile	Ile	Gly	Gly	Phe	Leu	Ala	Ser
	50					55					60				
Ala	Leu	Gly	Gly	Ser	Arg	Val	Leu	Ile	Ser	Gly	Pro	Thr	Ser	Ser	Phe
65					70					75					80
Ile	Ser	Ile	Leu	Tyr	Cys	Ile	Gly	Val	Lys	Tyr	Gly	Glu	Asp	Gly	Leu
				85					90					95	
Phe	Thr	Ile	Thr	Leu	Met	Ala	Gly	Ile	Phe	Leu	Val	Ile	Phe	Gly	Leu
			100					105					110		
Ala	Gly	Leu	Gly	Thr	Phe	Ile	Lys	Tyr	Met	Pro	Tyr	Pro	Val	Val	Thr
		115					120					125			
Gly	Leu	Thr	Thr	Gly	Ile	Ala	Val	Ile	Ile	Phe	Ser	Ser	Gln	Ile	Arg
		130				135					140				
Asp	Phe	Leu	Gly	Leu	Gln	Met	Gly	Asp	Gly	Val	Pro	Leu	Asp	Phe	Ile
145					150					155					160

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Gly Lys Trp Ala Ala Tyr Trp Asp Tyr Leu Trp Thr Trp Asp Ser Lys
      165      170      175
Thr Phe Ala Val Gly Leu Phe Thr Leu Leu Met Ile Tyr Phe Arg
      180      185      190
Asn Tyr Lys Pro Arg Tyr Pro Gly Val Met Ile Ser Ile Ile Ala
      195      200      205
Ser Thr Leu Val Trp Ile Leu Lys Ile Asp Ile Pro Thr Ile Gly Ser
      210      215      220
Arg Tyr Gly Thr Leu Pro Ser Ser Leu Pro Gly Pro Val Phe Pro His
      225      230      235
Ile Ser Ile Thr Lys Met Leu Gln Leu Met Pro Asp Ala Leu Thr Ile
      245      250      255
Ser Val Leu Ser Gly Ile Glu Thr Leu Leu Ala Ala Val Val Ala Asp
      260      265      270
Gly Met Thr Gly Trp Arg His Gln Ser Asn Cys Gln Leu Ile Gly Gln
      275      280      285
Gly Ile Ala Asn Ile Gly Thr Ser Leu Phe Ala Gly Met Pro Val Thr
      290      295      300
Gly Ser Leu Ser Arg Thr Thr Ala Ser Ile Lys Cys Gly Ala Ser Thr
      305      310      315
Pro Ile Ala Gly Ile Ile His Ala Ile Cys Leu Ser Phe Ile Leu Leu
      325      330      335
Leu Leu Ala Pro Leu Thr Ile Lys Ile Pro Leu Thr Cys Leu Ala Ala
      340      345      350
Val Leu Ile Leu Ile Ala Trp Asn Met Ser Glu Ile His His Phe Ile
      355      360      365
His Leu Phe Thr Ala Pro Lys Lys Asp Val Leu Val Leu Leu Thr Val
      370      375      380
Phe Ile Leu Thr Val Met Thr Thr Ile Thr Ser Ala Val Gln Val Gly
      385      390      395      400
Met Ile Leu Gln Pro Phe Tyr Ser
      405

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(2) INFORMATIONS POUR LA SEQ ID NO: 512:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 147 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 506999..507439

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 512:

```

Ala Ile Tyr Leu Met Leu Ser Pro Gln Gln Asn Ile Leu Met Asn Pro
1           5           10           15
Asn Asn Leu Lys Met Thr Cys Tyr Phe Ser Lys Asn Glu Val Pro Pro
      20           25           30
Phe Thr Glu Ile Tyr Glu Ile Asn Gly Pro Phe Phe Phe Gly Ile Ala
      35           40           45
Asp Arg Leu Lys Asn Leu Leu Asn Glu Ile Glu Lys Pro Pro Lys Ile
      50           55           60
Phe Ile Leu Cys Met Thr Arg Val Pro Thr Ile Asp Ala Ser Ala Met
      65           70           75           80
His Ala Leu Glu Glu Phe Phe Leu Glu Cys Asp Arg Gln Gly Thr Leu

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85 90 95
 Leu Leu Leu Ala Gly Val Lys Lys Thr Pro Leu Ser Asp Leu Arg Arg
 100 105 110
 Tyr His Val Asp Glu Leu Ile Gly Val Asp His Ile Phe Ser Asn Ile
 115 120 125
 Lys Gly Ala Leu Leu Phe Ala Lys Ala Leu Ile Lys Leu Glu Ser Lys
 130 135 140
 Ser Ser Gln
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 513:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 252 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(507649..508404)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 513:

Ser Phe Arg Val Cys Ser Arg Tyr Lys Asn Trp Lys Asn Ala Phe Asp
 1 5 10 15
 Gly Cys Ser Ser Asn Asp Ser Trp Ala Lys Glu Phe Ser Gly Tyr Ser
 20 25 30
 Cys Gln Leu His Asn Cys Leu Glu Arg Ile Gly Phe Ser Leu Thr His
 35 40 45
 Leu Tyr Glu Leu Ala Ile Gly Gly Thr Ala Ile Gly Thr Gly Leu Asn
 50 55 60
 Val Pro Glu Gly Phe Val Glu Lys Val Ile Gln Tyr Leu Arg Arg Glu
 65 70 75 80
 Thr Gly Glu Pro Phe Val Pro Ala Ser Asn Tyr Phe Ala Ala Leu Ser
 85 90 95
 Asn His Asp Ala Leu Val Gln Ala His Gly Ser Leu Thr Val Leu Ala
 100 105 110
 Cys Ala Leu Val Lys Ile Ala Thr Asp Leu Ser Xaa Leu Gly Ser Gly
 115 120 125
 Pro Arg Cys Gly Leu Gly Glu Ile Phe Phe Pro Glu Asn Glu Pro Gly
 130 135 140
 Ser Ser Ile Met Pro Gly Lys Ile Asn Pro Thr Gln Ser Glu Ala Leu
 145 150 155 160
 Gln Met Val Cys Ser Gln Val Ile Gly Asn Asn Gln Ser Ile Ile Phe
 165 170 175
 Ser Gly Thr Lys Gly Asn Phe Glu Leu Asn Val Met Lys Pro Val Ile
 180 185 190
 Ile Tyr Asp Phe Leu Gln Ser Val Asn Leu Leu Ala Gly Ala Met Arg
 195 200 205
 Ser Phe Ala Asp Cys Phe Val Cys Gly Leu Lys Val Asn Lys Gly Gln
 210 215 220
 Leu Gln Gln Asn Val Glu Arg Ser Leu Met Leu Val Thr Ala Leu Val
 225 230 235 240
 Pro Phe Trp Gly Thr Ile Asn Val Gln Arg Leu Leu
 245 250

(2) INFORMATIONS POUR LA SEQ ID NO: 514:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 100 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 508291..508590

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 514:

Thr	Ile	Met	Gln	Leu	Thr	Thr	Ile	Pro	Arg	Lys	Leu	Phe	Cys	Pro	Arg
1			5					10					15		
Val	Ile	Gly	Thr	Thr	Ser	Ile	Lys	Cys	Val	Leu	Pro	Ile	Phe	Ile	Ser
		20					25					30			
Arg	Ala	Asn	Ser	Lys	Ala	Leu	Ala	Ser	Thr	Thr	Phe	Phe	Lys	Cys	Ser
		35				40					45				
Asn	Thr	Gly	Ile	Lys	Asp	Pro	Phe	Ile	Leu	Cys	Thr	Ala	Ala	Ile	Cys
	50				55					60					
Ile	Ala	Val	Gly	Lys	Thr	Ser	Phe	Glu	Asp	Trp	Val	Tyr	Ser	Arg	Asp
65				70				75						80	
His	Trp	Asp	Ala	Arg	Asp	Val	Tyr	Phe	Gln	Ala	Leu	Pro	His	Asp	Ala
			85					90					95		
Glu	Leu	Leu	Asn												
			100												

(2) INFORMATIONS POUR LA SEQ ID NO: 515:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(508478..508915)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 515:

Met	Xaa	Gln	Glu	Asn	Asp	Ser	Leu	Gly	Ile	Val	Leu	Val	Pro	Glu	Asp
1			5					10					15		
Lys	Leu	Phe	Gly	Ala	Gln	Thr	Gly	Xaa	Ser	Gln	Glu	Phe	Phe	Ser	Tyr
		20					25					30			
Gly	Lys	Glu	Ser	Met	Pro	Leu	Glu	Ile	Ile	His	Ala	Leu	Val	Lys	Ile
		35				40					45				
Lys	Lys	Cys	Ala	Ala	Lys	Ala	Asn	Gly	Asp	Leu	Gly	Cys	Leu	Asp	Ala
	50				55				60						
Lys	Arg	Arg	Asp	Met	Ile	Val	Ala	Ala	Thr	Asp	Glu	Ile	Leu	Ser	Gly
65				70				75					80		
Glu	Phe	Asp	Glu	His	Phe	Pro	Leu	Lys	Val	Trp	Gln	Thr	Gly	Ser	Gly
			85					90					95		
Thr	Gln	Ser	Asn	Met	Asn	Val	Asn	Glu	Val	Ile	Ala	Asn	Leu	Ala	Ile
			100					105					110		
Gln	Arg	His	Gly	Gly	Glu	Leu	Gly	Ser	Lys	His	Pro	Val	His	Pro	Asn

Gln Ala Ser Ile Asp Thr Phe Phe Tyr
305 310

(2) INFORMATIONS POUR LA SEQ ID NO: 517:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 511039..511527

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 517:

Lys	Lys	Gln	Ser	Ala	Ala	Ser	Leu	Glu	Gly	Lys	Ser	Phe	Cys	Ser	Ser	1	5	10	15
Arg	Val	Phe	Cys	Ser	Leu	Ser	Ser	Ile	Ile	Arg	Ala	Pro	Leu	Leu	Phe	20	25	30	
Ala	Asn	Thr	Ser	Met	Arg	Ser	Thr	Val	Val	Gly	Gly	Cys	Gly	Val	Met	35	40	45	
Phe	Thr	Gly	Met	Arg	Ala	Ile	Leu	Arg	Asn	Thr	Gln	Ala	Ser	Leu	Trp	50	55	60	
Ser	Lys	Ile	Pro	Ser	Leu	Ser	Gln	Ser	Pro	Lys	Val	Ala	Pro	Ile	Ala	65	70	75	80
Leu	Pro	Leu	Met	Ile	Gly	Pro	Ser	Trp	Leu	Cys	Ala	Cys	Ala	Pro	Leu	85	90	95	
Ala	Met	Gln	Gln	Leu	Pro	Phe	Ser	Ile	Val	Cys	Ala	Leu	Leu	Cys	Leu	100	105	110	
Ser	Trp	Leu	Met	Met	Thr	Ile	Thr	Thr	Ile	Val	Leu	Gln	Thr	Ala	Asn	115	120	125	
Lys	Ala	Gly	Ser	Gln	Thr	Ile	Ile	Ala	Thr	Gln	Thr	Ile	Leu	Gly	Leu	130	135	140	
Ala	Val	Val	Ile	Val	Gly	Ala	Gln	Leu	Leu	Val	Ser	Gly	Leu	Gln	Gln	145	150	155	160
Thr	Phe	Leu																	

(2) INFORMATIONS POUR LA SEQ ID NO: 518:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 213 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 511547..512185

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 518:

Met	Leu	His	Ser	Leu	Phe	Arg	Leu	Thr	Leu	Leu	Phe	Tyr	Ala	Leu	Phe	1	5	10	15
Asn	Ala	Leu	Gly	Ser	Leu	Pro	Val	Phe	Ile	Ala	Leu	Leu	Lys	Asn	Phe				

```

                20                25                30
Ser Phe Lys Lys Gln Gln Arg Ile Ile Leu Arg Glu Ser Ile Phe Ala
      35                40                45
Leu Leu Leu Leu Leu Leu Phe Val Thr Phe Gly Arg Gly Phe Phe Arg
      50                55                60
Leu Leu Gly Ile Thr Leu Pro Ala Phe Gln Phe Thr Gly Gly Leu Leu
      65                70                75                80
Leu Gly Ser Ile Ala Ile Asp Met Met Lys Ala Leu Pro Ser Gln Ser
      85                90                95
Glu Thr Leu Glu Lys Asp Lys Asp Glu Pro Val Phe Phe Pro Leu Ala
      100                105                110
Phe Pro Val Ile Thr Gly Pro Ala Met Ile Thr Ser Thr Leu Gly His
      115                120                125
Met Glu Glu Gly Ile Phe Pro Lys Glu Ile Val Leu Gly Ala Ile Val
      130                135                140
Xaa Ala Trp Leu Phe Ser Leu Ile Thr Leu Leu Phe Ser Ser Ser Ile
      145                150                155                160
Asn Arg Leu Phe Gly Gln Met Gly Leu Leu Ala Leu Glu Arg Leu Phe
      165                170                175
Gly Ile Ser Leu Ala Leu Met Ala Gly Asn Leu Met Leu Lys Ala Leu
      180                185                190
Ser Thr Ala Phe Asn Ile Gly Tyr Tyr Met Leu His Leu Lys Ala Leu
      195                200                205
Leu Tyr Val Lys Arg
      210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 519:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 237 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 512382..513092

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 519:

```

Ser Leu Pro Ser Tyr Ser Ser Tyr Ser Arg Cys Phe Met Arg Xaa Ala
1      5      10      15
Lys Glu Gly Val Thr Thr Asn Glu Leu Asp Leu Leu Ser Arg Glu Leu
      20      25      30
His Lys Arg His Asn Ala Ile Pro Ala Pro Leu Asn Tyr Gly His Pro
      35      40      45
Pro Phe Pro Lys Thr Ile Cys Thr Ser Leu Asn Glu Val Ile Cys His
      50      55      60
Gly Ile Pro Asn Asp Ile Pro Leu Gln Asn Gly Asp Ile Met Asn Ile
      65      70      75      80
Asp Val Ser Cys Ile Val Asp Gly Phe Tyr Gly Asp Cys Ser Arg Met
      85      90      95
Val Met Ile Gly Glu Val Ser Glu Ile Lys Arg Lys Val Cys Glu Ala
      100      105      110
Ser Leu Glu Ala Leu Asn Ala Ala Ile Ser Ile Leu Glu Pro Asn Leu
      115      120      125
Pro Leu Tyr Glu Ile Gly Glu Val Ile Glu Asn Cys Ala Ala Lys Tyr
      130      135      140

```

Gly Phe Ser Val Val Asp Gln Phe Val Gly His Gly Val Gly Val Lys
 145 150 155 160
 Phe His Glu Asn Pro Phe Val Ala His His Arg Asn Ser Cys Lys Ile
 165 170 175
 Pro Leu Ala Pro Gly Met Ile Phe Thr Ile Glu Pro Met Ile Asn Val
 180 185 190
 Gly Lys Lys Glu Gly Phe Ile Asp Pro Ile Asn His Trp Glu Ala Arg
 195 200 205
 Thr Cys Asp His Gln Pro Ser Ala Gln Trp Glu His Ala Ile Leu Ile
 210 215 220
 Thr Asp Ser Gly Cys Glu Val Leu Thr Leu Leu Asp Lys
 225 230 235

(2) INFORMATIONS POUR LA SEQ ID NO: 520:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 411 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(513055..514287)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 520:

Thr Lys Lys Arg Val Leu Met Gly Phe Gly Thr Val Arg Gly Lys Gly
 1 5 10 15
 Lys Ala Val Lys Ser Phe Phe Leu Arg Pro Leu Gln Asn Leu Glu Val
 20 25 30
 Gly Leu Phe Ser Leu Pro Ile Val Leu Leu Leu Gly Glu Ile Gly Cys
 35 40 45
 Val Ser Ser Ile Ser Ser Val Ser Leu Val Ala Val Leu Ser Ile Val
 50 55 60
 Gly Val Phe Val Ala Leu Val Ser Phe Phe Arg Ser Trp Gly Tyr Gly
 65 70 75 80
 Leu Ser Val Val Gly Ala Ile Phe Phe Gly Leu Ala Leu Cys Asn Asn
 85 90 95
 Phe Pro Val Ser Val Phe Trp Gly Gly Leu Leu Thr Val Ser Phe Ile
 100 105 110
 Ile Ser Tyr Gly Ile Leu Leu Leu Ser Val Ser Leu Val Glu Gly His
 115 120 125
 Ile Lys Glu Lys Ala Val Ser Leu Ser Glu Leu Thr Ala Ser His Asn
 130 135 140
 Ser Leu Gln Asp Ser Tyr Asn Arg Glu Val Gln Glu Arg Lys Glu Lys
 145 150 155 160
 Glu Leu Leu Ala Gln Ser Lys Ile Thr Ala Leu Glu Gln Glu Leu Ser
 165 170 175
 Val Ser His Glu Gln Leu Gln Glu Val Ser Arg Lys Tyr Thr His Thr
 180 185 190
 Ser Glu Asp Leu Gln Ile Leu Ile Asp Gln Arg Asp Ser Trp Leu Lys
 195 200 205
 Asp Tyr Met Thr Leu His Gln Glu Tyr Val Arg Val Ala Gly Asp
 210 215 220
 Glu Glu Asn Val Ile Phe Pro Trp Lys Val Phe Gln Gly Asn Ser Glu
 225 230 235 240
 Lys Asp Ser Gly Tyr Gln Gln Arg Val Gln Asp Ala Glu His Lys Ile



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(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 515808..516422

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 524:

(xi)	DESCRIPTION OF THE SEQUENCE														
Arg	Gly	Tyr	Pro	Met	Ser	Ser	Ala	Ile	Ile	Pro	Thr	Leu	Pro	Glu	Lys
1				5					10					15	
Asn	Thr	Val	Ile	Pro	Asp	Ser	Thr	Leu	Ile	Glu	Pro	Thr	Ser	Ile	Glu
			20					25					30		
Ile	Asn	Lys	Lys	Ser	Ala	Met	Tyr	Phe	Cys	Ile	Ala	Val	Met	Leu	Lys
		35					40					45			
Leu	Ser	Val	Ala	Thr	Thr	Asp	Tyr	Ser	His	Ala	Ile	Met	Ala	Val	Leu
	50					55					60				
Gln	Glu	Asn	Thr	Leu	Glu	Gln	Gln	Arg	Lys	Thr	Lys	Glu	Leu	Ile	Asn
65					70					75				80	
Ile	Pro	Leu	Leu	Tyr	Val	Pro	Asp	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Asp
				85					90					95	
Asp	Glu	Tyr	Thr	Asn	His	Ser	Thr	Ile	Gln	Ala	Phe	Gln	Thr	Ser	Asn
			100					105					110		
Gln	Gln	Ile	Thr	Ala	Asn	Arg	Glu	Leu	Ile	Gln	Gln	Glu	Leu	Ser	Ala
		115					120					125			
Ala	Gln	Gln	Arg	Ala	Gln	Ala	Asn	Gln	Lys	Ser	Val	Asn	Ala	Thr	Ser
	130					135					140				
Thr	Glu	Ser	Met	Lys	Ile	Leu	Gln	Ala	Val	Ser	Ala	Leu	Leu	Thr	Ser
145					150				155					160	
Leu	Ile	Asp	Leu	Thr	Ile	Lys	Ala	Asn	Leu	Thr	Thr	Ser	Leu	Arg	Thr
				165					170					175	
Asn	Ile	Leu	Gly	Cys	Thr	Gly	Phe	Pro	Met	His	Pro	Asn	Asn	Lys	Pro
			180					185					190		
Cys	Glu	Thr	Lys	Gly	Arg	Leu	Thr	Ala	Lys	Asn	Arg	Ala			
		195					200					205			

(2) INFORMATION POUR LA SEQ ID NO: 525:

(i) CARACTERISTIQUES DE LA SEQUENCE:
(ii) LONGUEUR: 232 acides aminés

(A) LONGUEUR: 232 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 516476..517171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 525:

(xi) DESCRIPTION OF SEQUENCE															
Glu	Leu	Ser	Ser	Pro	Ile	Ser	Thr	Asn	Lys	Leu	Pro	Phe	Gly	Glu	Ser
1				5					10					15	
Pro	Lys	Thr	Ala	Ser	Leu	Leu	Val	Leu	Val	Thr	Ser	Cys	Ser	Ala	Pro
			20					25					30		
Ser	Ile	Ala	Phe	Phe	Leu	Gln	Tyr	Phe	Phe	Gln	Val	Arg	Gly	Pro	Ile
		35					40					45			

```

Glu Trp Leu Ala Leu Ser Val Lys Gly Ile His Gln His Tyr Phe Trp
 50          55          60
Gln Trp Leu Thr Tyr Pro Leu Val Thr Ala Asp Thr Leu Lys Leu Gly
65          70          75          80
Asp Leu Arg Ser Leu Glu Ile Thr Gln Arg Leu Leu Met Arg Asn Val
          85          90          95
Leu Asp Phe Ile Leu Phe Tyr Lys Ala Thr Asp Val Ile Ile Arg Lys
          100          105          110
Leu Gly Thr Gly Ser Phe Val Phe Leu Leu Thr Thr Gln Val Ser Ile
          115          120          125
Ala Gly Ile Ser Ile Trp Ala Phe Leu Trp Leu Ile Gly Ser Thr Gln
          130          135          140
Ala Phe Phe Gly Pro Glu Ser Leu Ile Cys Ala Leu Leu Ile Val Arg
          145          150          155          160
Val Phe Leu Asp Pro Glu Lys Arg Leu Thr Leu Pro Leu Phe Pro Ile
          165          170          175
Ser Leu Ser Arg Lys Trp Ser Phe Val Leu Leu Leu His Phe Tyr Phe
          180          185          190
Leu Ile Leu Ile Leu Ser Gly Ala Tyr Ala Ile Leu Leu Gly Ser Val
          195          200          205
Leu Ser Met Ala Leu Ala Ile Cys Phe Cys Tyr Lys Glu Asn Ile Pro
          210          215          220
Asn Pro Tyr Arg Gly Ser Tyr Arg
225          230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 526:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(517400..517888)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 526:

```

Met Cys Ile Glu Lys Asp Leu Phe Phe Met Lys Lys Ala Leu Asp Glu
1          5          10          15
Ala Arg Lys Ala Tyr Glu Gln Asp Glu Val Pro Val Gly Cys Ile Ile
          20          25          30
Val His Gly Asp Lys Ile Ile Ala Arg Gly His Asn Ser Val Glu Gln
          35          40          45
Leu Lys Asp Pro Thr Ala His Ala Glu Met Ile Cys Ile Ser Ala Ala
          50          55          60
Ala Glu Tyr Leu Glu Asn Trp Arg Leu Lys Asp Thr Ile Leu Tyr Cys
65          70          75          80
Thr Leu Glu Pro Cys Leu Met Cys Ala Gly Ala Ile Gln Leu Ala Arg
          85          90          95
Ile Pro Arg Ile Val Trp Gly Ala Pro Asp Leu Arg Leu Gly Ala Gly
          100          105          110
Gly Ser Trp Leu Asn Val Phe Leu Glu Lys His Pro Phe His Gln Val
          115          120          125
Glu Cys Cys Ser Gly Val Cys Tyr Gln Glu Ser Glu Gln Leu Met Lys
          130          135          140
Asn Phe Phe Leu Glu Lys Arg Lys Ala Lys Asp Glu Gly Arg Asn Ser

```

160

Asp 1	Asn	Ser	Met	Ala 5	Phe	Glu	Thr	Phe	Ser 10	Val	Ala	Leu	Asp	Lys 15	Asp
Lys	Thr	Leu	Ile 20	Phe	Glu	Thr	Gly	Lys 25	Ile	Ala	Arg	Gln	Ala 30	Ser	Gly
Ala	Val	Leu 35	Val	Lys	Met	Asn	Glu 40	Thr	Trp	Val	Phe	Ser 45	Ser	Ala	Cys
Ala 50	Ala	Ser	Leu	Ser	Glu	Ala 55	Val	Gly	Phe	Leu	Pro 60	Phe	Arg	Val	Asp
Tyr 65	Gln	Glu	Lys	Phe	Ser 70	Ser	Ala	Gly	Arg	Thr 75	Ser	Gly	Gly	Phe	Leu 80
Lys	Arg	Glu	Gly	Arg 85	Pro	Ser	Glu	Arg	Glu 90	Ile	Leu	Val	Ser	Arg 95	Leu

Ile Asp Arg Ser Leu Arg Pro Ser Phe Pro Asn Arg Leu Met Gln Asp
 100 105 110
 Ile Gln Val Leu Ser Tyr Val Trp Ser Tyr Asp Gly Lys Thr Leu Pro
 115 120 125
 Asp Pro Pro Ser Leu Phe Ala Glu Leu Leu Pro Leu
 130 135 140

(2) INFORMATIONS POUR LA SEQ ID NO: 529:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 518923..519516

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 529:

Val Pro Pro Ser Leu Asp Leu Val Met Ala Gly Thr Ala Ser Ala Val
 1 5 10 15
 Leu Met Ile Glu Gly His Cys Asp Phe Leu Thr Glu Glu Gln Val Leu
 20 25 30
 Glu Ala Ile Ala Phe Gly Gln Thr Tyr Ile Ala Lys Ile Cys Asp Ala
 35 40 45
 Ile Glu Ala Trp Gln Lys Ala Ile Gly Lys Gln Lys Asn Phe Ser Ala
 50 55 60
 Val Leu Asp Met Pro Glu Asp Val Gln Asn Val Val Ser Asp Phe Ile
 65 70 75 80
 Arg Glu Lys Phe Glu Lys Ala Leu Ser Phe Arg Asp Lys Glu Ala Leu
 85 90 95
 Glu Gln Ala Ser Lys Glu Leu Glu Glu Ser Val Ile Ala Asn Leu Val
 100 105 110
 Gln Glu Glu Asn Ser Asp Phe Ser Leu Leu Asn Val Lys Ala Ala Phe
 115 120 125
 Lys Thr Ala Lys Ser Asn Gln Met Arg Ala Leu Ile Gln Asp Leu Gly
 130 135 140
 Ile Arg Val Asp Gly Arg Thr Thr Thr Glu Ile Arg Pro Ile Ser Ile
 145 150 155 160
 Glu Thr Pro Leu Leu Pro Arg Thr His Gly Ser Cys Leu Phe Thr Arg
 165 170 175
 Gly Glu Thr Gln Ser Met Ala Val Cys Thr Leu Gly Gly Glu Asn Met
 180 185 190
 Ala Gln Asp Ser Lys Ile
 195

(2) INFORMATIONS POUR LA SEQ ID NO: 530:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 307 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 519577..520497

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 530:

```

Lys Val Gly Arg Ile Gly Ser Pro Gly Arg Arg Glu Ile Gly His Gly
1      5      10      15
Lys Leu Ala Glu Xaa Ala Leu Ser His Val Leu Pro Glu Thr Ser Arg
20      25      30
Phe Pro Tyr Ile Ile Arg Leu Glu Ser Asn Ile Thr Glu Ser Asn Gly
35      40      45
Ser Ser Ser Met Ala Ser Val Cys Gly Gly Cys Leu Ala Leu Met Asp
50      55      60
Ala Gly Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu
65      70      75      80
Ile Leu Asp Arg Asp Gln Ala Ile Ile Leu Ser Asp Ile Ser Gly Ile
85      90      95
Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Lys
100      105      110
Gly Ile Thr Ala Phe Gln Met Asp Ile Lys Ile Glu Gly Ile Thr His
115      120      125
Lys Ile Met Glu Gln Ala Leu Ala Gln Ala Lys Gln Gly Arg Ser His
130      135      140
Ile Leu Asn Leu Met Thr Gln Val Leu Ala Ser Pro Lys Gly Thr Val
145      150      155      160
Ser Lys Tyr Ala Pro Arg Ile Glu Thr Met Gln Ile Asn Thr Ser Lys
165      170      175
Ile Ala Thr Val Ile Gly Pro Gly Gly Lys Gln Ile Arg Gln Ile Ile
180      185      190
Glu Arg Ser Gly Ala Gln Val Asp Ile Asn Asp Asp Gly Val Ile Asn
195      200      205
Ile Ala Ala Ser Thr Gln Glu Ser Ile Asn Lys Ala Lys Glu Leu Ile
210      215      220
Glu Gly Leu Thr Gly Glu Val Glu Val Gly Lys Val Tyr Asn Gly Arg
225      230      235      240
Val Thr Ser Ile Ala Thr Phe Gly Val Phe Val Glu Val Leu Pro Gly
245      250      255
Lys Glu Gly Leu Cys His Ile Ser Glu Leu Ser Lys Gln Lys Val Asp
260      265      270
Asn Ile Ser Asp Phe Val Lys Glu Gly Asp Lys Leu Ala Val Lys Leu
275      280      285
Leu Ser Ile Asn Glu Lys Gly Gln Leu Lys Leu Ser His Lys Ala Thr
290      295      300
Leu Glu Asp
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 531:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(520718..521986)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 531:

Pro Val Leu Ile Ser Leu Lys Cys Leu Leu Gly Leu Glu Gln Val Glu
 1 5 10 15
 Ser Glu Ile Cys Ser Ser Arg Arg Ser Val Met Leu Leu Gly Ile Ile
 20 25 30
 Phe Ile Asp Glu Ile Asp Ala Val Gly Arg His Arg Gly Ala Gly Ile
 35 40 45
 Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu Asn Gln Leu Leu Val
 50 55 60
 Glu Met Asp Gly Phe Gly Thr Asn Glu Gly Val Ile Leu Met Ala Ala
 65 70 75 80
 Thr Asn Arg Pro Asp Val Leu Asp Lys Ala Leu Leu Arg Pro Gly Arg
 85 90 95
 Phe Asp Arg Arg Val Val Val Asn Leu Pro Asp Ile Lys Gly Arg Phe
 100 105 110
 Glu Ile Leu Ala Val His Ala Lys Arg Ile Lys Leu Asp Pro Thr Val
 115 120 125
 Asp Leu Met Ala Val Ala Arg Ser Thr Pro Gly Ala Ser Gly Ala Asp
 130 135 140
 Leu Glu Asn Leu Leu Asn Glu Ala Ala Leu Leu Ala Ala Arg Lys Asp
 145 150 155 160
 Arg Thr Ala Val Thr Ala Val Glu Val Ala Glu Ala Arg Asp Lys Val
 165 170 175
 Leu Tyr Gly Lys Glu Arg Arg Ser Leu Glu Met Asp Ala Gln Glu Lys
 180 185 190
 Lys Thr Thr Ala Tyr His Glu Ser Gly His Ala Ile Val Gly Leu Cys
 195 200 205
 Val Glu His Ser Asp Pro Val Asp Lys Val Thr Ile Ile Pro Arg Gly
 210 215 220
 Leu Ser Leu Gly Ala Thr His Phe Leu Pro Glu Lys Asn Lys Leu Ser
 225 230 235 240
 Tyr Trp Lys Lys Glu Leu Tyr Asp Gln Leu Ala Val Leu Met Gly Gly
 245 250 255
 Arg Ala Ala Glu Gln Ile Phe Leu Gly Asp Val Ser Ser Gly Ala Gln
 260 265 270
 Gln Asp Ile Ala Gln Ala Thr Lys Ile Val Arg Ser Met Ile Cys Glu
 275 280 285
 Trp Gly Met Ser Asp His Leu Gly Thr Val Ala Tyr Asp Glu His Ser
 290 295 300
 Glu Ala Ala Pro Thr Gly Tyr Gly Ser Tyr His Glu Lys Asn Tyr Ser
 305 310 315 320
 Glu Glu Thr Ala Lys Val Ile Asp Asn Glu Leu Lys Thr Leu Leu Asp
 325 330 335
 Ala Ala Tyr Gln Arg Ala Leu Asp Ile Ile Asn Ser His Lys Glu Glu
 340 345 350
 Leu Glu Leu Met Thr Gln Met Leu Ile Glu Phe Glu Thr Leu Asp Ser
 355 360 365
 Lys Asp Val Lys Glu Ile Met Asp His Ser Trp Asp Ala Asp Lys Lys
 370 375 380
 Arg Ala Arg Met Lys Glu Glu Gly Met Leu Tyr Lys Lys Ile Ser Asp
 385 390 395 400
 Asp Leu Pro Pro Pro Pro Pro Gln Glu Asn Val Gln Asp Gly Thr Ser
 405 410 415
 Leu Lys Phe Asn Thr Ser Thr
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 532:

Ser Gly Met Pro Ile Pro Glu Ala Gly Tyr Thr Ile Ser Pro Arg Thr
 145 150 155 160
 Asp Val Gly Leu Ser Val Leu Glu Pro Leu Val Val Tyr Gly Pro Val
 165 170 175
 Asp Ala Gln Ile Val Asn Leu Ala Ala Leu Glu Asn Arg Val Arg Ser
 180 185 190
 Leu Pro Lys Ser Thr Glu Ser Leu Arg Val Phe Gly Ser Asp Leu Tyr
 195 200 205
 Ala Leu Ile Gly Lys Tyr Leu Ser Pro Ala Leu Gly Ile Gly Ser Glu
 210 215 220
 Ser Leu Lys Lys Glu Ile Lys Asp Leu His Gln Gln Val Glu Asn Ser
 225 230 235 240
 Leu Thr Gln Val Ile Glu Gly Asp Gln Ala Val Ala Leu Tyr Lys Thr
 245 250 255
 Val Leu Glu Thr Leu His Arg Ile Ser Leu Ala Leu Val Ser Pro Glu
 260 265 270
 Glu Gly Thr Arg Phe His Gln Leu Arg Ser Val Arg Leu Tyr Arg Glu
 275 280 285
 Asp Phe Asn Arg Cys Val Lys Leu Leu Arg Glu Ser Asp Glu Thr Gln
 290 295 300
 Val Gln Leu Asp Lys Leu Arg Gly Glu Leu Val Gln Ala Val Trp Tyr
 305 310 315 320
 Phe Asn Asn Gln Glu Leu Ser Ser Arg Ala Leu Glu Lys Gln Asp Pro
 325 330 335
 Glu Val Phe Ser Arg Trp Phe Glu Gly Ala Lys Gln Glu Trp Ala Ala
 340 345 350
 Phe Ser Ser Asn Lys Ser Leu Ser Phe Arg Ala Pro Asp Gln Pro Arg
 355 360 365
 Asn Leu Val Leu Glu Lys Thr Phe Arg Ser Glu Glu Pro Thr Pro His
 370 375 380
 Tyr Ser Gly Tyr Leu Phe Thr Phe Met Pro Ile Ile Leu Val Leu Leu
 385 390 395 400
 Phe Ile Tyr Phe Ile Phe Ser Arg Gln Val Lys Gly Met Asn Gly Ser
 405 410 415
 Ala Met Ser Phe Gly Lys Ser Pro Ala Arg Leu Leu Ala Lys Gly Gln
 420 425 430
 Lys Gln Ser Asn Phe Cys Gly Cys Ser Arg Asp Arg Gly Ser Gln Arg
 435 440 445
 Arg Thr Arg
 450

(2) INFORMATIONS POUR LA SEQ ID NO: 534:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 323 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(523623..524591)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 534:

Cys Tyr Asp Asn Pro Phe Ile Phe Glu Asn Asp Lys Gln Leu Glu Gly
 1 5 10 15
 Phe Phe Ser Ser Leu Asp Lys Lys Lys Lys Tyr Leu Leu Ala Leu Ser

```

Ser Leu Ile Cys Ile Ser Ile Ile Ser Ser Leu Gln Glu Ile Val Ser
      35              40              45
Tyr Ile Ala Lys Asp Val Pro Tyr Ala Thr Val Phe Lys Val Thr Ala
      50              55              60
Tyr Gln Ile Pro Tyr Leu Leu Pro Phe Ile Leu Pro Ala Ser Cys Phe
      65              70              75              80
Ile Ser Ala Phe Thr Leu Phe Arg Lys Leu Ser Asp Asn Asn Gln Ile
      85              90              95
Thr Phe Leu Lys Ala Ser Gly Ala Ser Gln Gly Met Ile Ile Phe Pro
      100             105             110
Val Leu Ile Ala Ser Gly Val Leu Cys Cys Phe Asn Phe Tyr Thr Cys
      115             120             125
Ser Glu Leu Ala Ser Ile Cys Arg Phe Gln Thr Gly Lys Ala Ile Ala
      130             135             140
Asn Ile Ala Met Thr Ser Pro Ala Leu Leu Leu Gln Thr Leu Gln Lys
      145             150             155             160
Lys Glu Asn Asp Arg Ile Phe Ile Ala Ile Asp His Cys Gly Lys Ser
      165             170             175
Lys Phe Asp Asn Val Ile Ile Ala Leu Lys His Asn Gln Glu Ile Ser
      180             185             190
Asn Ile Gly Phe Ile Glu Thr Ile Ile Pro Asp Val Asn Lys Asp Ser
      195             200             205
Val Gln Ala Lys Asn Val Leu Val Ile Ser Lys Ile Pro Leu Phe Ser
      210             215             220
Glu Ala Arg Thr Ser Asn Pro Asn Glu Phe Tyr Leu Glu Thr Leu Asp
      225             230             235             240
Glu Phe Leu Ile Pro Lys Ile Thr Ala Thr Leu Phe Ala Gly Lys Ser
      245             250             255
Tyr Met Lys Thr Arg Thr Asp Tyr Leu Pro Trp Lys Gln Leu Ile Gln
      260             265             270
Asp Ala Arg Leu His Leu Ala Glu Ile Leu Arg Arg Ile Ala Ile Gly
      275             280             285
Leu Leu Cys Ser Thr Met Thr Phe Ser Gly Leu Ala Leu Gly Thr Tyr
      290             295             300
Lys Pro Arg Phe Arg Lys Pro Val Leu Ile Tyr Ala Leu Phe Pro Ile
      305             310             315             320
Leu Asn Leu Ile Phe Leu Ile Val Gly Lys Asn Thr Ile His Pro Ile
      325             330             335
Ser Ala Val Met Leu Phe Leu Phe Pro Gln Leu Leu Ser Trp Leu Ile
      340             345             350
Phe Ser Trp Arg Ile Tyr Thr Glu Asn Gln Gly His Ala
      355             360             365

```

(2) INFORMATIONS POUR LA SEQ ID NO: 536:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 116 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 525731..526078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 536:

Lys Ser Arg Ala Cys Ile Asp Met Val Ile Trp Lys Arg Tyr Leu Leu

```

1           5           10           15
Ser Arg Phe Trp Ile Ser Leu Ser Ser Leu Phe Phe Leu Ala Val Ile
                20           25           30
Phe Tyr Ala Ser Ile His His Ser Leu His Ala Phe Arg Glu Gly Lys
                35           40           45
Thr Ala Ile Ala Gly Ala Pro Leu Gln Leu Ser Leu Leu Tyr Tyr Leu
                50           55           60
Ser Gln Ile Ser Leu Lys Ala Glu Phe Ile Leu Pro Thr Thr Arg Cys
65           70           75           80
Asn Cys Phe Asp Asn Tyr Thr Ile Phe His Ala Glu Gln Lys Arg Asn
                85           90           95
Ser Ile Thr Ala Gly Phe Arg Ala Phe Pro Glu Asn Phe Xaa Thr Ser
                100           105           110
Thr Ser Tyr Ile
                115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 537:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 525939..526400

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 537:

```

Lys Gln Asn Ser Phe Ser Leu Gln Leu Val Ala Ile Ala Ser Thr Ile
1           5           10           15
Thr Leu Phe Ser Met Gln Ser Lys Arg Glu Ile Leu Leu Leu Gln Ala
                20           25           30
Ser Gly Leu Ser Leu Lys Thr Leu Xaa Arg Pro Leu Val Ile Ser Ser
                35           40           45
Ser Leu Ile Thr Leu Leu Leu Tyr Ala Asn Phe Gln Trp Leu His Pro
                50           55           60
Ile Cys Glu Lys Ile Ser Val Thr Lys Glu His Met Asp Lys Gly Thr
65           70           75           80
Leu Glu Lys Ala Gln Glu Lys Ile Pro Ala Leu Tyr Leu Lys Asp Gln
                85           90           95
Thr Val Leu Ile Phe Ser Ser Ile Asn Arg Arg Ala Ala Thr Leu Asn
                100           105           110
Asn Val Phe Trp Ile Lys Gly Pro Lys Thr Ile Tyr Ala Ile Lys Lys
                115           120           125
Leu Ala Phe Thr Thr Pro Ser Leu Leu Ser Gly Leu Lys Cys Pro Ile
                130           135           140
Phe Pro Lys Met Lys Ile Thr Lys Cys Leu
                145           150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 538:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 526301..526735

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 538:

```

Asn Asp Leu Cys Asn Gln Lys Thr Cys Ile Tyr Tyr Ser Ile Ala Pro
1      5      10      15
Ile Gly Leu Glu Val Ser Tyr Phe Ser Glu Asp Glu Asn His Glu Val
      20      25      30
Ser Leu Thr Gln Phe Phe Asp Met Lys Glu Phe Pro Glu Leu Glu Phe
      35      40      45
Ser Tyr Tyr Asp Asn Pro Phe Ser Lys Ile Phe Ile Thr Gly Arg Asp
      50      55      60
Cys Ser Phe Ser Ala Phe Leu Gln Ala Ile Pro Trp His Ala Ala Lys
65      70      75      80
Phe Gly Leu Leu Thr Thr Val Pro Gln Arg Ile Leu Ser Leu Leu Thr
      85      90      95
Leu Phe Tyr Tyr Met Leu Ile Ser Pro Leu Leu Cys Ile Ala Ala Val
      100      105      110
Ile Leu Ser Ala His Leu Cys Leu Arg Phe His Arg Leu Pro Lys Ile
      115      120      125
Thr Trp Ala Tyr Leu Val Leu Trp Glu Pro Leu Ile Phe Ser Leu Leu
      130      135      140
Phe
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 539:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 491 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(526851..528323)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 539:

```

Arg Lys Leu Ser Ile Ser Xaa Gly Lys Ile His Glu Ser Met His Glu
1      5      10      15
Asn Asp Pro Leu Thr Lys Thr Ile Val Trp Asn Ser Asp Glu Ile Thr
      20      25      30
Lys Leu Ala Ser Ser Leu Val Tyr Thr Asn Asp Met Pro Ile Arg Leu
      35      40      45
Phe Tyr Gln Lys Ala Leu Thr Asn Met Ser Ala Glu Leu Thr Val Asn
      50      55      60
Val His Asn Ala Leu Met Ala Leu Phe Leu Ala Arg Tyr Glu Ala Thr
65      70      75      80
Ala Val Ser Gln Gln Pro Arg Lys Glu Asn Leu Ser Tyr Phe Asn Asp
      85      90      95
Phe Leu His Phe Leu Arg Lys Ala Ala Ala Leu Leu Asn Glu Lys Asp
      100      105      110
Leu Leu Asp Leu Gln Glu Lys His Ser Lys Ser Leu Val Ser Ser Leu

```

	115		120		125														
Ser	Ala	Lys	Leu	Tyr	Asp	His	Thr	Ile	Asp	Phe	Val	Glu	Ala	Ala	Asn				
	130					135					140								
Tyr	Ile	Phe	Leu	Asn	Ile	Ser	Ser	Lys	Leu	Gln	Pro	Glu	Glu	Gly	Lys				
145					150					155					160				
Lys	Pro	Leu	Ser	Ala	Gly	Gln	Tyr	Val	Ala	Glu	Ile	Tyr	Asp	Glu	Leu				
				165					170					175					
His	Arg	Leu	Phe	Ser	Lys	Tyr	Pro	Asn	Gly	Pro	Leu	Phe	Lys	Ala	Ile				
			180					185					190						
Asp	Arg	Met	Leu	Asp	Pro	Tyr	Leu	Lys	Glu	Phe	Asp	Pro	Ile	Leu	Leu				
	195						200					205							
Gly	Ile	Leu	Pro	Cys	Leu	Glu	Gly	Lys	Leu	Ile	Gln	Gly	Asp	Lys	Glu				
	210					215					220								
Ile	Lys	Val	Leu	Arg	Thr	Pro	Ser	Pro	Val	Ser	Gln	Ser	Ser	Ile	Leu				
225					230					235									
Tyr	Ala	Asn	Cys	Asn	Gly	Glu	Phe	Leu	His	Phe	Leu	Asp	Ala	Lys	Thr				
				245					250					255					
Cys	Gln	Gly	Asp	Lys	Ile	Leu	Val	Ile	Ile	Pro	Arg	Pro	Trp	Arg	Pro				
			260					265					270						
Glu	His	Ala	Thr	Ser	Arg	Ser	Arg	Ile	Ile	Glu	Glu	Ser	Leu	Gln	Asp				
	275						280					285							
Tyr	Ser	Ser	Val	Tyr	Met	Ser	Ala	Phe	Pro	Glu	Pro	Glu	Asp	Phe	Leu				
	290					295					300								
Tyr	Gly	Leu	Glu	Gln	Val	His	Gly	Glu	Leu	Glu	Thr	Phe	Ala	Asp	Phe				
305					310					315					320				
Phe	Ser	Leu	Val	Gln	Glu	Phe	Phe	Lys	Pro	Lys	Ala	Gln	Gly	Tyr					
				325				330					335						
Cys	Val	Leu	Pro	Glu	Glu	Met	Lys	Glu	Arg	Met	Gly	Val	Phe	Phe	Arg				
			340					345				350							
Arg	Tyr	Leu	Phe	Leu	Leu	Leu	Lys	Asn	Val	Phe	Phe	Ser	Lys	Xaa	Lys				
			355				360					365							
Ile	Leu	Phe	Lys	Asn	Asp	Lys	Val	Leu	Leu	Leu	His	Leu	Ile	Tyr	Tyr				
	370					375					380								
Phe	Val	Val	Phe	Asn	Leu	Ile	Glu	Gln	Leu	Asp	Pro	Asn	Thr	Leu	Val				
385				390						395					400				
Ile	Met	Ser	Lys	Asp	Gly	Leu	Asp	Tyr	Ala	Ser	Val	Phe	Val	Ser	Gly				
				405					410					415					
Phe	Ala	Phe	Phe	Glu	Asn	Arg	Gly	Asn	Trp	Asp	Glu	Asp	Ser	Leu	Lys				
			420				425					430							
Arg	Met	Val	Ala	Arg	Met	Leu	Ala	Pro	Thr	Leu	Val	Ala	Arg	Asp	Arg				
	435						440					445							
Leu	Val	Phe	Ala	Gln	His	Val	Glu	Leu	Leu	Ser	Lys	Phe	Leu	Asn	Cys				
	450					455					460								
Leu	Arg	Lys	Asn	Arg	His	Asn	Leu	Lys	Asp	Leu	Arg	Thr	Leu	Phe	Ser				
465				470					475						480				
Tyr	Asp	Leu	Glu	Gly	Trp	Gln	Phe	Ser	Gly	Ile									
				485					490										

(2) INFORMATIONS POUR LA SEQ ID NO: 540:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 190 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(528292..528861)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 540:

Lys	Asp	Tyr	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Gly	Met	Glu	Lys	Thr	Arg
1				5					10					15	
Lys	Phe	Glu	Lys	Ala	Leu	Glu	Asn	Leu	Glu	Gln	Leu	Lys	Lys	Ile	Ser
			20					25					30		
Tyr	Asp	Tyr	Ser	Ser	Gly	Asn	Ala	Glu	Ala	Ser	Ser	His	Asn	Lys	Ala
		35					40					45			
Leu	Ser	Glu	Met	Lys	Lys	Ala	Met	His	Tyr	Ile	Asp	His	Tyr	Phe	Lys
		50				55					60				
Gln	Ala	Gly	Ala	Leu	Ser	Gln	Lys	Asp	Val	Asp	Lys	Val	Ile	Lys	Glu
65					70					75					80
Thr	Asp	Phe	Leu	Ile	Ala	Gly	Val	Gln	Asp	Val	Phe	Ser	Phe	Leu	Glu
			85					90						95	
Asp	Arg	Lys	Glu	Glu	Val	Tyr	Arg	Ser	Leu	Ser	Gln	Asp	Tyr	Arg	His
			100					105					110		
Leu	Asn	His	Thr	Tyr	Asp	Val	Thr	Arg	Glu	His	Leu	Asn	Asn	Lys	Met
		115				120						125			
Val	Glu	Pro	Lys	Glu	Ile	Leu	Asn	Gly	Ser	Leu	Glu	Asn	Cys	Gln	Asp
	130					135					140				
Arg	Glu	Glu	Phe	Leu	Asn	Asn	Leu	Val	Glu	Val	Lys	Arg	Asp	Arg	Ser
145					150					155					160
Tyr	Glu	Leu	Phe	Tyr	Met	Ala	Asn	Glu	Asp	Asn	Lys	Arg	Phe	Tyr	Thr
			165					170						175	
Asp	Ala	Leu	Ala	Gln	Ile	Ile	Tyr	Lys	Xaa	Arg	Glu	Asp	Pro		
			180					185					190		

(2) INFORMATIONS POUR LA SEQ ID NO: 541:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(529142..529723)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 541:

Phe	Arg	Arg	Arg	Ser	Ser	Cys	Ser	Thr	Asp	Ala	Gly	Tyr	Phe	Leu	Phe
1				5					10					15	
Gly	Ser	His	His	Gly	Leu	Gly	Ser	Ala	Pro	Leu	Asp	Phe	Ala	Ser	Arg
			20					25					30		
Glu	Leu	Ala	Arg	Asn	Lys	Pro	Pro	Val	Arg	Ile	Val	Ala	Pro	Gly	Glu
		35					40					45			
Cys	Phe	Arg	Asn	Glu	Asp	Val	Ser	Ala	Arg	Ser	His	Val	Ile	Phe	His
		50				55					60				
Gln	Val	Glu	Ala	Phe	Cys	Val	Asp	Lys	Asp	Ile	Ser	Phe	Ser	Asp	Leu
65					70					75					80
Thr	Ser	Met	Leu	Ala	Gly	Phe	Tyr	His	Ile	Phe	Phe	Gly	Arg	Lys	Val
			85					90						95	
Glu	Leu	Arg	Phe	Arg	His	Ser	Tyr	Phe	Pro	Phe	Val	Glu	Pro	Gly	Ile
			100					105					110		
Glu	Val	Asp	Ile	Ser	Cys	Glu	Cys	His	Gly	Ala	Gly	Cys	Ser	Leu	Cys

		115					120					125							
Lys	His	Ser	Gly	Trp	Leu	Glu	Val	Ala	Gly	Ala	Gly	Met	Ile	His	Pro				
	130					135					140								
Asn	Val	Leu	Arg	Lys	Ala	Ser	Phe	Asp	Pro	Glu	Glu	Tyr	Ser	Gly	Tyr				
145					150					155					160				
Ala	Leu	Gly	Met	Gly	Ile	Glu	Arg	Leu	Ala	Met	Leu	Lys	Tyr	Gly	Ile				
			165					170						175					
Ser	Asp	Ile	Arg	Leu	Phe	Ser	Glu	Asn	Asp	Leu	Arg	Phe	Leu	Arg	Gln				
			180					185						190					
Phe	Ser																		

(2) INFORMATIONS POUR LA SEQ ID NO: 542:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(529624..530166)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 542:

Met	Thr	Ile	Gln	Glu	Glu	Leu	Glu	Ala	Val	Lys	Gln	Gln	Phe	Ser	Cys				
1			5					10					15						
Asp	Val	Ser	Leu	Ala	His	Ser	Ser	Lys	Asp	Leu	Phe	Asp	Val	Lys	Val				
		20					25					30							
Lys	Tyr	Leu	Gly	Lys	Lys	Gly	Ile	Phe	Arg	Gly	Phe	Ala	Asp	Gln	Leu				
	35					40					45								
Arg	Lys	Cys	Pro	Ile	Glu	Gln	Lys	Ala	Thr	Val	Gly	Ala	Ser	Ile	Asn				
	50				55					60									
Ala	Cys	Lys	Gln	Tyr	Val	Glu	Glu	Val	Leu	Leu	Glu	Arg	Gly	Lys	Ala				
65			70					75				80							
Val	Leu	Ala	Lys	Glu	Glu	Ala	Glu	Glu	Phe	Leu	Lys	Glu	Lys	Ile	Asp				
			85				90					95							
Ile	Ser	Leu	Pro	Gly	Ser	Glu	Glu	Ala	Leu	Gly	Gly	Lys	His	Val					
		100					105					110							
Ile	Lys	Lys	Val	Leu	Asp	Asp	Val	Val	Asp	Ile	Phe	Val	Arg	Phe	Gly				
	115					120					125								
Phe	Cys	Val	Arg	Glu	Ala	Pro	Asn	Ile	Glu	Ser	Glu	Lys	Asn	Asn	Phe				
	130				135						140								
Ser	Leu	Leu	Asn	Phe	Glu	Glu	Asp	His	Pro	Ala	Arg	Gln	Met	Gln	Asp				
145				150				155						160					
Thr	Phe	Tyr	Leu	Asp	Pro	Thr	Thr	Val	Leu	Val	Arg	Pro	Arg	Trp	Ile				
			165					170						175					
Leu	Arg	Leu	Gly	Ser															
			180																

(2) INFORMATIONS POUR LA SEQ ID NO: 543:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(530223..530543)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 543:

Met	Val	Arg	Ala	Thr	Gly	Ser	Val	Ala	Ser	Arg	Ser	Arg	Arg	Lys	Arg
1				5					10					15	
Val	Leu	Lys	Gln	Ala	Lys	Gly	Phe	Trp	Gly	Asp	Arg	Lys	Gly	His	Phe
			20					25					30		
Arg	Gln	Ser	Arg	Ser	Ser	Val	Met	Arg	Ala	Met	Ala	Phe	Asn	Tyr	Met
			35				40					45			
His	Arg	Lys	Asp	Arg	Lys	Gly	Asp	Phe	Arg	Ser	Leu	Trp	Ile	Thr	Arg
	50					55					60				
Leu	Asn	Val	Ala	Ser	Arg	Ile	His	Gly	Leu	Ser	Tyr	Ser	Arg	Leu	Ile
65					70					75					80
Asn	Gly	Leu	Lys	Gln	Ala	Gly	Ile	His	Leu	Xaa	Glu	Lys	Cys	Cys	Leu
				85					90					95	
Arg	Trp	Leu	Phe	Met	Thr	Leu	Lys	Gly	Leu	Leu					
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 544:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(530737..531378)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 544:

Glu	Lys	Ser	Leu	Phe	Leu	Gly	Lys	Gly	Gly	Leu	Trp	Phe	Phe	Leu	Gly
1				5					10					15	
Ser	Pro	Ser	Ala	Ile	Thr	Asn	Phe	Ser	Arg	Val	Asp	Val	Ala	Leu	Asn
			20					25					30		
Leu	Arg	Ile	Asn	Arg	Gln	Ile	Arg	Ala	Pro	Arg	Val	Arg	Val	Ile	Gly
			35				40					45			
Ser	Ala	Gly	Glu	Gln	Leu	Gly	Ile	Leu	Ser	Ile	Lys	Glu	Ala	Leu	Asp
	50					55					60				
Leu	Ala	Lys	Glu	Ala	Asp	Leu	Asp	Leu	Val	Glu	Val	Ala	Ser	Asn	Ser
65					70					75					80
Glu	Pro	Pro	Val	Cys	Lys	Ile	Met	Asp	Tyr	Gly	Lys	Tyr	Arg	Tyr	Asp
				85				90					95		
Ile	Thr	Lys	Lys	Glu	Lys	Asp	Ser	Lys	Lys	Ala	Gln	His	Gln	Val	Arg
			100					105					110		
Ile	Lys	Glu	Val	Lys	Leu	Lys	Pro	Asn	Ile	Asp	Asp	Asn	Asp	Xaa	Leu
		115					120					125			
Thr	Lys	Ala	Lys	Gln	Ala	Arg	Ala	Phe	Ile	Glu	Lys	Gly	Asn	Lys	Val
		130				135					140				
Lys	Val	Ser	Cys	Met	Phe	Arg	Gly	Arg	Glu	Leu	Ala	Tyr	Pro	Glu	His
145					150					155					160
Gly	His	Lys	Val	Val	Gln	Arg	Met	Cys	Gln	Gly	Leu	Glu	Asp	Ile	Gly

Met 1	Thr	Asp	Ser	Phe 5	Pro	Phe	Ser	Val	Gln 10	Glu	Ser	Val	Pro	Leu 15	Ser
Arg	Phe	Ser	Thr 20	Phe	Arg	Ile	Gly	Gly 25	Pro	Ala	Arg	Tyr	Phe 30	Lys	Glu
Leu	Thr	Ser 35	Leu	Ser	Glu	Ala	Leu 40	Thr	Val	Phe	Ser	Tyr 45	Leu	His	Thr
His	Pro	Leu 50	Pro	Tyr	Ile	Ile 55	Ile	Gly	Lys	Gly	Ser 60	Asn	Cys	Leu	Phe
Asp 65	Asp	Gln	Gly	Phe	Asp 70	Gly	Leu	Val	Leu	Tyr 75	Asn	Asn	Ile	Gln	Gly 80
Gln	Glu	Phe	Leu	Ser 85	Asp	Thr	Gln	Ile	Lys 90	Val	Leu	Ser	Gly	Ser 95	Ser
Phe	Ala	Leu 100	Leu	Gly	Lys	Arg	Leu	Ser 105	Ser	Gln	Gly	Phe	Ser 110	Gly	Leu
Glu	Phe	Ala 115	Val	Gly	Ile	Pro	Gly 120	Thr	Val	Gly	Gly	Ala 125	Val	Phe	Met
Asn	Ala	Gly 130	Thr	Thr	Leu	Ala 135	Asn	Thr	Ala	Ser	Ser 140	Leu	Ile	Asn	Val
Glu 145	Ile	Ile	Asp	His	Ser 150	Gly	Ile	Leu	Leu	Ser 155	Ile	Pro	Arg	Glu	Lys 160
Leu	Leu	Phe	Ser	Tyr 165	Arg	Thr	Ser	Pro	Phe 170	Gln	Lys	Lys	Pro	Ala 175	Phe
Ile	Ala	Ser 180	Ala	Thr	Phe	Gln	Leu	Thr 185	Lys	Asp	Pro	Gln	Ala 190	Ala	Lys
Arg	Ala	Lys 195	Ala	Leu	Ile	Glu	Glu 200	Arg	Ile	Leu	Lys	Gln 205	Pro	Tyr	Glu
Tyr	Pro	Ser 210	Ala	Gly	Cys	Ile 215	Phe	Arg	Asn	Pro	Glu 220	Gly	Leu	Ser	Ala
Gly 225	Ala	Leu	Ile	Asp	Arg 230	Ala	Gly	Leu	Lys	Gly 235	Leu	Lys	Ile	Gly	Gly 240
Gly	Gln	Ile	Ser	Glu 245	Lys	His	Gly	Asn	Phe 250	Ile	Ile	Asn	Thr	Gly 255	Asn
Ala	Cys	Thr 260	Ala	Asp	Ile	Leu	Glu	Leu 265	Ile	Glu	Ile	Ile	Gln 270	Lys	Ile
Leu	Lys	Asn 275	Lys	Val	Phe	Pro	Tyr 280	Ile	Lys	Lys	Ser	Val 285	Ser	Ser	Pro

Phe Ala Ser Ser Leu Val Val Cys Glu Lys Glu Ile Thr
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 546:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 187 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(533244..533804)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 546:

Ile	Leu	Phe	Ser	Asn	Ile	Ile	Lys	Leu	Ser	His	Ser	Ile	Phe	Arg	Gln
1				5					10					15	
Val	Val	Glu	Pro	Gly	Asp	Thr	Ile	Val	Asp	Ala	Thr	Cys	Gly	Asn	Gly
			20					25					30		
Lys	Asp	Ala	Leu	Phe	Leu	Ala	Gln	Leu	Leu	Arg	Gly	Lys	Gly	Arg	Leu
		35					40					45			
Val	Val	Tyr	Asp	Ile	Gln	Gln	Glu	Ala	Leu	Asp	Arg	Ala	Thr	Ala	Asn
	50					55					60				
Phe	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Glu	Arg	Ala	Ile	Ile	Glu	Met	Lys
65					70				75						80
Leu	Cys	Ser	His	Glu	Tyr	Leu	Gln	Glu	Gln	Gly	Ala	Lys	Leu	Phe	His
			85						90				95		
Tyr	Asn	Leu	Gly	Tyr	Leu	Pro	Ser	Gly	Asp	Lys	Gln	Ile	Thr	Thr	Cys
			100					105					110		
Ser	Glu	Ser	Thr	Val	Thr	Ser	Ile	Tyr	Lys	Ala	Leu	Glu	Leu	Val	Ala
		115					120					125			
Pro	Ser	Gly	Ile	Val	Ser	Val	Val	Cys	Tyr	Pro	Gly	His	Gln	Glu	Gly
		130				135					140				
Ala	Ala	Glu	Leu	Cys	Cys	Val	Glu	Gln	Val	Ala	Thr	Glu	Leu	Asp	Pro
145					150					155					160
Ser	Met	Trp	Glu	Val	Cys	Thr	His	Tyr	Ser	Val	Asn	Arg	Arg	Asn	Ala
			165						170					175	
Pro	Arg	Leu	Phe	Leu	Phe	Arg	Arg	Arg	Gln	Gly					
			180					185							

(2) INFORMATIONS POUR LA SEQ ID NO: 547:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 243 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(533944..534672)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 547:

Ser Gly Glu Val Trp Gly Trp Ser Arg Cys Ser Leu Ser His Thr Lys

```

1           5           10           15
Tyr Phe Pro Val Lys Pro Gln Asp Leu Lys Leu Pro Tyr Phe Trp Glu
      20           25           30
Glu Arg Ser Pro Gln Ile Ala Asn His Val Phe Tyr Val Pro Asn Tyr
      35           40           45
Tyr Ser Arg Tyr Glu Glu Phe Val Ile Pro Thr Trp Gln Glu Leu Phe
      50           55           60
Ala Asn Asn Gly Pro Ile Cys Cys Glu Leu Cys Ser Gly Asn Gly Asp
      65           70           75           80
Trp Val Val Glu Gln Ala Leu Lys Asp Ala Ser Val Asn Trp Ile Ala
      85           90           95
Val Glu Lys Arg Phe Asp Arg Val Arg Lys Ile Trp Ser Lys Met Gly
      100          105          110
Thr Tyr Arg Val Asn Asn Leu Leu Ile Val Cys Gly Glu Ala Gln Thr
      115          120          125
Phe Phe Ser His Tyr Val Ser Asp Ala Ser Phe Gln Lys Ile Val Val
      130          135          140
Asn Phe Pro Asp Pro Trp Pro Lys Phe Arg His Arg Lys His Arg Leu
      145          150          155          160
Phe Gln Asp Leu Phe Val Gln Asp Met Met Arg Thr Leu Val Val Gly
      165          170          175
Gly Gln Leu Thr Leu Ala Thr Asp Asp Tyr Asn Tyr Leu Val Asn Ala
      180          185          190
Ile Thr Val Met Leu Lys Tyr Leu Ser Pro Gly Leu Lys Ser Pro His
      195          200          205
Tyr Ile Asn Val Lys Asp Asn Tyr Gly Gly Ser Trp Phe Glu Asn Leu
      210          215          220
Trp Arg Ser Lys Gly Gln Glu Ile Phe Cys Thr Glu Phe Ile Lys Arg
      225          230          235          240
Val Gly Ile

```

(2) INFORMATIONS POUR LA SEQ ID NO: 548:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(534878..535915)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 548:

```

Met Gln Ala Asp Ile Leu Asp Gly Lys Gln Lys Arg Val Asn Leu Asn
1           5           10           15
Ser Lys Arg Leu Val Asn Cys Asn Gln Val Asp Val Asn Gln Leu Val
      20           25           30
Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn Gly Cys Ala
      35           40           45
Asn Asn Trp Leu Pro Thr Glu Ile Pro Met Gly Lys Asp Ile Glu Leu
      50           55           60
Trp Lys Ser Asp Arg Leu Ser Glu Asp Glu Arg Arg Val Ile Leu Leu
      65           70           75           80
Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly Asn Asn Ile
      85           90           95

```

```

Val Leu Ala Ile Phe Lys His Val Thr Asn Pro Glu Ala Arg Gln Tyr
      100      105      110
Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His Thr Phe Leu
      115      120      125
Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Lys Glu Ile Phe Asn Ala
      130      135      140
Tyr Asn Glu Arg Ala Ala Ile Lys Ala Lys Asp Asp Phe Gln Met Glu
      145      150      155      160
Ile Thr Gly Lys Val Leu Asp Pro Asn Phe Arg Thr Asp Ser Val Glu
      165      170      175
Gly Leu Gln Glu Phe Val Lys Asn Leu Val Gly Tyr Tyr Ile Ile Met
      180      185      190
Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu Ser Phe His
      195      200      205
Arg Gln Asn Lys Met Ile Gly Ile Gly Glu Gln Tyr Gln Tyr Ile Leu
      210      215      220
Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu Ile Asn Gly
      225      230      235      240
Ile Lys Glu Glu Asn Pro Glu Ile Trp Thr Pro Glu Leu Gln Gln Glu
      245      250      255
Ile Val Glu Leu Ile Lys Arg Ala Val Asp Leu Glu Ile Glu Tyr Ala
      260      265      270
Gln Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ala Ser Met Phe
      275      280      285
Ile Asp Tyr Val Gln His Ile Ala Asp Arg Arg Leu Glu Arg Ile Gly
      290      295      300
Leu Lys Pro Ile Tyr His Thr Lys Asn Pro Phe Pro Trp Met Ser Glu
      305      310      315      320
Thr Ile Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr Arg Asp Thr
      325      330      335
Glu Tyr Gln His Ala Ala Ser Leu Thr Trp
      340      345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 549:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1066 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(535956..539153)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 549:

```

Arg Arg Leu Cys Phe Lys Ile Glu Asn Asn Ala Tyr Ser Met Phe Thr
1      5      10      15
Arg Ile Val Met Val Asp Leu Gln Glu Lys Gln Cys Thr Ile Val Lys
      20      25      30
Arg Asn Gly Met Phe Val Pro Phe Asp Arg Asn Arg Ile Phe Gln Ala
      35      40      45
Leu Glu Ala Ala Phe Arg Asp Thr Arg Arg Ile Asp Asp His Met Pro
      50      55      60
Leu Pro Glu Asp Leu Glu Ser Ser Ile Arg Ser Ile Thr His Gln Val
      65      70      75      80
Val Lys Glu Val Val Gln Lys Ile Thr Asp Gly Gln Val Val Thr Val

```

Trp His Leu Asp Tyr Glu Asp Phe Leu Glu Leu Arg Lys Asn Thr Gly
 565 570 575
 Asp Glu Arg Arg Arg Ala His Asp Val Asn Thr Ala Ser Trp Ile Pro
 580 585 590
 Asp Leu Phe Phe Lys Arg Leu Gln Gln Lys Gly Thr Trp Thr Leu Phe
 595 600 605
 Ser Pro Asp Asp Val Pro Gly Leu His Asp Ala Tyr Gly Glu Glu Phe
 610 615 620
 Glu Arg Leu Tyr Glu Glu Tyr Glu Arg Lys Val Asp Thr Gly Glu Ile
 625 630 635 640
 Arg Leu Phe Lys Lys Val Glu Ala Glu Asp Leu Trp Arg Lys Met Leu
 645 650 655
 Ser Met Val Phe Glu Thr Gly His Pro Trp Met Thr Phe Lys Asp Pro
 660 665 670
 Ser Asn Ile Arg Ser Ala Gln Asp His Lys Gly Val Val Arg Cys Ser
 675 680 685
 Asn Leu Cys Thr Glu Ile Leu Leu Asn Cys Ser Glu Thr Glu Thr Ala
 690 695 700
 Val Cys Asn Leu Gly Ser Ile Asn Leu Val Gln His Ile Val Gly Asp
 705 710 715 720
 Gly Leu Asp Glu Glu Lys Leu Ser Glu Thr Ile Ser Ile Ala Val Arg
 725 730 735
 Met Leu Asp Asn Val Ile Asp Ile Asn Phe Tyr Pro Thr Lys Glu Ala
 740 745 750
 Lys Glu Ala Asn Phe Ala His Arg Ala Ile Gly Leu Gly Val Met Gly
 755 760 765
 Phe Gln Asp Ala Leu Tyr Lys Leu Asp Ile Ser Tyr Ala Ser Gln Glu
 770 775 780
 Ala Val Glu Phe Ala Asp Tyr Ser Ser Glu Leu Ile Ser Tyr Tyr Ala
 785 790 795 800
 Ile Gln Ala Ser Cys Leu Leu Ala Lys Glu Arg Gly Thr Tyr Ser Ser
 805 810 815
 Tyr Lys Gly Ser Lys Trp Asp Arg Gly Leu Leu Pro Ile Asp Thr Ile
 820 825 830
 Gln Leu Leu Ala Asn Tyr Arg Gly Glu Ala Asn Leu Gln Met Asp Thr
 835 840 845
 Ser Ser Arg Lys Asp Trp Glu Pro Ile Arg Ser Leu Val Lys Glu His
 850 855 860
 Gly Met Arg His Cys Gln Leu Met Ala Ile Ala Pro Thr Ala Thr Ile
 865 870 875 880
 Ser Asn Ile Ile Gly Val Thr Gln Ser Ile Glu Pro Thr Tyr Lys His
 885 890 895
 Leu Phe Val Lys Ser Asn Leu Ser Gly Glu Phe Thr Ile Pro Asn Val
 900 905 910
 Tyr Leu Ile Glu Lys Leu Lys Lys Leu Gly Ile Trp Asp Ala Asp Met
 915 920 925
 Leu Asp Asp Leu Lys Tyr Phe Asp Gly Ser Leu Leu Glu Ile Glu Arg
 930 935 940
 Ile Pro Asp His Leu Lys His Ile Phe Leu Thr Ala Phe Glu Ile Glu
 945 950 955 960
 Pro Glu Trp Ile Ile Glu Cys Ala Ser Arg Arg Gln Lys Trp Ile Asp
 965 970 975
 Met Gly Gln Ser Leu Asn Leu Tyr Leu Ala Gln Pro Asp Gly Lys Lys
 980 985 990
 Leu Ser Asn Met Tyr Leu Thr Ala Trp Lys Lys Gly Leu Lys Thr Thr
 995 1000 1005
 Tyr Tyr Leu Arg Ser Ser Ser Ala Thr Thr Val Glu Lys Ser Phe Val
 1010 1015 1020
 Asp Ile Asn Lys Arg Gly Ile Gln Pro Arg Trp Met Lys Asn Lys Ser

1025 1030 1035 1040
 Ala Ser Ala Gly Ile Ile Val Glu Arg Ala Lys Lys Ala Pro Val Cys
 1045 1050 1055
 Ser Leu Glu Glu Gly Cys Glu Ala Cys Gln
 1060 1065

(2) INFORMATIONS POUR LA SEQ ID NO: 550:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 247 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 539779..540519

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 550:

Pro	Asn	Ala	Ile	Thr	Ala	Phe	Gly	Leu	Cys	Cys	Gly	Leu	Phe	Ile	Ile	1	5	10	15
Phe	Lys	Ser	Val	Leu	Lys	Thr	Ser	Ser	Leu	Glu	Leu	Met	His	Arg		20	25	30	
Leu	Gln	Gly	Leu	Ser	Leu	Leu	Leu	Ile	Ser	Ala	Met	Ile	Ala	Asp	Phe	35	40	45	
Ser	Asp	Gly	Ala	Val	Ala	Arg	Ile	Met	Lys	Ala	Glu	Ser	Ala	Phe	Gly	50	55	60	
Ala	His	Phe	Asp	Ser	Leu	Ser	Asp	Ala	Ile	Thr	Phe	Gly	Ile	Ala	Pro	65	70	75	80
Pro	Leu	Ile	Ala	Ile	Lys	Ser	Leu	Asn	Gly	Glu	Tyr	Gly	Gly	Thr	Phe	85	90	95	
Cys	Ser	Ser	Phe	Leu	Leu	Val	Thr	Cys	Ile	Ile	Tyr	Ser	Leu	Cys	Gly	100	105	110	
Val	Leu	Arg	Leu	Val	Arg	Tyr	Asn	Leu	Phe	Ala	Ala	Thr	Gly	Glu	Lys	115	120	125	
Ala	Thr	Thr	Phe	Thr	Gly	Leu	Pro	Ile	Pro	Ala	Ala	Ala	Ala	Cys	Val	130	135	140	
Val	Ser	Leu	Gly	Val	Leu	Leu	Ala	Ser	Asp	Thr	Leu	Asn	Ser	Leu	Pro	145	150	155	160
Glu	Arg	Ala	Arg	Val	Leu	Leu	Val	Ser	Leu	Gly	Leu	Leu	Leu	Ser	Gly	165	170	175	
Cys	Leu	Met	Ile	Ser	Thr	Trp	Arg	Phe	Pro	Gly	Leu	Lys	His	Phe	His	180	185	190	
Phe	Arg	Val	Ser	Ser	Ser	Leu	Leu	Val	Leu	Gly	Ile	Gly	Leu	Val	Ala	195	200	205	
Cys	Leu	Phe	Phe	Ser	Gly	Leu	Val	Asp	His	Phe	Thr	Gln	Val	Phe	Xaa	210	215	220	
Leu	Val	Ser	Trp	Leu	Tyr	Val	Leu	Val	Val	Ala	Pro	Val	Phe	Pro	Phe	225	230	235	240
Ile	Asn	Lys	Arg	Ser	Ser	Ser										245			

(2) INFORMATIONS POUR LA SEQ ID NO: 551:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 149 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 540523..540969

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 551:

```

Tyr Met Gly Val Phe Ala Ile Ser Leu Leu Ser Gln Thr Val Cys Leu
1          5          10          15
Tyr Phe Thr Phe Phe Ser Leu Gly Ile Ala Leu Gly Val Leu Phe Ser
20          25          30
Phe Lys Ile Phe Thr Lys Lys Leu Ser Arg Gln Tyr Glu Ile Ile Arg
35          40          45
Asp Leu Glu His Ser Lys Ala Ile Leu Gln Met Ser Leu Asp Thr Arg
50          55          60
Arg Ser Gln Glu Gln Ile Met Glu Glu Phe Ser His Lys Leu Thr Ser
65          70          75          80
Val Ser Gln Ala Phe Ala Arg Asp Met Lys Thr Glu Ser Gln Glu Phe
85          90          95
Phe Ser Glu Lys Thr Gln Ala Ile Thr Ser Val Leu Ala Pro Val His
100         105         110
Asn Thr Leu Ser Ala Phe Lys Gln Asn Leu Glu Asn Phe Glu Thr Lys
115         120         125
Gln Ala Glu Asp Arg Gly Val Ser Lys Asn Asn Ser Leu Asn Tyr Ser
130         135         140
Leu Gln Asn Arg Ser
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 552:

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 300 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 540906..541805

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 552:

```

Ala Ser Arg Arg Pro Arg Ser Leu Lys Glu Gln Leu Ser Gln Leu Leu
1          5          10          15
Thr Ala Glu Gln Lys Leu Glu Arg Glu Thr Gln Ala Leu Thr Asn Ile
20          25          30
Leu Lys His Pro Gly Ser Arg Gly Arg Trp Gly Glu Ile Gln Leu Glu
35          40          45
Arg Ile Leu Glu Ile Ser Gly Met Leu Lys Tyr Cys Asp Tyr Ser Thr
50          55          60
Gln Thr Val Asp Ser Ser Glu Ser Ser Ser Arg Ala Asp Ile Val Ile
65          70          75          80
Arg Leu Pro Gln Asn Arg Ser Leu Val Ile Asp Ala Lys Thr Pro Phe
85          90          95
Ser Glu Glu Tyr Leu Thr Asp Asn His Ala Asp Pro Thr Asp Leu Val

```

(2) INFORMATION POUR LA SEQ ID NO: 553:

(A) LONGUEUR: 477 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(541825..543255)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 553:

Ala	Phe	Arg	Ser	Ile	Ser	Val	Ala	Arg	Arg	Arg	Leu	Asn	Lys	Val	Leu
1				5					10					15	
Pro	Leu	Phe	Ala	Leu	Asp	Lys	Val	Pro	Ser	Leu	Gly	Lys	Glu	Phe	Val
			20					25					30		
Leu	Glu	Lys	Glu	Val	Phe	Ala	Glu	Gly	Glu	Val	Leu	His	His	Asp	Cys
		35					40					45			
Phe	Thr	Asn	Asp	Ile	Ile	Phe	Val	Glu	Leu	Val	Phe	Asp	Leu	Pro	Ala
	50					55					60				
Leu	Ser	Ala	Glu	Glu	Leu	Pro	Trp	Leu	Arg	Leu	Leu	Val	Phe	Val	Leu
65					70				75						80
Leu	Gln	Leu	Gly	Ser	Gly	Asn	Arg	Ser	Tyr	Lys	Glu	His	Leu	Glu	Phe
			85						90					95	
Leu	Leu	Glu	His	Thr	Gly	Gly	Val	Asp	Val	Leu	Tyr	Glu	Phe	Ser	Ser
			100					105					110		
Gln	Ala	Thr	Asp	Thr	Asp	Arg	Leu	Ser	Pro	Ser	Ile	Ser	Ile	Arg	Gly
		115					120					125			
Lys	Ala	Leu	Ile	Ser	Lys	Ala	Glu	Tyr	Leu	Phe	Gln	Val	Ile	Arg	Glu
	130					135					140				

```

Thr Leu Thr Thr Val Asp Phe Ser Asp Ile Ala Arg Leu Lys Glu Leu
145          150          155          160
Leu Met Gln His Ala Glu Ser Leu Thr Asn Ser Val Arg Asn Ser Pro
          165          170          175
Met Gly Tyr Ala Val Ser Leu Ala Cys Cys Asn Lys Ser Ile Ala Gly
          180          185          190
Gly Leu Ala Tyr Gln Met Ala Gly Leu Pro Tyr Val Lys Tyr Ile Arg
          195          200          205
Glu Leu Leu Ser Asn Phe Asp Ser Gln Ala Gln Glu Ile Ile Asp Arg
          210          215          220
Leu Gln Thr Leu Tyr Lys Lys Cys Phe Val Gly Arg Arg Gln Leu Val
225          230          235          240
Ile Ser Ser Ser Lys Ala Asn Tyr Gln Val Leu His Asp Gln Arg Phe
          245          250          255
Phe Gly Leu Leu Asp Glu Arg Leu Glu Gly Gly Glu Leu Trp Lys Asn
          260          265          270
Pro Val Leu Asp Val Val Lys Asp Ser Arg Gly Ile Val Ile Pro Ala
          275          280          285
Arg Gly Ala Tyr Asn Val Leu Ala Phe Pro Leu Gly Ser Leu Ala Tyr
          290          295          300
Asp His Pro Asp Ala Ala Val Leu Ser Val Ala Ala Glu Val Leu Gly
305          310          315          320
Asn Val Ile Leu His Ala Lys Ile Arg Glu Gln Gly Gly Ala Tyr Gly
          325          330          335
Ser Gly Ala Ser Ala Asn Leu Gly Arg Gly Ala Phe Tyr Cys Tyr Ser
          340          345          350
Tyr Arg Asp Pro Glu Val Ala Thr Thr Tyr Gln Val Leu Leu Gln Gly
          355          360          365
Ile Arg Asp Met Ala Ala Gly Asp Phe Ser Glu Glu Asp Val His Glu
          370          375          380
Gly Ile Leu Gly Val Ile Gln Asn Leu Asp Asp Pro Ile Ser Pro Gly
385          390          395          400
Ser Arg Gly Ser Ala Ser Tyr Tyr Arg Ser Arg Ser Gly Lys Val Pro
          405          410          415
Phe Val Arg Gln Ala Phe Arg Gln Ala Val Leu Ser Thr Thr Lys Ala
          420          425          430
Gln Ile Cys Glu Val Val Arg Asn Arg Leu Glu Gly Cys Leu Ser Glu
          435          440          445
Ala Ser Phe Val Ser Phe Ala Gly Glu Glu Met Leu Gln Lys Ser Ala
          450          455          460
Lys Glu Leu Asn Glu Ala Phe Gln Ile Glu Ala Ala Phe
465          470          475

```

(2) INFORMATIONS POUR LA SEQ ID NO: 554:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 304 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(543222..544133)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 554:

Lys Arg Ser Ala Leu Phe Met Lys Val Ser Ile Arg Ser Val Val Val

(2) INFORMATION POUR LA SEQ ID NO: 555:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544179..544565)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 555:

Trp	Ser	Gly	Ser	Arg	Thr	Arg	Ala	Tyr	Gly	Leu	Met	Xaa	Xaa	Ser	Leu
1				5					10					15	
Ser	Tyr	Pro	Ile	Arg	Asp	Pro	Phe	Phe	Ser	Met	Thr	Arg	Arg	Ser	Leu
			20					25					30		
Asn	Thr	Phe	Met	Asn	Ala	Phe	Thr	Gly	Ala	Asp	Phe	Thr	Cys	Tyr	Pro
		35					40					45			

```

Ala Ala Ser Gln Ile Pro Glu Asp Phe Tyr Asn Leu Leu Ser Val Tyr
  50                      55                      60
Ile Asp Ala Val Phe His Pro Leu Leu Thr Glu Asn Ser Phe Leu Gln
  65                      70                      75                      80
Glu Ala Trp Arg Tyr Glu Arg Thr Glu Glu Gly Asn Leu Ser Tyr Thr
                      85                      90                      95
Gly Ile Val Phe Asn Glu Met Lys Gly Ala Leu Met Ser Gly Glu Ser
                      100                      105                      110
Arg Leu Ser Glu Val Arg Met Pro His Cys Ser Leu Arg Ser Leu Thr
                      115                      120                      125
Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 556:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 92 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544487..544762)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 556:

```

Lys Ile Glu Trp Asp Met Lys Thr Gly Asp Thr Tyr Arg Asn Phe Val
  1                      5                      10                      15
Val Lys Leu Ser Gln Asp Leu Pro Glu Ile Glu Ser Lys Leu Ile Glu
                      20                      25                      30
Val Glu His Thr Pro Thr Gly Ala Thr Ile Met Met Ile Val Asn Asp
                      35                      40                      45
Asp Asp Glu Asn Val Phe Asn Ile Ser Phe Arg Thr Cys Pro Gln Asp
                      50                      55                      60
Ser Ser Gly Val Ala His Val Leu Glu His Met Ala Leu Cys Xaa Gly
  65                      70                      75                      80
Leu Arg Val Thr Gln Phe Gly Ile Leu Phe Ser Gln
                      85                      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 557:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 440 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(544951..546270)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 557:

```

Ser Arg Val Ala Ala Lys Ala Thr Pro Gly Val Val Tyr Ile Glu Asn
  1                      5                      10                      15
Phe Pro Lys Thr Gly Asn Gln Ala Ile Ala Ser Pro Gly Asn Lys Arg

```

(2) INFORMATION POUR LA SEQ ID NO: 558:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 299 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(546584..547480)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 558:

Val	Val	Ser	Trp	Glu	Arg	Asn	Cys	Val	Arg	Ile	Ile	Lys	Gln	Gly	Phe	1	5	10	15
Thr	Asp	Tyr	Tyr	Thr	Gly	Tyr	Tyr	Arg	Glu	Ser	Arg	Val	Phe	Ser	His	20	25	30	
Tyr	Thr	Met	Cys	Arg	Phe	Thr	Asp	Leu	Thr	Phe	Val	Gly	Gly	Val	Thr	35	40	45	
Pro	Gly	Lys	Gly	Gly	Ser	Gln	Phe	Leu	Asp	Leu	Pro	Ile	Phe	Asp	Ser	50	55	60	
Val	Leu	Glu	Ala	Lys	Arg	Ala	Thr	Gly	Cys	Arg	Ala	Ser	Met	Ile	Phe	65	70	75	80
Val	Pro	Pro	Pro	Phe	Ala	Ala	Glu	Ala	Ile	Phe	Glu	Ala	Glu	Asp	Xaa	85	90	95	
Gly	Ile	Glu	Leu	Ile	Val	Cys	Ile	Thr	Glu	Gly	Ile	Pro	Ile	Lys	Asp	100	105	110	
Met	Leu	Glu	Val	Ala	Ser	Leu	Met	Glu	Lys	Ser	Ala	Ser	Ser	Leu	Ile	115	120	125	
Gly	Pro	Asn	Cys	Pro	Gly	Val	Ile	Lys	Pro	Gly	Val	Cys	Lys	Ile	Gly	130	135	140	
Ile	Met	Pro	Gly	Tyr	Ile	His	Leu	Pro	Gly	Lys	Val	Gly	Val	Val	Ser	145	150	155	160
Xaa	Ser	Gly	Thr	Leu	Thr	Tyr	Glu	Ala	Val	Trp	Gln	Leu	Thr	Gln	Arg	165	170	175	
Lys	Ile	Gly	Gln	Ser	Val	Cys	Ile	Gly	Ile	Gly	Gly	Asp	Pro	Leu	Asn	180	185	190	
Gly	Thr	Ser	Phe	Ile	Asp	Ala	Leu	Gln	Glu	Phe	Glu	Lys	Asp	Ser	Gln	195	200	205	
Thr	Glu	Ala	Val	Leu	Met	Ile	Gly	Glu	Ile	Gly	Gly	Ser	Ala	Glu	Glu	210	215	220	
Glu	Ala	Ala	Asp	Trp	Ile	Arg	Gln	His	Ser	Ser	Lys	Pro	Val	Ile	Ala	225	230	235	240
Phe	Ile	Ala	Gly	Ala	Thr	Ala	Pro	Lys	Gly	Lys	Arg	Met	Gly	His	Ala	245	250	255	
Gly	Ala	Ile	Ile	Ser	Gly	Lys	Ser	Gly	Asp	Ala	Phe	Ser	Lys	Gln	Glu	260	265	270	
Ala	Leu	Arg	Gln	Ala	Gly	Val	Thr	Val	Val	Glu	Phe	Pro	Ala	Leu	Ile	275	280	285	
Gly	Glu	Ala	Val	Ala	Ser	Val	Leu	Lys	Pro	Arg						290	295		

(2) INFORMATIONS POUR LA SEQ ID NO: 559:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 546789..547382

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 559:

```

Arg Ile Gln Ser Ala Ala Ser Ser Ser Ala Leu Pro Pro Ile Ser Pro
1      5      10      15
Ile Ile Arg Thr Ala Ser Val Trp Leu Ser Phe Ser Asn Ser Trp Arg
20      25      30
Ala Ser Ile Lys Asp Val Pro Phe Lys Gly Ser Pro Pro Ile Pro Ile
35      40      45
His Thr Leu Cys Pro Ile Phe Leu Cys Val Ser Cys Gln Thr Ala Ser
50      55      60
Tyr Val Ser Val Pro Asp Xaa Glu Thr Thr Pro Thr Phe Pro Gly Arg
65      70      75      80
Trp Ile Tyr Pro Gly Met Met Pro Ile Leu Gln Thr Pro Gly Leu Ile
85      90      95
Thr Pro Gly Gln Phe Gly Pro Ile Lys Glu Leu Ala Leu Phe Ser Ile
100     105     110
Arg Glu Ala Thr Ser Ser Ile Ser Leu Ile Gly Ile Pro Ser Val Ile
115     120     125
Gln Thr Ile Ser Ser Ile Pro Xaa Ser Ser Ala Ser Lys Met Ala Ser
130     135     140
Ala Ala Asn Gly Gly Gly Thr Lys Ile Ile Glu Ala Arg Gln Pro Val
145     150     155     160
Ala Arg Leu Ala Ser Lys Thr Glu Ser Lys Met Gly Lys Ser Lys Asn
165     170     175
Trp Leu Pro Pro Phe Pro Gly Val Thr Pro Pro Thr Lys Val Arg Ser
180     185     190
Val Lys Arg His Ile Val
195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 560:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 142 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(547476..547901)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 560:

```

Pro Lys Gln Leu Gly Leu Ser Tyr Ile Ala Leu Asp Gly Thr Ile Gly
1      5      10      15
Cys Leu Val Asn Gly Ala Gly Leu Ala Met Ser Thr Leu Asp Ile Leu
20      25      30
Lys Leu Tyr Gly Gly Ser Ala Ala Asn Phe Leu Asp Val Gly Gly Ser
35      40      45
Ala Ser Glu Lys Gln Ile Gln Glu Ala Ile Ser Leu Val Leu Ser Asp
50      55      60
Lys Ser Val Arg Val Leu Phe Ile His Ile Phe Gly Gly Ile Met Asp
65      70      75      80
Cys Ala Val Val Ala Ser Gly Leu Val Ser Ala Met Gln Gly Gln Lys
85      90      95

```

Glu Thr Ile Pro Thr Val Ile Arg Leu Glu Gly Thr Asn Val Asp Lys
 100 105 110
 Gly Lys Gly Met Ile Ile Asn Ala Gly Ile Pro Cys Glu Phe Val Thr
 115 120 125
 Ser Met Ser Glu Gly Ala Glu Leu Ala Val Gln Leu Ser Arg
 130 135 140

(2) INFORMATIONS POUR LA SEQ ID NO: 561:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 245 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(547900..548634)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 561:

Met His Leu His Glu Tyr Gln Ala Lys Asp Leu Leu Thr Ala Tyr Gln
 1 5 10 15
 Leu Pro Ile Pro Pro Tyr His Val Ala Thr Ser Val Pro Glu Val Glu
 20 25 30
 Ala Ala Ile Gln Xaa Glu Gln Trp Lys Ala Gly Val Val Lys Ala Gln
 35 40 45
 Val His Ala Gly Gly Arg Gly Lys Asn Gly Gly Val Val Ile Ala His
 50 55 60
 Ser Pro Glu Asp Leu Leu Ala Ala Ala Asp Lys Leu Leu His Met Gln
 65 70 75 80
 Phe Ser Ser Asn Gln Thr Ala Gly Leu Ser Leu Pro Val Asn Lys Val
 85 90 95
 Leu Ile Ser Pro Leu Val Glu Ile Ala Ser Glu Tyr Tyr Leu Ala Ile
 100 105 110
 Val Ile Asp Arg Lys His Arg Cys Pro Val Ile Met Leu Ser Lys Ala
 115 120 125
 Gly Gly Val Asp Ile Glu Glu Val Ala Glu Lys Gln Pro Asp Gln Leu
 130 135 140
 Leu Lys Met Thr Leu Pro Ser Ser Gly Lys Ile Tyr Gly Tyr Gln Leu
 145 150 155 160
 Arg Arg Ile Ala Lys Phe Met Glu Trp Asp Gln Pro Ile Ala Asp Gln
 165 170 175
 Gly Asn Arg Ile Ile Arg Gln Leu Leu Gln Cys Phe Tyr Glu Lys Asp
 180 185 190
 Ala Ser Leu Leu Glu Ile Asn Pro Leu Val Leu Thr Lys Asp Gly Ser
 195 200 205
 Leu Val Ile Leu Asp Ala Lys Met Thr Ile Asp Asp Asn Ala Leu Tyr
 210 215 220
 Arg His Pro Glu Leu Ala Asp Cys Tyr Asp Pro Ser Gln Glu Asn Ile
 225 230 235 240
 Arg Asp Val Leu Ala
 245

(2) INFORMATIONS POUR LA SEQ ID NO: 562:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 256 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 548692..549459

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 562:

Phe	Asp	Tyr	Ser	Val	Phe	Lys	Phe	Phe	Gly	Asn	Lys	Leu	Arg	Ser	Leu
1				5					10					15	
Phe	Lys	Arg	Thr	Leu	Ser	Ser	Asp	Leu	Leu	Glu	Tyr	Ala	Glu	Val	Leu
			20					25					30		
Leu	Tyr	Glu	Gly	Asp	Phe	Gly	Pro	Lys	Leu	Thr	Glu	Ala	Phe	Cys	Glu
		35				40						45			
Glu	Leu	Arg	Arg	Cys	Lys	Asn	Pro	Asp	Glu	Arg	Ala	Val	Lys	Glu	Leu
	50					55					60				
Ile	Arg	Ser	Phe	Leu	Ser	Lys	Ile	Ile	Ser	Lys	Leu	Pro	Gln	Arg	Glu
65					70					75					80
Pro	Leu	Ser	Val	Arg	Pro	Phe	Ser	Thr	Leu	Val	Leu	Gly	Thr	Asn	Gly
				85					90					95	
Ser	Gly	Lys	Thr	Thr	Thr	Val	Ala	Lys	Leu	Ala	His	Tyr	Tyr	Leu	Ser
			100					105					110		
Gln	Asn	Gln	Lys	Val	Leu	Ile	Val	Ala	Thr	Asp	Thr	Phe	Arg	Ser	Ala
		115					120					125			
Gly	Met	Asp	Gln	Met	Arg	Cys	Trp	Ala	Glu	Thr	Leu	Asn	Cys	Gly	Phe
	130					135					140				
Ile	Ser	Gly	Lys	Pro	Gly	Gly	Asp	Ala	Ala	Ala	Ile	Ala	Phe	Asp	Gly
145					150					155					160
Ile	Ser	Ala	Ala	Val	Ala	Arg	Asp	Tyr	Asp	His	Val	Ile	Ile	Asp	Thr
				165					170					175	
Ser	Gly	Arg	Leu	His	Thr	His	Thr	Asn	Leu	Leu	Lys	Glu	Leu	Gln	Lys
			180					185					190		
Ile	Ala	Thr	Val	Cys	Asn	Lys	Ala	Phe	Pro	Gly	Ala	Pro	His	Glu	Thr
		195					200					205			
Leu	Met	Thr	Ile	Asp	Ala	Thr	Leu	Gly	Ser	Asn	Thr	Ile	Glu	Ser	Gly
	210					215					220				
Cys	Asn	Tyr	Ser	Met	Lys	Pro	Tyr	Leu	Ser	Lys	Trp	Thr	Tyr	Phe	His
225					230					235					240
Lys	Ser	Gly	Arg	Phe	Cys	Gln	Arg	Arg	Leu	Ser	Leu	Pro	Tyr	Arg	Arg
				245					250					255	

(2) INFORMATIONS POUR LA SEQ ID NO: 563:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 241 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(549663..550385)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 563:



```

Phe Leu Pro Thr Thr Leu Leu Tyr Ile Val Ser Trp Phe Ile Ala Val
   35                               40                               45
Ala Ser Gly Tyr Cys Phe Leu Glu Val Leu Thr Trp Thr His Ser Arg
   50                               55                               60
Lys Asn Val Asn Met Val Ser Leu Ala Glu Tyr Thr Leu Gly His Lys
  65                               70                               75
Ser Lys Ile Ile Met Trp Leu Ile Tyr Leu Leu Phe Tyr Ser Leu
                               85                               90
Leu Val Ala Tyr Phe Cys Asp Gly Gly Asn Ile Leu Met Arg Val Met
                               100                            105
Gly Cys Arg Ser Trp Asp Thr Pro Trp Ile Arg His Ala Met Pro Val
                               115                            120
Val Phe Phe Ala Leu Phe Ser Pro Leu Leu Met Ala Lys Thr Ser Ile
  130                               135                            140
Ile Asp Gln Cys Asn Arg Val Phe Val Phe Gly Leu Gly Ile Ala Phe
  145                               150                            155
Ala Met Phe Cys Tyr Phe Gly Phe Pro Leu Met Lys Thr Asp Leu Leu
                               165                            170
Val Arg Ser Ala Trp Gly Ala Thr Leu Lys Gly Phe Pro Ile Leu Phe
                               180                            185
Leu Ala Phe Gly Phe Gln Asn Val Val Pro Thr Leu Tyr His Tyr Met
  195                               200                            205
Asp Lys Asn Val Lys Asp Val Lys Lys Ala Ile Val Ile Gly Ser Ser
  210                               215                            220
Ile Pro Leu Val Leu Tyr Ile Ile Trp Glu Ala Ile Val Leu Gly Ala
  225                               230                            235
Val Pro Ile Ser Phe Leu Glu Gln Ala Lys Val Glu Gly Trp Thr Ala
                               245                            250
Ile Gly Ala Leu Gln Thr Ala Leu Lys Cys Ala Ala Phe Tyr Val Ala
                               260                            265
Gly Glu Phe Phe Gly Phe Phe Ala Leu Ile Ser Ser Phe Ile Gly Val
  275                               280                            285
Ser Leu Gly Leu Lys Asp Phe Phe Ile Asp Ala Phe Gln Trp Asp Glu
  290                               295                            300
Lys Lys Arg Lys Val Glu Ile Phe Phe Leu Val Phe Val Phe Pro Leu
  305                               310                            315
Val Trp Ala Val Phe Tyr Pro Gly Ile Val Leu Lys Cys Leu Glu Cys
                               325                            330
Thr Gly Ala Leu Gly Glu Thr Ile Val Leu Gly Val Cys Pro Val Leu
                               340                            345
Met Val Trp Lys Gly Arg Tyr Gly Lys Lys Arg Tyr Tyr Gly Lys Arg
  355                               360                            365
Ile Leu Pro Gly Gly Lys Gly Thr Leu Leu Val Met Ser Gly Leu Val
  370                               375                            380
Leu Leu Asn Leu Val Leu Ile Ala Gln Lys Phe Leu Gly Tyr
  385                               390                            395

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(2) INFORMATIONS POUR LA SEQ ID NO: 566:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 606 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(553096..554913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 566:

```

Met Cys Gly Ile Phe Gly Tyr Leu Gly Glu Lys Asn Ala Val Pro Leu
1          5          10          15
Val Leu Glu Gly Leu Ser Glu Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20          25          30
Gly Ile Ala Thr Leu Ile Glu Gly Arg Leu Phe Val Glu Lys Ala Val
35          40          45
Gly Pro Val Ser Gln Leu Cys Ser Ala Val Ser Ser Asp Ile His Ser
50          55          60
Gln Ala Ala Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser
65          70          75          80
Arg Phe Asn Ala His Pro His Ile Asp Met Asp Ala Ser Cys Ala Leu
85          90          95
Val His Asn Gly Ile Ile Glu Asn Phe Gln Lys Leu Lys Glu Glu Leu
100          105          110
Glu Glu Gln Gly Val Val Phe Ser Asp Thr Asp Thr Glu Val Ile
115          120          125
Val Gln Leu Phe Ala Arg Arg Tyr Lys Glu Thr Arg Asp Leu Ile Gln
130          135          140
Ser Phe Ser Trp Thr Leu Lys Arg Leu Gln Gly Ser Phe Ala Cys Ala
145          150          155          160
Leu Met His Gln Asp His Pro Glu Val Leu Leu Cys Ala Ala His Glu
165          170          175
Ser Pro Leu Ile Leu Gly Leu Gly Glu Asp Glu Val Phe Ile Ser Ser
180          185          190
Asp Ile His Ala Phe Leu Lys Tyr Ser Gly Cys Thr Gln Thr Leu Ala
195          200          205
Ser Gly Glu Leu Val Val Leu Arg Ile Gly Lys Ser Ile Glu Thr Tyr
210          215          220
Asn Phe Glu Leu Ala Arg Ile Gln Lys Glu Val Arg Cys Ile Asp His
225          230          235          240
Thr Glu Asp Ser Leu Asp Lys Lys Gly Phe Asp Tyr Tyr Met Leu Lys
245          250          255
Glu Ile Tyr Glu Gln Pro Glu Val Phe Glu Arg Ile Leu His Leu Thr
260          265          270
Cys Glu Glu Asn Ser Phe Thr Glu Ser Phe Leu Lys Gly Phe Ser Leu
275          280          285
Asp Glu Ile Gln Ser Leu His Ile Val Ala Cys Gly Ser Ser Tyr His
290          295          300
Ala Gly Tyr Leu Ala Lys Tyr Val Ile Glu Ser Ile Ala Ser Ile Pro
305          310          315          320
Val Tyr Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Gln Pro Tyr Ile
325          330          335
Ala Glu His Ser Leu Ala Ile Leu Ile Ser Gln Ser Gly Glu Thr Ala
340          345          350
Asp Thr Leu Ala Ala Leu Asn Glu Phe Arg Lys Leu Ser Lys Ala Arg
355          360          365
Val Leu Gly Ile Cys Asn Val Arg Glu Ser Ala Leu Ala Ser Arg Val
370          375          380
Asp His Cys Leu Phe Ile Glu Ala Gly Leu Glu Val Gly Val Ala Ser
385          390          395          400
Thr Lys Ala Phe Thr Ala Gln Leu Leu Leu Leu Ile Leu Leu Gly Leu
405          410          415
Arg Leu Ala Asn His Arg Gln Val Ile Ala Gln Glu Asp Leu Ala Gln
420          425          430
Ala Ile Gln Gly Leu Lys Asp Leu Pro Asn Leu Thr Arg Leu Phe Leu
435          440          445

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Asp	Ser	Ser	Ile	His	Asp	Trp	Arg	Cys	Arg	Gln	Ile	Glu	Glu	Thr	Ser
450					455					460					
Phe	Ile	Phe	Leu	Gly	Arg	Arg	Phe	Met	Tyr	Pro	Ile	Cys	Met	Glu	Ala
465				470						475					480
Ala	Leu	Lys	Leu	Lys	Glu	Ile	Ala	Tyr	Val	Glu	Ala	Asn	Ala	Tyr	Pro
			485						490					495	
Ala	Gly	Glu	Met	Lys	His	Gly	Pro	Ile	Ala	Leu	Ile	Arg	Glu	Gly	Thr
		500					505						510		
Pro	Val	Ile	Val	Tyr	Cys	Gly	Asp	Arg	Ser	Val	Tyr	Thr	Lys	Thr	Ile
	515					520						525			
Gly	Ala	Ile	Met	Glu	Val	Lys	Ala	Arg	Lys	Ala	Tyr	Val	Ile	Ala	Leu
530					535						540				
Ala	Pro	Glu	Ser	Asn	Arg	Asp	Ile	Ala	Ala	Val	Ser	Asp	Glu	Gln	Ile
545				550						555					560
Tyr	Ile	Pro	Asp	Ser	His	Asp	Leu	Ala	Ala	Pro	Ile	Leu	Phe	Thr	Ile
			565						570					575	
Ala	Gly	Gln	Ile	Met	Ala	Tyr	Thr	Met	Ala	Leu	Gln	Arg	Gly	Thr	Glu
		580					585						590		
Val	Asp	Arg	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu		
	595					600						605			

(2) INFORMATIONS POUR LA SEQ ID NO: 567:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 458 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(554927..556300)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 567:

Met	Thr	Arg	Asp	Val	Ser	Gln	Leu	Phe	Gly	Thr	Asp	Gly	Val	Arg	Gly
1				5					10					15	
Arg	Ala	Asn	Phe	Glu	Pro	Met	Thr	Val	Glu	Thr	Ser	Val	Leu	Leu	Gly
		20						25					30		
Lys	Ala	Ile	Ala	Gly	Val	Leu	Leu	Glu	Lys	His	Ala	Gly	Lys	His	Arg
	35					40						45			
Val	Val	Val	Gly	Lys	Asp	Thr	Arg	Leu	Ser	Gly	Tyr	Met	Phe	Glu	Asn
	50				55						60				
Ala	Leu	Ile	Ala	Gly	Leu	Thr	Ser	Met	Gly	Ile	Glu	Thr	Leu	Met	Leu
65				70					75						80
Gly	Pro	Ile	Pro	Thr	Pro	Gly	Val	Ala	Phe	Ile	Thr	Arg	Ala	Tyr	Arg
			85					90						95	
Ala	Asp	Ala	Gly	Ile	Met	Ile	Ser	Ala	Ser	His	Asn	Pro	Tyr	Arg	Asp
		100					105						110		
Asn	Gly	Ile	Lys	Ile	Phe	Ser	Ser	Asp	Gly	Phe	Lys	Ile	Gly	Gln	Ala
	115						120					125			
Val	Glu	Glu	Arg	Ile	Glu	Ala	Met	Val	Ala	Ser	Lys	Asp	Phe	Gly	Lys
	130					135					140				
Leu	Pro	Asp	Asp	His	Ala	Val	Gly	Lys	Asn	Lys	Arg	Val	Lys	Asp	Ala
145				150						155					160
Thr	Gly	Arg	Tyr	Ile	Glu	Tyr	Ala	Lys	Ala	Thr	Phe	Pro	Lys	Gly	Arg
			165					170						175	
Thr	Leu	Lys	Gly	Leu	Arg	Ile	Val	Leu	Asp	Cys	Ala	His	Gly	Ala	Thr

180 185 190
 Tyr Arg Val Ala Pro Ser Val Phe Glu Glu Leu Asp Ala Glu Val Ile
 195 200 205
 Cys Tyr Gly Cys Glu Pro Ser Gly Cys Asn Ile Asn Ala Gly Cys Gly
 210 215 220
 Ala Leu Trp Pro Ser Thr Ile Gln Lys Ala Val Ile Glu His Lys Ala
 225 230 235 240
 Asp Val Gly Ile Ala Leu Asp Gly Asp Gly Asp Arg Leu Ile Met Val
 245 250 255
 Asp Glu Lys Gly His Ile Val Asp Gly Asp Met Leu Leu Ser Ile Cys
 260 265 270
 Ala Ser Asp Leu Lys Arg Arg Gln Ala Leu Pro Asp Asn Arg Val Val
 275 280 285
 Ala Thr Val Met Thr Asn Phe Gly Val Leu Arg Tyr Leu Glu Ser Leu
 290 295 300
 Gly Ile Gln Val Thr Ile Ser Pro Val Gly Asp Arg His Val Leu Gln
 305 310 315 320
 His Met Leu Glu Asn Gln Ala Val Leu Gly Gly Glu Gln Ser Gly His
 325 330 335
 Met Ile Phe Leu Asp Tyr Asn Thr Thr Gly Asp Gly Ile Val Ser Ala
 340 345 350
 Leu Gln Val Leu Arg Ile Met Ile Glu Ser Glu Ser Thr Leu Ser Asp
 355 360 365
 Leu Thr Ala Cys Ile Val Lys Ser Pro Gln Ala Leu Ile Asn Val Pro
 370 375 380
 Val Thr Lys Lys Val Pro Leu Glu Ser Leu Ala Asn Val Gln Gly Val
 385 390 395 400
 Leu Lys Glu Val Lys Glu Val Leu Gly Asp Ser Gly Arg Ile Leu Leu
 405 410 415
 Arg Tyr Ser Gly Thr Glu Asn Ile Cys Arg Val Met Val Glu Gly Thr
 420 425 430
 Lys Lys His Gln Val Asp Ser Leu Ala Lys Thr Ile Val Asp Val Val
 435 440 445
 Glu Ala Glu Ile Gly Ala Gly Ile Ser Glu
 450 455

(2) INFORMATIONS POUR LA SEQ ID NO: 568:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 127 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 556524..556904

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 568:

Met Ile Tyr Phe Phe Val Phe Met Thr Pro Tyr Leu Ile Glu Ala Leu
 1 5 10 15
 Val Ala Cys Cys Ile Leu Leu Ser Leu Gly Met Val Leu Ile Phe Ala
 20 25 30
 Phe Thr Ile Cys Leu Leu Leu Lys Leu His Lys Ile Met Lys Leu Val
 35 40 45
 Ser Arg Ile Ser Ser Leu Phe Asn Phe Glu Ala Arg Trp Leu Ala Pro
 50 55 60

Leu	Leu	Ile	Gly	Lys	Lys	Phe	Ile	Leu	Asn	Trp	Leu	Arg	Lys	Lys	Tyr
65					70					75					80
Ala	Asp	Arg	Lys	Met	Ser	Gln	Leu	Ala	Asp	Glu	Leu	Glu	Asp	Asn	Glu
				85					90					95	
Asp	Ser	Glu	Asn	Ser	Cys	Ser	Ser	Arg	Leu	Leu	Cys	Gly	Ala	Lys	Leu
			100					105					110		
Ala	Ala	Ile	Ala	Leu	Cys	Ala	Trp	Leu	Leu	Ile	Arg	Lys	Lys	Asp	
			115					120					125		

(2) INFORMATIONS POUR LA SEQ ID NO: 569:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 271 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(557314..558126)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 569:

Arg	Ser	Phe	Lys	Gly	Asp	Ser	Met	Thr	Thr	Leu	Pro	Asn	Thr	Cys	Thr
1				5					10					15	
Ser	Asn	Ser	Asn	Ser	Ile	Asn	Thr	Phe	Thr	Xaa	Asp	Ile	Glu	Met	Ala
			20					25					30		
Lys	Gln	Ile	Gln	Gly	Ser	Arg	Lys	Asp	Pro	Leu	Ala	Lys	Thr	Ser	Trp
			35				40					45			
Ile	Ala	Gly	Leu	Ile	Cys	Val	Val	Ala	Gly	Val	Leu	Gly	Leu	Leu	Ala
	50					55					60				
Ile	Gly	Ile	Gly	Gly	Cys	Ser	Met	Ala	Ser	Gly	Leu	Gly	Leu	Ile	Gly
65					70					75					80
Ala	Ile	Ile	Ala	Ala	Val	Val	Val	Ala	Val	Gly	Leu	Cys	Cys	Leu	Val
				85					90					95	
Ser	Ala	Leu	Cys	Leu	Xaa	Val	Glu	Lys	Ser	Gln	Trp	Trp	Gln	Lys	Glu
			100					105					110		
Phe	Lys	Ser	Trp	Ile	Glu	Gln	Lys	Ser	Gln	Phe	Arg	Ile	Val	Met	Ala
			115				120					125			
Asp	Met	Leu	Glu	Ala	Asn	Gln	Lys	Leu	Gln	Ser	Glu	Val	Glu	Phe	Leu
	130					135					140				
Ser	Lys	Gly	Trp	Ser	Asp	Ala	Ala	Ala	Val	His	Lys	Glu	Asp	Val	Thr
145					150					155					160
Lys	Tyr	Glu	Gln	Val	Val	Glu	Lys	Tyr	Gly	Glu	Lys	Ile	Met	Lys	Leu
				165					170					175	
Tyr	Lys	Gln	Thr	Gly	Val	Leu	Thr	Ile	Glu	Lys	Val	Asn	Leu	Gln	Lys
			180					185					190		
Glu	Lys	Lys	Thr	Trp	Leu	Glu	Glu	Lys	Ala	Glu	Met	Glu	Gln	Lys	Leu
			195				200					205			
Thr	Thr	Val	Thr	Asp	Leu	Glu	Ala	Ala	Lys	Gln	Gln	Leu	Glu	Glu	Lys
	210					215					220				
Val	Thr	Asp	Leu	Glu	Ser	Glu	Lys	Gln	Glu	Leu	Arg	Glu	Glu	Leu	Asp
225					230					235					240
Lys	Ala	Thr	Glu	Asn	Leu	Asp	Glu	Met	Ala	His	Glu	Ala	Met	Glu	Phe
				245					250					255	
Glu	Lys	Glu	Lys	His	Gly	Ile	Lys	Pro	Gly	Arg	Arg	Gly	Ser	Ile	
			260					265					270		

(2) INFORMATIONS POUR LA SEQ ID NO: 570:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 142 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 557810..558235

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 570:

```

Asp Phe Ser Thr Xaa Lys His Lys Ala Asp Thr Lys Gln His Lys Pro
1      5      10      15
Thr Ala Thr Thr Thr Ala Ala Ile Ile Ala Pro Ile Asn Pro Asn Pro
20      25      30
Glu Ala Ile Glu His Pro Pro Ile Pro Ile Ala Arg Ser Pro Asn Thr
35      40      45
Pro Ala Thr Thr Gln Ile Asn Pro Ala Ile His Glu Val Leu Ala Arg
50      55      60
Gly Ser Phe Arg Glu Pro Trp Ile Cys Phe Ala Ile Ser Ile Ser Xaa
65      70      75      80
Val Lys Val Phe Ile Glu Leu Glu Phe Glu Val Gln Val Leu Gly Arg
85      90      95
Val Val Ile Glu Ser Pro Leu Asn Asp Arg His Ala Asp Gly Pro Lys
100     105     110
Lys Gln Pro Gln Thr Tyr Phe Cys Thr Asn Phe Cys Phe Leu Ala Lys
115     120     125
Lys Lys Glu Arg Phe Tyr Leu Leu Leu Asn Leu Leu Thr Ser
130     135     140

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(2) INFORMATIONS POUR LA SEQ ID NO: 571:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 302 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(558310..559215)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 571:

```

Lys Met His Ala Leu Leu Ile Asn Leu Thr Ala Gln Arg Met Glu Phe
1      5      10      15
Asp Tyr Ser Thr Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr
20      25      30
Leu Ser Ala Glu Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr
35      40      45
Gly Gly Ala Ser Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val
50      55      60
Leu Gly Val Ser Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys
65      70      75      80

```

Phe	Asp	Ala	Glu	Val	Ser	Arg	Lys	Gly	Val	Val	Gly	Ser	Val	Tyr	Thr
				85					90					95	
Gly	Phe	Leu	Ala	Gly	Ser	Trp	Phe	Phe	Lys	Gly	Gln	Tyr	Ser	Leu	Gly
			100					105					110		
Glu	Thr	Gln	Asn	Asp	Met	Lys	Thr	Arg	Tyr	Gly	Val	Leu	Gly	Glu	Ser
		115					120					125			
Ser	Ala	Ser	Trp	Thr	Ser	Arg	Gly	Val	Leu	Ala	Asp	Ala	Leu	Val	Glu
	130					135					140				
Tyr	Arg	Ser	Leu	Val	Gly	Pro	Val	Arg	Pro	Thr	Phe	Tyr	Ala	Leu	His
145					150					155					160
Phe	Asn	Pro	Tyr	Val	Glu	Val	Ser	Tyr	Ala	Ser	Met	Lys	Phe	Pro	Gly
				165					170					175	
Phe	Thr	Glu	Gln	Gly	Arg	Glu	Ala	Arg	Ser	Phe	Glu	Asp	Ala	Ser	Leu
		180						185					190		
Thr	Asn	Ile	Thr	Ile	Pro	Leu	Gly	Met	Lys	Phe	Glu	Leu	Ala	Phe	Ile
	195						200					205			
Lys	Gly	Gln	Phe	Ser	Glu	Val	Asn	Ser	Leu	Gly	Ile	Ser	Tyr	Ala	Trp
	210					215					220				
Glu	Ala	Tyr	Arg	Lys	Val	Glu	Gly	Gly	Ala	Val	Gln	Leu	Leu	Glu	Ala
225					230					235					240
Gly	Phe	Asp	Trp	Glu	Gly	Ala	Pro	Met	Asp	Leu	Pro	Arg	Gln	Glu	Leu
				245					250					255	
Arg	Val	Ala	Leu	Glu	Asn	Asn	Thr	Glu	Trp	Ser	Ser	Tyr	Phe	Ser	Thr
			260					265					270		
Val	Leu	Gly	Leu	Thr	Ala	Phe	Cys	Gly	Gly	Phe	Thr	Ser	Thr	Asp	Ser
	275						280					285			
Lys	Leu	Gly	Tyr	Glu	Ala	Asn	Ala	Gly	Leu	Arg	Leu	Ile	Phe		
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 572:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 718 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(559196..561349)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 572:

Leu	Leu	Val	Arg	Trp	Lys	Leu	Pro	Ile	Ile	Pro	Ser	Asn	Phe	Phe	Tyr
1				5					10					15	
Arg	Lys	Cys	Glu	Xaa	Pro	Gln	Ala	Leu	Pro	Thr	Gln	Glu	Glu	Phe	Pro
		20						25					30		
Leu	Phe	Ser	Lys	Lys	Glu	Gly	Arg	Pro	Leu	Ser	Ser	Gly	Tyr	Ser	Gly
	35					40						45			
Gly	Gly	Ala	Ile	Leu	Gly	Arg	Glu	Val	Ala	Ile	Leu	His	Asn	Ala	Ala
	50					55					60				
Val	Val	Phe	Glu	Gln	Asn	Arg	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Ala	Thr
65					70					75					80
Leu	Leu	Gly	Cys	Cys	Gly	Gly	Gly	Ala	Val	His	Gly	Met	Asp	Ser	Thr
			85						90					95	
Ser	Ile	Val	Gly	Asn	Ser	Ser	Val	Arg	Phe	Gly	Asn	Asn	Tyr	Ala	Met
		100						105					110		
Gly	Gln	Gly	Val	Ser	Gly	Gly	Ala	Leu	Leu	Ser	Lys	Thr	Val	Gln	Leu

115 120 125
 Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn Ile Ala Ser Leu Gly
 130 135 140
 Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys Glu Leu Val Asp Asn
 145 150 155 160
 Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg Val Tyr Gly Gly Ala
 165 170 175
 Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser Gly Asn Lys Gly Arg
 180 185 190
 Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu Thr
 195 200 205
 Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro Glu Gln Lys Asp Asn
 210 215 220
 Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln Ser Phe Ile Thr Ala
 225 230 235 240
 Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro Glu
 245 250 255
 Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala Gly
 260 265 270
 Gly Ala Ile Phe Ala Lys Arg Val Arg Ile Val Asp Asn Gln Glu Ala
 275 280 285
 Val Val Phe Ser Asn Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe
 290 295 300
 Thr Gly Ser Leu Arg Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu
 305 310 315 320
 Val Leu Ile Ser Gly Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser
 325 330 335
 Ser Lys Arg Asp Glu His Leu Pro His Thr Gly Gly Gly Ala Ile Cys
 340 345 350
 Thr Gln Asn Leu Thr Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr
 355 360 365
 Asn Asn Val Ala Cys Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly
 370 375 380
 Asn Val Leu Leu Glu Ala Phe Gly Gly Asp Ile Val Phe Lys Gly Asn
 385 390 395 400
 Ser Ser Phe Arg Ala Gln Gly Ser Asp Ala Ile Tyr Phe Ala Gly Lys
 405 410 415
 Glu Ser His Ile Thr Ala Leu Asn Ala Thr Glu Gly His Ala Ile Val
 420 425 430
 Phe His Asp Ala Leu Val Phe Glu Asn Leu Lys Glu Arg Lys Ser Ala
 435 440 445
 Glu Val Leu Leu Ile Asn Ser Arg Glu Asn Pro Gly Tyr Thr Gly Ser
 450 455 460
 Ile Arg Phe Leu Glu Ala Glu Ser Lys Val Pro Gln Cys Ile His Val
 465 470 475 480
 Gln Gln Gly Ser Leu Glu Leu Leu Asn Gly Ala Thr Leu Cys Ser Tyr
 485 490 495
 Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val Leu Ala Ala Gly Ser
 500 505 510
 Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val Gln Gly His Ala Ile
 515 520 525
 Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser Glu Pro Glu Gly Ala
 530 535 540
 His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr Thr Val Pro Met Val
 545 550 555 560
 Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser Phe Ser Ser Ser Gln
 565 570 575
 Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile Val Pro Gly Gly Ser
 580 585 590

```

Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly
    595                      600                      605
Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro
    610                      615                      620
Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser
    625                      630                      635                      640
Asn Leu Ser Val Ser Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile
    645                      650                      655
Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile
    660                      665                      670
Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu
    675                      680                      685
Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Glu
    690                      695                      700
Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg Phe Ala Asp
    705                      710                      715

```

(2) INFORMATIONS POUR LA SEQ ID NO: 573:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 594 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(561150..562931)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 573:

```

Phe Val Lys Lys Val Leu Phe Arg Arg Phe Glu Met Ser Ser Glu Lys
1      5      10      15
Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu Ser Val Val Ala Ala
20     25     30
Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys Val Asp Leu His Ala
35     40     45
Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala Val
50     55     60
Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp Ser
65     70     75     80
Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser Phe
85     90     95
Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser Thr
100    105    110
Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln Gln
115    120    125
Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser Asn
130    135    140
Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe Val
145    150    155    160
Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala Ser
165    170    175
Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu Lys
180    185    190
Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln Gly
195    200    205
Gly Ala Cys Gly Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly Leu

```

210 215 220
 Gln Val Lys His Cys Thr Thr Ala Val Asn Ala Glu Gly Ser Ser Ala
 225 230 235 240
 Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe Phe Val Thr Gly Ser
 245 250 255
 Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val Val
 260 265 270
 Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn Phe
 275 280 285
 Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val Ala
 290 295 300
 Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly Gly
 305 310 315 320
 Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu Leu
 325 330 335
 Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu Asp Lys Gly Ser Leu
 340 345 350
 Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly Asn
 355 360 365
 His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly Ala
 370 375 380
 Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val Val
 385 390 395 400
 Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly Ala Ile Ala Gln
 405 410 415
 Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu Gly
 420 425 430
 Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys Gly Ser Phe Ser Ser
 435 440 445
 Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn Leu
 450 455 460
 Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu Gly
 465 470 475 480
 Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe Gly Glu Asn Ile Ser
 485 490 495
 Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val Lys
 500 505 510
 Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Gly Ala Ile Leu Ala
 515 520 525
 Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Val Glu Phe Leu Leu Gln
 530 535 540
 Glu Met Arg Xaa Ser Thr Ser Ser Ser Asn Ser Arg Gly Val Ser Phe
 545 550 555 560
 Ile Gln Gln Lys Arg Arg Ala Thr Thr Leu Phe Arg Ile Phe Trp Gly
 565 570 575
 Arg Ser Asp Phe Arg Lys Arg Ser Ser Tyr Ser Pro Gln Arg Cys Ser
 580 585 590
 Ser Ile

(2) INFORMATIONS POUR LA SEQ ID NO: 574:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 321 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(563121..564083)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 574:

Met	Lys	Val	Arg	Leu	Gly	Val	Asp	Met	Met	Gly	Gly	Asp	His	Asp	Pro
1				5				10					15		
Leu	Val	Val	Trp	Glu	Ala	Leu	Gly	Glu	Val	Leu	Leu	Ser	Ser	Thr	Gly
			20					25					30		
Glu	Gln	Pro	Val	Glu	Phe	Thr	Val	Phe	Ala	Thr	Ser	Asp	Val	His	His
		35					40					45			
Gln	Leu	Met	Asn	Ser	Pro	Leu	Ser	Arg	Ser	Val	Arg	Ile	Val	Thr	Ala
	50					55				60					
Glu	Asp	Phe	Val	Ser	Met	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Val	Arg	Lys
65					70					75					80
Lys	Arg	Ser	Ser	Met	Ala	Leu	Gly	Leu	Asp	Ala	Leu	Gln	Gln	Gly	Asp
				85				90						95	
Leu	Asp	Gly	Phe	Val	Ser	Ser	Gly	Asn	Thr	Ala	Ala	Leu	Val	Thr	Leu
			100					105					110		
Ala	Arg	Ser	Lys	Ile	Pro	Met	Ile	Pro	Ala	Val	Pro	Arg	Pro	Ala	Leu
			115					120					125		
Leu	Val	Ser	Val	Pro	Thr	Leu	Ser	Gly	Phe	Ala	Val	Ile	Leu	Asp	Val
	130					135						140			
Gly	Ala	Thr	Val	Ser	Val	Asn	Pro	Asp	Glu	Met	Val	Gly	Phe	Ala	Arg
145					150					155					160
Met	Gly	Leu	Ala	Tyr	Arg	Gln	Ser	Leu	Ser	Ser	Asn	Ser	Asn	Gln	Pro
				165				170						175	
Phe	Thr	Leu	Gly	Leu	Leu	Asn	Ile	Gly	Ser	Glu	Glu	Arg	Lys	Gly	Thr
			180					185					190		
Asp	Ser	His	Lys	Gln	Thr	Phe	Arg	Met	Leu	Arg	Asn	Ile	Phe	Gly	Ser
		195					200					205			
Ala	Phe	Leu	Gly	Asn	Ile	Glu	Ser	Gly	Asp	Val	Phe	Ser	Gly	Lys	Val
	210					215						220			
Asp	Ile	Val	Val	Thr	Asp	Gly	Phe	Thr	Gly	Asn	Val	Phe	Leu	Lys	Thr
225					230					235					240
Ala	Glu	Gly	Leu	Phe	Asp	Phe	Leu	Arg	His	Ile	Leu	Gly	Asp	Arg	Leu
				245					250					255	
Glu	Lys	Ser	Ile	Lys	Met	Gln	Phe	Asp	Tyr	Thr	Ile	Tyr	Pro	Gly	Ser
			260					265					270		
Ile	Ile	Ser	Gly	Leu	Ser	Arg	Leu	Val	Ile	Lys	Cys	His	Gly	Lys	Ser
		275					280					285			
His	Gly	Thr	Ala	Leu	Phe	Gly	Gly	Ile	Ser	Gly	Ala	Ile	Asp	Leu	Ala
	290					295					300				
Arg	Ala	Asn	Val	Cys	Ser	Arg	Ile	Ala	Asp	Arg	Phe	Gly	Asp	Asn	Val
305					310					315					320
Val															

(2) INFORMATIONS POUR LA SEQ ID NO: 575:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 117 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 563593..563943

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 575:

```

Ala Lys Pro Ile Arg Ala Lys Pro Thr Ile Ser Ser Gly Phe Thr Asp
1      5      10      15
Thr Val Ala Pro Thr Ser Lys Ile Thr Ala Asn Pro Glu Arg Val Gly
      20      25      30
Thr Glu Thr Asn Asn Ala Gly Leu Gly Thr Ala Gly Ile Ile Gly Ile
      35      40      45
Leu Glu Arg Ala Ser Val Thr Lys Ala Ala Val Phe Pro Glu Glu Thr
      50      55      60
Lys Pro Ser Arg Ser Pro Cys Cys Asn Ala Ser Asn Pro Arg Ala Ile
65      70      75      80
Glu Asp Arg Phe Leu Arg Thr Ala Ala Asn Lys Glu Ser Ser Ile Glu
      85      90      95
Thr Lys Ser Ser Ala Val Thr Ile Arg Thr Glu Arg Asp Ser Gly Glu
      100      105      110
Phe Ile Asn Trp Trp
      115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 576:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 518 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 565400..566953

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 576:

```

Arg Ala Phe Arg Asn Ala Met Glu Asn Asp Ile Leu Leu Asn Ile Glu
1      5      10      15
Ser Lys Glu Ile Arg Tyr Ala His Leu Lys Asn Gly Gln Leu Phe Asp
      20      25      30
Leu Ile Ile Glu Arg Lys Lys Ile Arg Gln Leu Lys Gly Asn Ile Tyr
      35      40      45
Arg Gly Arg Val Thr Asn Ile Leu Arg Asn Ile Gln Ser Ala Phe Ile
      50      55      60
Asn Ile Asp Glu Arg Glu Asn Gly Phe Ile His Ile Ser Asp Val Leu
65      70      75      80
Glu Asn Ser Lys Lys Phe Glu Gln Met Phe Asp Ile Asp Ser Asp Ala
      85      90      95
Asp His Ala Glu Pro Arg Pro Glu Glu Thr Ser Glu Ala Pro Ile Glu
      100      105      110
Glu Leu Leu Lys Leu Asp Ser Pro Val Leu Val Gln Val Val Lys Glu
      115      120      125
Pro Ile Gly Thr Lys Gly Ala Arg Leu Thr Ser Asn Ile Ser Ile Pro
      130      135      140
Gly Arg Tyr Leu Val Leu Leu Pro Asn Ser Pro His Arg Gly Val Ser
145      150      155      160
Arg Lys Ile Glu Asp Pro Leu Met Arg Asp Gln Leu Lys Gln Leu Ile
      165      170      175

```



```

Lys Ile Ser Ala Glu Lys Ala Glu Ala Leu Cys Ser Gln Trp Leu Lys
1      5      10      15
Val Ile Ile Asp Asp Leu Lys Asn Pro Ile Ile Phe Pro Pro Tyr His
20      25      30
Lys Lys Ile Arg Ser Pro Ile Asp Leu Tyr Gln Phe Gly Ile Asp Phe
35      40      45
Phe Ser Ala Leu Ile Asp His Gln Lys Ser Gln Ile Leu His Pro Glu
50      55      60
Arg Leu Asp Gln Ile Gln Glu Tyr Ile Gln Ala Gly His Asn Val Val
65      70      75      80
Leu Leu Ala Asn His Gln Thr Glu Ser Asp Pro Gln Leu Met Tyr Cys
85      90      95
Leu Leu Gly Ala Ser His Pro Gln Leu Met Glu Ser Met Ile Phe Val
100     105     110
Ala Gly Asp Arg Ile Thr Ser Asp Pro Leu Ala Arg Pro Phe Ser Met
115     120     125
Gly Cys Asp Leu Leu Cys Ile Tyr Ser Lys Arg His Ile Asn His Pro
130     135     140
Pro Glu Leu Lys Glu Glu Lys Leu Met His Asn Gln Lys Ser Met Arg
145     150     155     160
Thr Leu Lys Met Leu Leu Ser Glu Gly Gly Lys Phe Phe Tyr Val Ala
165     170     175
Pro Ser Gly Gly Arg Asp Arg Lys Asn Leu Gln Gly Glu Leu Tyr Pro
180     185     190
Ala Glu Phe His Pro Asp Ser Val Glu Met Phe Arg Leu Leu Ala Lys
195     200     205
Ser Ser Gly Lys Thr Thr His Phe Phe Pro Leu Ala Met Lys Thr Tyr
210     215     220
Asp Ile Leu Pro Pro Pro Pro Thr Ile Glu Glu Ala Ile Gly Glu His
225     230     235     240
Arg Val Ile Ser Phe Ala Pro Val Ala Phe Asn Phe Gly Asp Glu Leu
245     250     255
Leu Leu Asp Glu Leu Cys Ser Ser Glu Glu Ala Asp Ile Tyr Asp Lys
260     265     270
His Ala Leu Arg Ala Leu Arg Ala Ser Arg Ala Phe Ser Ile Val Thr
275     280     285
Asp Leu Tyr Lys Glu Ile Leu Thr
290     295

```

(2) INFORMATIONS POUR LA SEQ ID NO: 578:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 769 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 568093..570399

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 578:

```

Leu Leu Leu Cys Ile Pro Ser Phe Leu Thr Ala Cys Ser Lys Ser Phe
1      5      10      15
Gln Thr Ile Arg Asp Glu Asn Pro Leu Thr Ile Leu Thr Pro Ala Leu
20      25      30

```

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 251 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 571269..572021

Thr	Gly	Leu	Arg	Ser	Leu	Gly	Asp	Ser	Ala	Ile	Leu	Ser	Ile	Phe	Ile
1				5					10					15	
Tyr	Arg	Ser	Tyr	Arg	Ile	Thr	Met	Ala	Tyr	Phe	Asp	Ser	Arg	Asn	Tyr
			20					25					30		
Val	Phe	Ser	Leu	Phe	Ile	Ile	Ala	Met	Leu	Ile	Leu	Leu	Glu	Ser	Arg
		35					40					45			
Pro	Ile	Glu	Tyr	Phe	Ser	Gln	Arg	Val	Phe	Ala	Thr	Ile	Ala	Lys	Ile
	50					55					60				

Gly	Lys	Gln	Ser	Pro	Ile	Cys	Trp	Trp	Trp	Thr	Ile	Met	Ile	Ala	Ala
65					70					75					80
Pro	Leu	Ser	Ala	Phe	Leu	Lys	Glu	Ser	Gly	Ala	Met	Ile	Ile	Ala	
				85				90						95	
Ala	Thr	Leu	Leu	Ser	Lys	Gln	Phe	Tyr	Lys	Phe	Ser	Pro	Ser	Pro	Lys
			100					105					110		
Phe	Cys	Tyr	Ala	Thr	Met	Gly	Leu	Leu	Phe	Ser	Asn	Ile	Ser	Ile	Ser
		115					120					125			
Gly	Leu	Thr	Ser	Ser	Phe	Ser	Ser	Arg	Ala	Leu	Leu	Thr	Ile	Leu	Pro
		130				135						140			
Glu	Ile	Lys	Trp	Thr	Asn	Ser	Phe	Ile	Ile	Ser	His	Phe	Cys	Trp	Lys
145					150					155					160
Val	Ile	Leu	Ala	Ile	Leu	Val	Ser	Thr	Thr	Ile	Leu	Phe	Cys	Leu	Phe
				165					170					175	
Arg	Lys	Glu	Phe	Lys	Lys	Phe	Pro	Lys	Thr	Ile	Pro	Ser	Thr	Thr	Met
			180					185					190		
Met	Asn	Asp	Arg	Leu	Pro	Ser	Trp	Ile	Ile	Phe	Ile	His	Val	Val	Leu
		195					200					205			
Val	Gly	Cys	Val	Ile	Leu	Ser	Arg	Ala	Ile	Pro	Leu	Phe	Leu	Gly	Phe
	210					215				220					
Leu	Phe	Ile	Phe	Tyr	Leu	Gly	Phe	Gln	Arg	Phe	Thr	Ile	Phe	Tyr	Gln
225					230					235					240
His	Pro	Ile	Gln	Asn	Ser	Lys	Ser	Ser	Val	Ser					
				245					250						

(2) INFORMATIONS POUR LA SEQ ID NO: 580:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 79 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 572519..572755

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 580:

Gly	Tyr	Asn	Ser	Ala	Gly	Phe	Ile	Arg	Ser	Trp	Asn	Met	Gln	His	Thr
1				5					10					15	
Ile	Met	Leu	Ser	Leu	Glu	Asn	Asp	Asn	Asp	Lys	Leu	Ala	Ser	Met	Met
			20					25					30		
Asp	Arg	Val	Val	Ala	Ala	Ser	Ser	Ser	Ile	Leu	Ser	Ala	Ser	Lys	Asp
		35					40					45			
Ser	Glu	Ser	Asn	Arg	Gln	Phe	Thr	Ile	Ser	Lys	Ala	Pro	Asp	Lys	Glu
	50					55					60				
Ala	Pro	Cys	Arg	Val	Ser	Tyr	Val	Ala	Ala	Ser	Ala	Leu	Ser	Glu	
65					70					75					

(2) INFORMATIONS POUR LA SEQ ID NO: 581:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 263 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

Ser Ser Ala His Arg Leu Ser Ser Gln Cys Phe Phe Ser Phe Lys Ser
 20 25 30
 Lys Arg Asn Arg Lys Thr Gly Phe Ser Lys Ser Phe Cys Val Tyr Ser
 35 40 45
 Lys Phe Phe Leu Glu Glu Gln Ser Glu Gly Cys Thr Thr Ala Lys Ala
 50 55 60
 Arg Leu Val Arg Thr Pro Ser Leu Glu Lys Tyr Lys Thr Tyr Leu Ser
 65 70 75 80
 Glu Thr Leu Ser Ser Arg Ala Ile Ile Phe Ser Pro Arg Ala Thr Pro
 85 90 95
 Lys Ala Ala Pro Val Glu Lys Lys Lys Gly Val Ser Met Pro Ile Cys
 100 105 110
 Ser Ala Lys Glu Arg Ile Ser Ser Ser Asp Ser Pro Val Leu Lys Ile
 115 120 125
 Trp Phe Lys Ala Asn Asn Ala Val Ala Ala Leu Leu Leu Pro Pro Ala
 130 135 140
 Arg Pro Ala Pro Thr Gly Ile Cys Leu Thr Thr Arg Gln Leu Thr Gly
 145 150 155 160
 Val Val Met Pro Val Tyr Arg Arg Lys Ser Ala Thr Leu Phe His Ile
 165 170 175
 Glu Leu Leu Gly Val Ser Arg
 180

(2) INFORMATIONS POUR LA SEQ ID NO: 583:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 77 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(573660..573890)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 583:

Met Tyr Gly Ser Val Thr Val Asn Asp Met Ile Ser Ala Ala Glu Gln
 1 5 10 15
 Gln Gly Val Val Leu Thr Arg Lys Asn Phe Pro Arg Ser His Ser Gly
 20 25 30
 Ile Lys Asn Leu Gly Arg His Val Val Gly Leu Lys Leu Lys Glu Gly
 35 40 45
 Val Thr Ala Asp Leu His Leu Glu Val Arg Ala Asp His Glu Ile Ile
 50 55 60
 Glu Gln Lys Glu Leu Gln Ser Ala Glu Glu Glu Glu Gly
 65 70 75

(2) INFORMATIONS POUR LA SEQ ID NO: 584:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 81 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(574923..575243)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 586:

```

Ser Cys Leu Ser Cys Gln Glu Val Phe Arg Cys Phe His Gly Arg Tyr
1          5          10          15
Ser Cys Cys Ser Arg Arg His His Arg Glu Phe Gly Phe Val Arg Phe
20          25          30
Arg Gln Asp Cys Gly Ser Gly Gly His Asn Gly Ile Lys Asn Thr Thr
35          40          45
Gln Ile Leu Gln Ser Asn His Tyr Trp Gln Leu Arg Leu Gly Val Gly
50          55          60
Arg Pro Ser Tyr Pro Gly Ala Glu Gly Val Ala Asp Tyr Val Leu Ser
65          70          75          80
Ser Phe Ser Leu Asn Glu Lys Glu Lys Leu Asn Asp Phe Leu Glu Lys
85          90          95
Gly Ile Glu Glu Ile Leu Pro Trp Leu Gly Cys
100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 587:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(575057..575458)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 587:

```

Met Val Lys Leu Val Val Gly Ile Gly Asn Pro Gly Arg Gln Tyr Val
1          5          10          15
Trp Thr Arg His Asn Ile Gly Phe Leu Leu Leu Asp Ser Leu Ala Ser
20          25          30
Arg Phe Leu Gly Ala Phe Arg Glu Ala Pro Arg Leu Tyr Ala Ser Phe
35          40          45
Ala Lys Val Glu Ile Ser Ser Glu Ala Val Val Leu Met Lys Pro Thr
50          55          60
Thr Tyr Val Asn Leu Thr Gly Lys Ala Val Leu Ala Ala Lys Lys Phe
65          70          75          80
Phe Asp Val Ser Met Glu Asp Ile Leu Val Val Ala Asp Asp Ile Ile
85          90          95
Gly Asn Ser Val Leu Cys Val Phe Gly Lys Ile Val Ala Leu Val Gly
100          105          110
Thr Met Glu Leu Arg Ile Pro Arg Arg Phe Cys Asn Pro Ile Ile Ile
115          120          125
Gly Asn Tyr Val Leu Gly
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 588:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 588:

(xi)	DESCRIPTION DE LA SÉQUENCE														
Leu	Leu	Leu	Cys	Ser	Arg	Phe	Leu	Asn	Glu	Gly	Arg	Glu	Ile	Lys	Ala
1				5					10					15	
Leu	Val	Lys	Asp	Ile	Gln	Tyr	His	Val	Thr	Thr	Tyr	Asp	Val	Ile	His
			20					25					30		
Leu	Asp	Phe	Glu	Glu	Leu	Val	Asp	Gly	Arg	Asp	Val	Arg	Leu	Asn	Val
			35				40					45			
Pro	Ile	Arg	Cys	Ile	Asn	Thr	Val	Asp	Cys	Val	Gly	Val	Lys	Leu	Gly
	50				55						60				
Gly	Ser	Leu	Arg	Gln	Val	Ile	Arg	Cys	Ile	Arg	Val	Val	Cys	Lys	Pro
				70						75				80	
65	Lys	Asp	Ile	Val	Pro	Phe	Leu	Glu	Leu	Asp	Val	Gln	Ser	Leu	Gly
				85						90				95	
Ser	Gln	Thr	Leu	Lys	Leu	Ser	Asp	Ile	Cys	Ile	Pro	Glu	Gly	Ile	Arg
			100					105					110		
Pro	Val	Thr	Ser	Leu	Lys	Glu	Val	Ala	Val	Thr	Val	Ala	Arg	Arg	
			115				120					125			

(i) CARACTERISTIQUES DE LA SEQUENCE:
(2) LONGUEUR: 474 acides aminés

(i) CARACTERISTIQUES DE L'ESPECE
(A) LONGUEUR: 474 acides aminés
 Poids: 52,7 acide aminé

(D) CONFIGURATION: linéaire

... DANS LE

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 589:

(xi) DESCRIPTION DE LA SEQUENCE

Met Lys Ile Ile His Thr Ala Ile Glu Phe Ala Pro Val Ile Lys Ala
10 15

Met Lys Ile Ile His Thr Ala Ile Glu Phe Ala 15
1 5 10
Gly Asp Ala Leu Tyr Gly Leu Ala Lys Ala Leu Ala Ala 30

Gly Gly Leu Gly Asp Ala Leu Tyr 25 30
20
Pro Leu Tyr Pro Lys 45
Leu Phe Thr

Asn His Thr Thr Glu Val Val Ile Ile 45
35 40
Pro Lys Glu Gln Asp Leu Cys Ser Ile Gln Lys Leu Ser Tyr Phe
60

Leu Pro Lys Glu Gln Asp Leu Cys Ser 110 60
50 55
Gly Glu Gln Glu Ala Thr Ala Phe Ser Tyr Phe Tyr Glu Gly
75 80

65 Phe Ala Gly Glu Gln Glu Ala Thr Ala Phe 75 80
70 75 80
65 Val Thr Leu Phe Lys Leu Asp Thr 85 90
95 95

Ile Lys Val Thr Leu Phe Lys Leu Asp Thr 95
85
Ser Thr Ile Tyr Thr Ser Asp Asp Ala Phe Arg Phe Cys Ala
110

Asn Ala Glu Thr Ile Tyr Thr Ser Asp Asp Ala 110
105
100
Ala Ala Ala Ser Tyr Ile Gln Lys Glu Gly Ala Asn Ile
125

Phe. Ser Ala Ala Ala Ala Ser Tyr Ile Gln Lys Cys 125
115 His Asp Trp His Thr Gly Leu Val Ala Gly Leu Leu Lys 140

Val His Leu His Asp Trp His Thr Gly Leu Val Ala Ser
130 135 140

Gln	Gln	Pro	Cys	Ser	Gln	Leu	Gln	Lys	Ile	Val	Leu	Thr	Leu	His	Asn
145					150					155					160
Phe	Gly	Tyr	Arg	Gly	Tyr	Thr	Thr	Arg	Glu	Ile	Leu	Glu	Ala	Ser	Ser
				165					170						175
Leu	Asn	Glu	Phe	Tyr	Ile	Ser	Gln	Tyr	Gln	Leu	Phe	Arg	Asp	Pro	Gln
			180					185					190		
Thr	Cys	Val	Leu	Leu	Lys	Gly	Ala	Leu	Tyr	Cys	Ser	Asp	Phe	Val	Thr
		195					200					205			
Thr	Val	Ser	Pro	Thr	Tyr	Ala	Lys	Glu	Ile	Leu	Glu	Asp	Tyr	Ser	Asp
	210					215					220				
Tyr	Glu	Ile	His	Asp	Ala	Ile	Thr	Ala	Arg	Gln	His	His	Leu	Arg	Gly
225					230					235					240
Ile	Leu	Asn	Gly	Ile	Asp	Thr	Thr	Ile	Trp	Gly	Pro	Glu	Thr	Asp	Pro
			245						250					255	
Asn	Leu	Ala	Lys	Asn	Tyr	Thr	Lys	Glu	Leu	Phe	Glu	Thr	Pro	Ser	Ile
			260					265					270		
Phe	Phe	Glu	Ala	Lys	Ala	Glu	Asn	Lys	Lys	Ala	Leu	Tyr	Glu	Arg	Leu
		275					280					285			
Gly	Leu	Ser	Leu	Glu	His	Ser	Pro	Cys	Val	Cys	Ile	Ile	Ser	Arg	Ile
	290					295					300				
Ala	Glu	Gln	Lys	Gly	Pro	His	Phe	Met	Lys	Gln	Ala	Ile	Leu	His	Ala
305					310					315					320
Leu	Glu	Asn	Ala	Tyr	Thr	Leu	Ile	Ile	Ile	Gly	Thr	Cys	Tyr	Gly	Asn
			325						330					335	
Gln	Leu	His	Glu	Glu	Phe	Ala	Asn	Leu	Gln	Glu	Ser	Leu	Ala	Asn	Ser
			340					345					350		
Pro	Asn	Val	Arg	Ile	Leu	Leu	Thr	Tyr	Ser	Asp	Val	Leu	Ala	Arg	Gln
		355					360					365			
Ile	Phe	Ala	Ala	Ala	Asp	Met	Ile	Cys	Ile	Pro	Ser	Met	Phe	Glu	Pro
	370					375					380				
Cys	Gly	Leu	Thr	Gln	Met	Ile	Gly	Met	Arg	Tyr	Gly	Thr	Val	Pro	Leu
385					390					395					400
Val	Arg	Ala	Thr	Gly	Gly	Leu	Ala	Asp	Thr	Val	Ala	Asn	Gly	Ile	Asn
			405						410					415	
Gly	Phe	Ser	Phe	Phe	Asn	Pro	His	Asp	Phe	Tyr	Glu	Phe	Arg	Asn	Met
			420					425					430		
Leu	Leu	Glu	Ala	Val	Thr	Thr	Tyr	Arg	Thr	Asn	His	Asp	Lys	Trp	Gln
		435					440					445			
His	Ile	Val	Arg	Ala	Cys	Leu	Asn	Phe	Ser	Ser	Asp	Leu	Glu	Thr	Ala
	450					455					460				
Ala	Asn	Lys	Tyr	Leu	Glu	Ile	Tyr	Lys	Gln						
465						470									

(2) INFORMATIONS POUR LA SEQ ID NO: 590:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 208 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(578017..578640)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 590:

Met Arg Val Ser Leu Pro Asn Phe Leu Thr Val Phe Arg Leu Phe Ile

```

1          5          10          15
Thr Pro Ile Phe Met Ile Leu Tyr Leu Lys Gly Arg Trp Phe Gly Leu
20          25          30
Ser Ala Ala Phe Leu Pro Tyr Val Leu Leu Phe Leu Leu Ile Ile Thr
35          40          45
Glu Ile Thr Asp Ala Val Asp Gly Tyr Ile Ala Arg Lys Phe Ser Gln
50          55          60
Val Thr Asp Leu Gly Lys Leu Leu Asp Pro Met Ala Asp Ser Val Tyr
65          70          75          80
Arg Ile Ser Leu Tyr Leu Thr Phe Thr Gln Pro Pro Val Asn Leu Pro
85          90          95
Leu Ile Leu Val Phe Ile Phe Leu Ala Arg Asp Ser Val Ile Ser Thr
100          105          110
Leu Arg Thr Leu Cys Ala Ser Arg Gly Gln Val Leu Ala Ala Arg Met
115          120          125
Ser Gly Lys Leu Lys Ala Ile Leu Gln Ala Ile Ser Phe Phe Phe Ile
130          135          140
Ile Phe Ser Met Phe Leu Cys Ala Lys Gly Ile Ile Ser Thr Asp Asp
145          150          155          160
Leu Glu Phe Phe Ser Thr Val Ile Val Ser Leu Val Ala Phe Tyr Ser
165          170          175
Ile Cys Ser Gly Val Glu Tyr Ile Trp Val Asn Lys Ser His Leu Leu
180          185          190
Gln Lys Asn Asp Ser Arg Met Ala Ser His Arg Glu Val Tyr Cys Leu
195          200          205

```

(2) INFORMATIONS POUR LA SEQ ID NO: 591:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 1003 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 579096..582104

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 591:

```

Met Ser Ser Gln Pro Leu Thr Leu Gln Ala Met Met Ala Ala Ile Leu
1          5          10          15
Asn Phe Trp Ser Glu Gln Gly Cys Ile Ile His Gln Gly Tyr Asp Leu
20          25          30
Glu Val Gly Ala Gly Thr Phe Asn Pro Ala Thr Phe Leu Gln Ser Leu
35          40          45
Gly Pro Glu Pro Phe Arg Thr Ala Tyr Ile Glu Pro Ser Arg Arg Pro
50          55          60
Gln Asp Gly Arg Tyr Gly Gln His Pro Asn Arg Leu Gln Lys Tyr His
65          70          75          80
Gln Leu Gln Val Ile Leu Lys Pro Val Pro Glu Asn Phe Leu Ser Leu
85          90          95
Tyr Leu Glu Ser Leu Lys Val Ile Gly Leu Asn Leu Val Asp His Asp
100          105          110
Ile Arg Phe Val His Asp Asp Trp Glu Asn Pro Thr Ile Gly Ala Trp
115          120          125
Gly Leu Gly Trp Glu Val Trp Leu Asn Gly Met Glu Ile Thr Gln Leu
130          135          140

```


Thr	Tyr	Phe	Gln	Ala	Val	Gly	Ser	Lys	Pro	Leu	Asp	Ala	Ile	Ser	Gly
145					150					155					160
Glu	Ile	Thr	Tyr	Gly	Val	Glu	Arg	Ile	Ala	Met	Tyr	Leu	Gln	Lys	Lys
				165					170					175	
Asn	Ser	Val	Tyr	Asp	Val	Met	Trp	Asn	Gly	Ser	Leu	Thr	Tyr	Gly	Asp
			180					185					190		
Ile	Thr	Gln	Tyr	Ala	Glu	Gln	Ala	Trp	Ser	Gln	Tyr	Asn	Phe	Glu	Thr
		195					200					205			
Ala	Asn	Thr	Thr	Met	Trp	Leu	Lys	His	Phe	Asp	Asp	Phe	Ser	Ala	Glu
	210					215					220				
Ala	Leu	Ala	Thr	Leu	Asp	Gln	Gly	Leu	Pro	Leu	Pro	Ala	Tyr	Asp	Phe
225					230					235					240
Val	Ile	Lys	Ala	Ser	His	Ala	Phe	Asn	Met	Leu	Asp	Ser	Arg	Gly	Val
				245					250					255	
Ile	Ser	Val	Thr	Glu	Arg	Thr	Arg	Tyr	Ile	Ala	Lys	Ile	Arg	Gln	Leu
			260					265						270	
Ala	Arg	Ala	Ala	Ala	Asp	Lys	Tyr	Val	Ala	Trp	Arg	Glu	Ser	Leu	Gly
		275					280					285			
Phe	Pro	Leu	Leu	Lys	Thr	Pro	Pro	Ser	Thr	Pro	Thr	Val	Thr	Pro	Lys
	290					295					300				
Lys	Ile	Pro	Thr	Ile	Cys	Gln	Pro	Glu	Asp	Phe	Leu	Leu	Glu	Ile	Gly
305					310					315					320
Ser	Glu	Glu	Leu	Pro	Ala	Thr	Phe	Val	Pro	Thr	Gly	Ile	Gln	Gln	Leu
				325					330					335	
Glu	Ser	Leu	Ala	Lys	Lys	Leu	Leu	Ala	Asp	His	Gly	Ile	Ala	Tyr	Lys
			340					345					350		
His	Leu	Glu	Val	Leu	Gly	Thr	Pro	Arg	Arg	Leu	Ala	Leu	Cys	Ile	Glu
	355						360					365			
Gly	Leu	Ser	His	Val	Thr	Ile	Arg	Pro	Glu	Ser	Glu	Lys	Lys	Gly	Pro
	370					375					380				
Pro	Leu	Ser	Leu	Leu	Phe	Met	Thr	Asp	Gly	Ser	Val	Ser	Pro	Gln	Gly
385					390					395					400
Glu	Gln	Phe	Phe	Pro	Ser	His	Gly	Leu	Ser	Ile	Ser	His	Arg	Ser	Ala
				405					410					415	
Leu	Asp	Gln	Pro	Ser	Ala	Ile	Cys	Arg	Val	Arg	Ser	Ile	Asn	Gly	Thr
			420					425					430		
Asp	Tyr	Leu	Phe	Leu	Val	Ile	Pro	Glu	Glu	Arg	Lys	Glu	Thr	Ala	Ala
	435						440					445			
Ile	Leu	Val	Asn	Glu	Leu	Pro	Gln	Leu	Ile	Arg	Ser	Ile	Arg	Phe	Pro
	450					455					460				
Gln	Lys	Met	Thr	Trp	Asp	Asn	Gly	Gly	Val	Glu	Tyr	Ala	Arg	Pro	Ile
465					470					475					480
Arg	Trp	Leu	Val	Ala	Leu	Tyr	Gly	Asp	Gln	Ile	Leu	Pro	Ile	Ser	Leu
				485					490					495	
Gly	Phe	Val	Ser	Ser	Gly	Asn	Thr	Ser	Trp	Gly	His	Arg	Gln	Leu	Asp
			500					505					510		
Asn	Arg	Gln	Leu	Thr	Ile	Pro	Ser	Ser	Asn	Met	Tyr	Val	Asp	Thr	Leu
	515						520					525			
Arg	Ser	Ala	Cys	Val	Ile	Val	Ser	Gln	Lys	Glu	Arg	Arg	Ala	Ile	Ile
	530					535					540				
Lys	Gln	Gly	Leu	Gln	Asn	Leu	Thr	Gly	Asp	Gln	Ile	Val	Ala	Ile	Ala
545					550					555					560
Pro	Glu	His	Leu	Val	Asp	Glu	Thr	Val	Phe	Leu	Thr	Glu	His	Pro	Phe
			565						570					575	
Val	Ile	Ser	Ala	Gln	Phe	Asp	Pro	Ala	Phe	Cys	Ser	Leu	Pro	Lys	Glu
			580					585					590		
Leu	Leu	Ile	Ala	Glu	Met	Ile	Gln	His	Gln	Arg	Tyr	Phe	Pro	Thr	Gln
	595						600					605			
Asn	Met	Gln	Gly	Glu	Ile	Thr	Asn	Arg	Phe	Leu	Ile	Val	Cys	Asp	Asn

610	615	620
Ser Pro Thr Asp Ser Ile Val Glu Gly Asn Glu Lys Ala Leu Ala Pro		
625	630	635
Arg Leu Thr Asp Gly Asn Phe Leu Phe Lys Gln Asp Leu Leu Thr Pro		
645	650	655
Leu Ser Ser Phe Val Glu Lys Leu Lys Ser Val Thr Tyr Phe Glu Ser		
660	665	670
Leu Gly Ser Leu Ala Asp Lys Thr Ser Arg Leu Lys Leu His Leu Glu		
675	680	685
Glu Ala Tyr Ala Leu Leu Pro Leu Cys Ala Lys Glu Asp Ile Asp Thr		
690	695	700
Ala Ile His Tyr Cys Lys Ala Asp Leu Val Ser Ser Val Val Asn Glu		
705	710	715
Phe Pro Glu Leu Gln Gly Ile Met Gly Arg Tyr Tyr Leu Gln Asn Ala		
725	730	735
Ser Leu Ser Arg Ala Ala Ala Leu Ala Ile Gly Glu His Leu Gln His		
740	745	750
Ile Thr Leu Gly Ser Asn Ile Ser Thr Thr Gly Ala Leu Leu Ser Ile		
755	760	765
Leu Asp Arg Ile Asp Asn Leu Leu Ser Cys Phe Ile Leu Gly Leu Leu		
770	775	780
Pro Thr Ser Ser His Asp Pro Tyr Ala Leu Arg Arg Gln Ser Leu Glu		
785	790	795
Ile Leu Thr Leu Leu Tyr Thr Thr Gln Ser Ser Val Asp Ile Glu Asp		
805	810	815
Leu Phe Ala Arg Leu Ile Arg His Phe Pro Ser Ser Ile Pro Asn Thr		
820	825	830
Val Trp Ser Pro Glu Glu Val Leu Ser Lys Leu Asn Thr Phe Val Trp		
835	840	845
Gly Arg Leu Arg Thr Ile Leu Ser Ser Leu Gly Phe Asp Lys Glu Ile		
850	855	860
Ile Ala Thr Val Leu Thr Asp Asn Cys Pro Lys Asn Pro Leu Thr Ile		
865	870	875
Ile Gln Ser Ala Gln Ser Ile Gln Glu Leu Lys Asn Thr Gln Ile Leu		
885	890	895
Lys Thr Ile Ala Ala Thr His Asn Arg Leu Lys Lys Ile Leu Ala Ser		
900	905	910
Leu Ser Phe Ser Val Thr Glu Gln Met Phe Ser Leu Gln Ser Ala Glu		
915	920	925
Asp Leu Leu Phe Lys Gln Ala Leu Asp Arg Phe Val Glu Glu Thr Thr		
930	935	940
Ala Leu Pro Ile Ser Ser Lys Asp Tyr Leu His Leu Leu Lys Glu Leu		
945	950	955
Ala Gln Ser Thr Glu Leu Phe Leu Asp Ser Val Arg Val Ala Ser Asp		
965	970	975
Asp Glu Ser Thr Arg Asn Gln Arg Ile Ala Leu Leu Ile Ala Ala Gln		
980	985	990
Lys Cys Phe Gly Phe Tyr Ala Trp Asp Val Leu		
995	1000	

(2) INFORMATIONS POUR LA SEQ ID NO: 592:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 164 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(582206..582697)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 592:

```

Lys Arg Ser Ser Leu Met Arg Phe Leu Leu Ala Leu Phe Ser Leu Ile
1      5      10      15
Leu Val Leu Pro Ala Thr Glu Ala Phe Ser Thr Glu Asp Lys Gln Cys
20      25      30
Gln Gln Glu Ala Glu Glu Asp Cys Ser Gln Val Ala Asp Thr Cys Val
35      40      45
Phe Tyr Ser Tyr Ala Glu Gly Leu Glu His Ala Arg Asp Glu Gly Lys
50      55      60
Leu Thr Leu Val Val Leu Leu Asp Thr Ser Gly Tyr Ser Phe Glu Thr
65      70      75      80
Leu Ala Tyr Ala Ala His Ala Met Glu Ser Leu Leu Ser Thr Phe
85      90      95
Ala Asp Phe Val Leu Ser Arg Arg Glu Ala Val Pro Leu Ile Ile
100     105     110
Pro Pro Gly Ser Arg Ser Tyr Gly Trp Arg Asp Ser Val Val Leu Arg
115     120     125
Ser Phe Leu Arg Ser Asn Ile Ser Ile Thr Ala Cys Asp Cys Tyr Leu
130     135     140
Ser Tyr Trp Gly Phe Phe Cys Arg Asp His Gly Tyr Tyr Arg Asp Ala
145     150     155     160
Val Asn Lys Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 593:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 104 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(582811..583122)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 593:

```

Asn Ile Ser Ser Leu Val Leu Asn Leu Leu Gly Phe Met Arg Ser Leu
1      5      10      15
His Phe Leu Leu Thr Ala Phe Thr Phe Ser Leu Phe Cys Gly Ala Ala
20      25      30
Leu Thr Ala Ser Ser Pro Lys Thr Leu Ser Phe Val Ala Ala Glu Ala
35      40      45
Ala Gly Val Gly Ala Ala Arg Pro Ser Ser Val Ala Ser Leu Leu Asp
50      55      60
Ser Ala His Glu Val Ala Lys Ser Ala Gly Val Gly Tyr Gly Ser Ala
65      70      75      80
Tyr Ile Leu Asn Glu Leu Gln Asn Leu Gln Ser Gln Glu Leu Glu Gly
85      90      95
Leu Leu Ala Ser Gln Glu Asn Ile
100

```

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 111 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

{viii) POSITION DANS LE GENOME: complement(583182..583514)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 594:

(X1)	DESCRIPTION														
Ser 1	Ser 1	Ile 5	Phe 5	Leu 5	Arg 5	Lys 5	Ser 5	Phe 10	Ile 10	Val 10	Ala 10	Glu 10	Tyr 15	Arg 15	Ala 15
Ile 20	Phe 20	Val 20	Met 20	Ala 20	Met 20	Asn 20	His 20	Tyr 25	Asn 25	Asp 25	Arg 25	Gln 30	Thr 30	Leu 30	Pro 30
Ser 35	Met 35	Asp 35	Glu 35	Met 40	Met 40	Ser 40	Leu 40	Val 45	Val 45	Gly 45	Thr 45	Glu 45	Ala 45	Met 45	Thr 45
Leu 50	Leu 50	Val 50	Ala 55	Arg 55	Arg 55	Met 55	Asn 55	Thr 60	Glu 60	Leu 60	Met 60	Arg 60	Asp 60	Ile 60	Val 60
Val 65	Gln 65	Ser 70	Ile 70	Gln 70	Lys 70	Leu 70	Leu 75	Asp 75	Lys 75	His 75	Trp 75	Arg 75	Asp 80	Arg 80	Lys 80
Arg 85	Lys 85	Leu 85	Cys 85	His 85	Gln 90	Thr 90	Gly 90	Lys 90	Gly 90	Leu 90	Asp 95	Ser 95	Leu 95	Gln 95	Glu 95
Tyr 100	Val 100	Arg 105	Leu 105	Ser 105	Gly 105	Glu 105	Arg 105	Val 110	Lys 110	Val 110	Ser 110	Leu 110	Val 110	Ser 110	

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 144 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(583438..583869)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 595:

(X1)	DESCRIPTION														
Xaa	His	Ser	Tyr	Glu	Gln	Phe	Thr	Pro	Arg	Glu	Lys	Ala	Arg	Val	Ile
1				5					10					15	
Glu	Glu	Val	Ile	Gln	Gln	Val	Arg	Cys	Trp	Gly	Ser	Pro	Ile	Thr	Ile
			20					25					30		
His	Glu	Tyr	Leu	Arg	Gln	Leu	Ala	Ser	Leu	Val	Lys	Val	Pro	Glu	Pro
		35					40					45			
Ala	Val	Leu	Ser	Tyr	Leu	Ser	Ser	Ile	Thr	Ser	Ala	Ala	Glu	Asp	Lys
	50					55					60				
Gly	Lys	Lys	Val	Ser	Ala	Lys	Glu	Pro	Ser	Ser	Glu	Ser	Glu	Gln	Thr
65					70					75				80	
Ser	Thr	Glu	Gly	Lys	Ile	Ser	Lys	Lys	Ile	Ser	Pro	Arg	Met	Ile	Leu
				85					90					95	
Glu	Ala	Asp	Val	Ile	Arg	Cys	Leu	Leu	Phe	Xaa	Lys	Pro	Glu	Asp	Glu
			100					105					110		

Phe Val Pro Ala Thr Val Lys Gln Tyr Leu Ser Pro Glu Glu Phe His
 115 120 125
 Cys Gly Arg Ile Ser Ser Tyr Ile Cys Tyr Gly Tyr Glu Ser Leu Gln
 130 135 140

(2) INFORMATIONS POUR LA SEQ ID NO: 596:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(583827..584435)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 596:

Ser Gly Leu Gly Ile Ser Leu Lys Thr Gly Phe Cys Leu Leu Arg Ser
 1 5 10 15
 Ile Met Phe Pro Ile Gln Asp Ala Leu Gly Tyr Thr Ile Gly Phe Ser
 20 25 30
 Ser Arg Arg Phe Lys Glu Gly Gly Arg Gly Gly Lys Tyr Ile Asn Ser
 35 40 45
 Pro Glu Thr Ile Leu Phe Lys Lys Ser Arg Val Leu Tyr Gly Leu Gln
 50 55 60
 Phe Ser Arg Lys Arg Ile Ala Lys Glu Arg Arg Val Ile Leu Val Glu
 65 70 75 80
 Gly Gln Ala Asp Cys Leu Gln Met Ile Asp Phe Gly Phe Asn Cys Thr
 85 90 95
 Leu Ala Ala Gln Gly Thr Ser Phe Thr Glu Thr His Val His Glu Leu
 100 105 110
 Val Lys Leu Gly Val Ser Lys Ala Tyr Leu Leu Phe Asp Gly Asp Ala
 115 120 125
 Ala Gly Glu Lys Ala Ser Leu Arg Val Gly Asp Leu Cys Gln Ala Ala
 130 135 140
 Gly Ile Thr Ala Ile Val Cys Arg Leu Pro Ser Gly Gln Asp Pro Asp
 145 150 155 160
 Ser Phe Leu Met Gln Arg Gly Pro Glu Glu Leu Arg Glu Leu Leu Asp
 165 170 175
 Arg Gly Glu Asp Tyr Leu Ser Phe Leu Val Trp His Lys Xaa Ile Leu
 180 185 190
 Met Asn Ser Leu Leu Gln Glu Lys Lys Leu Glu
 195 200

(2) INFORMATIONS POUR LA SEQ ID NO: 597:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 223 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(584299..584967)

(2) INFORMATIONS POUR LA SEQ ID NO: 599:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 457 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 585240..586610

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 599:

Glu	Pro	Val	Pro	Leu	Leu	Arg	Ile	Lys	Asn	Phe	Phe	Asp	His	Ala	Ile
1				5					10					15	
Leu	Asp	Lys	Ala	Met	Thr	His	Lys	Leu	Thr	Pro	Met	Met	Gln	Gln	Trp
			20					25					30		
His	Gln	Cys	Lys	Glu	Gln	Ala	Gly	Asp	Cys	Leu	Leu	Leu	Phe	Arg	Leu
		35					40					45			
Gly	Glu	Phe	Tyr	Glu	Ala	Phe	Phe	Asp	Asp	Ala	Leu	Ile	Leu	Ala	Gln
	50					55				60					
Asn	Leu	Asp	Ile	Thr	Leu	Thr	Gln	Arg	Gln	Asn	Val	Pro	Met	Ser	Gly
65					70				75					80	
Ile	Pro	Ala	Thr	Cys	Leu	Asp	Gly	Tyr	Val	Asp	Arg	Leu	Val	Ser	Arg
				85				90					95		
Gly	Phe	Lys	Val	Ala	Ile	Ala	Glu	Gln	Ala	Asp	Asn	Thr	Glu	Gly	Ser
			100					105					110		
Lys	Gly	Leu	Val	Pro	Arg	Thr	Ile	Asn	Arg	Leu	Ile	Thr	Pro	Gly	Ala
		115					120					125			
Leu	Leu	Ser	Ser	Ser	Leu	Leu	Pro	Glu	Lys	Ala	Asn	Asn	Tyr	Val	Leu
	130					135					140				
Ala	Ile	Asn	Gln	Val	Gly	Ser	Leu	Tyr	Gly	Leu	Ser	Cys	Leu	Asp	Leu
145					150					155				160	
Ser	Ile	Gly	Thr	Phe	Leu	Val	Ala	Glu	Tyr	Asp	Asn	Thr	Lys	Asp	Leu
				165					170					175	
Ile	Glu	Ala	Ile	Cys	Arg	Leu	Ala	Pro	Thr	Glu	Leu	Leu	Ser	His	Ala
		180					185						190		
Lys	Phe	Tyr	Gln	Lys	Asn	Ala	Ala	Val	Ile	Lys	Gln	Leu	Gln	Gln	His
		195				200						205			
Leu	Arg	Ile	Thr	Leu	Ser	Glu	Tyr	Val	Ser	Trp	Ala	Phe	Glu	Tyr	Gln
	210					215					220				
Ser	Ala	Thr	Lys	Lys	Leu	Tyr	Thr	Cys	Phe	Gln	Val	Ser	Ser	Leu	Asp
225					230					235				240	
Gly	Phe	Gly	Leu	Gln	Gly	Leu	Val	Pro	Ala	Ile	Asn	Ala	Ala	Gly	Ala
			245						250					255	
Leu	Leu	Ser	Tyr	Ile	Gln	Asp	Lys	Leu	Leu	Leu	Pro	Ile	Ser	His	Leu
		260					265						270		
Ser	Ile	Pro	Lys	Ile	Tyr	Gly	Gln	Lys	His	Leu	Leu	Ile	Asp	Lys	
		275					280					285			
Ala	Ser	Gln	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Pro	Ile	His	Gly	Glu	His
		290				295					300				
Gly	Lys	Gly	Ser	Leu	Leu	Gln	Val	Met	Glu	Arg	Thr	Ser	Thr	Pro	Met
305					310					315				320	
Gly	Gly	Arg	Leu	Leu	Arg	Asn	Thr	Leu	Ile	Asn	Pro	Phe	Tyr	Asp	Leu
				325					330					335	
Lys	Glu	Ile	Thr	Leu	Arg	Gln	Asp	Ser	Val	Glu	Phe	Phe	Leu	Gln	Gln

(2) INFORMATION POUR LA SEQ ID NO: 600:

(A) LONGUEUR: 425 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 586484..587758

Val 1	Phe	Asp	Cys	Ser 5	Pro	Ser	Met	Leu	Ser 10	His	Lys	Asn	Val 15	Ile	Asp
Arg	Ala	Tyr	Pro 20	Arg	Thr	Ser	Phe	Lys 25	Ser	Val	Arg	Arg	Asn 30	Ile	Phe
Ala	Asn	His 35	Tyr	His	Pro	Asp	Leu 40	Leu	Arg	Leu	Arg	Asn 45	Ile	Lys	Glu
Asn	Ser 50	Lys	Ser	Trp	Ile	Leu 55	Glu	Tyr	Gln	Glu	Arg 60	Ile	Arg	Asn	Glu
Thr 65	Gly	Ile	Lys	Lys	Leu 70	Lys	Val	Cys	Tyr	Ala 75	Gln	Ala	Leu	Gly	Tyr
Tyr	Ile	Glu	Val 85	Ser	Asn	Leu	Ala	Pro 90	Gln	Leu	Pro	Lys	Glu 95	Phe	
Ile	Arg	Arg	Gln 100	Ser	Arg	Leu	His 105	Ala	Glu	Arg	Phe	Thr 110	Thr	Gln	Glu
Leu	Gln 115	Gln	Phe	Gln	Asp	Glu 120	Val	Phe	Ser	Val	Glu	Asp 125	Lys	Leu	Gln
Thr 130	Leu	Glu	Thr	Lys	Leu	Phe 135	Lys	Glu	Leu	Cys	Phe 140	Tyr	Ile	Val	Glu
His 145	Arg	Asp	Leu	Ile 150	Leu	Lys	Leu	Ser	Thr	Ala 155	Val	Ala	Asp	Leu	Asp
Tyr	Val	Val	Ser 165	Leu	Ala	Glu	Leu	Ala 170	Ala	Glu	Tyr	Asp	Tyr	Arg	Arg
Pro	Leu	Val	Asp 180	His	Ser	Asp	Ala 185	Leu	Ser	Ile	Thr	Lys	Gly 190	Met	His
Pro	Val 195	Ala	Leu	Thr	Leu	Leu	Asp 200	Lys	Gly	Thr	Phe 205	Ile	Pro	Asn	Asp
Thr	Val 210	Met	His	Ser	Ala 215	Gln	Thr	Arg	Met	Ile 220	Leu	Thr	Gly	Pro	

130 135 140
 Leu Glu Val Ile Ser Leu Trp Phe Pro Leu Arg Thr Cys Ser Asp Arg
 145 150 155 160
 Glu Phe Ser Thr Arg Gln Arg Pro Cys Val Leu Tyr Glu Met Lys Arg
 165 170 175
 Cys Leu Ala Pro Cys Val Gly Leu Cys Ser Gln Thr Glu Tyr Gln Glu
 180 185 190
 Thr Leu Asp Lys Ala Ile Leu Phe Leu Lys Gly Asp Val Arg Ser Thr
 195 200 205
 Ile Ser Asn Leu Glu Lys Ala Ile Glu Lys Ala Ser Gln Glu Gln Lys
 210 215 220
 Phe Glu His Ala Ala Ala Leu Tyr Arg Thr Leu Thr Leu Ile Arg Gln
 225 230 235 240
 Thr Met Ala Lys Gln His Val Glu Lys Phe Gln Ala Tyr Asp Ile Asp
 245 250 255
 Val Leu Gly Leu Tyr Arg Lys Gly Ser Leu Ala Ile Val Ser Val Leu
 260 265 270
 Ser Val Tyr Ser Gly Lys Leu Leu Gly Ala Arg Tyr Phe Ile Phe Pro
 275 280 285
 Glu Asn Ala Gln Glu Asp Ser Ala Leu Phe Pro Ser Phe Ile Leu Gln
 290 295 300
 Tyr Tyr Ala Glu Asn Pro Arg Ile Pro Lys Glu Ile Phe Val Pro Val
 305 310 315 320
 Ser Leu Asp Ser Pro Glu Leu Pro Tyr Leu Leu Asn Thr Ala Glu Pro
 325 330 335
 Pro Lys Ile Arg Cys Pro Lys Thr Glu Tyr Gly Lys Glu Leu Ala
 340 345 350
 Leu Ala His Lys Asn Ala Ala Glu Gln Ala Lys Pro Phe Asn Ser Ile
 355 360 365
 Thr Pro Pro Tyr Glu Glu Leu Gln His Phe Phe Asn Leu Ser Gln Tyr
 370 375 380
 Pro Tyr Arg Ile Glu Cys Tyr Asp Asn Ala His Leu Gln Gly Glu His
 385 390 395 400
 Asn Val Gly Val Cys Ile Val Phe Glu Asn Asp Leu Phe Ser Pro Lys
 405 410 415
 Gln Tyr Arg Thr Phe Ser Ile Thr Ser His Gly Asp Asp Leu Ala Ala
 420 425 430
 Phe Glu Glu Val Leu Thr Arg Arg Phe Arg Ser Leu Thr Thr Glu Leu
 435 440 445
 Pro Asn Leu Ile Val Ile Asp Gly Gly Arg Asn Gln Phe Lys Arg Ala
 450 455 460
 Gln Arg Ile Leu Glu Glu Leu Asn Leu Thr Gly Ile Thr Val Val Thr
 465 470 475 480
 Ile Ala Lys Glu Ser Gly Asn His Ser Lys Ser Cys Ala Lys Lys Ser
 485 490 495
 Tyr Phe Val Lys Leu Ser Pro Lys Glu Ser Phe Phe Ile Pro His Pro
 500 505 510
 Gln Phe Phe Ser Ser Phe Ser Tyr Tyr Glu Met Lys Pro Thr Val Ser
 515 520 525
 Arg Phe Asn Thr Ile Val Lys Asn Met Gln Lys Gln Cys
 530 535 540

(2) INFORMATIONS POUR LA SEQ ID NO: 602:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 127 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 589198..589578

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 602:

Glu	Phe	Asn	Arg	Asp	Tyr	Arg	Ser	Asn	His	Arg	Gln	Gly	Ile	Trp	Gln
1				5					10					15	
Ser	Gln	Gln	Lys	Leu	Arg	Gln	Glu	Lys	Leu	Phe	Cys	Glu	Thr	Phe	Pro
			20					25					30		
Gln	Gly	Ile	Leu	Leu	His	Pro	Thr	Ser	Ala	Ile	Leu	Gln	Phe	Phe	Gln
		35					40					45			
Leu	Leu	Arg	Asp	Glu	Ala	His	Arg	Phe	Ala	Ile	Gln	His	Tyr	Arg	Lys
	50					55					60				
Lys	His	Ala	Lys	Ala	Val	Leu	Thr	Thr	Lys	Lys	Ile	Pro	Gly	Ile	Gly
65					70					75					80
Glu	Val	Lys	Thr	Lys	Arg	Leu	Leu	Gln	Lys	Phe	Lys	Ser	Trp	Lys	Arg
				85					90					95	
Val	Phe	Ile	Ala	Ser	Glu	Glu	Glu	Leu	Lys	Thr	Val	Gln	Gly	Ile	Thr
			100					105					110		
Ala	Lys	Asp	Ile	Gln	Arg	Ile	Gln	Glu	Glu	Gly	Ala	Lys	Pro	Glu	
		115					120						125		

(2) INFORMATIONS POUR LA SEQ ID NO: 603:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(589630..590061)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 603:

Ser	Arg	Tyr	Arg	Asp	Pro	Cys	Asp	Ser	Ser	Asp	His	Cys	Ser	Leu	Leu
1				5					10					15	
Ser	Lys	Asn	Arg	Trp	Gly	Phe	Ile	Ile	Arg	Xaa	Arg	Ile	Ser	Leu	Thr
			20					25					30		
Arg	Phe	Leu	Asp	Ala	Ile	Ser	Lys	Xaa	Xaa	Lys	Gly	Ile	Tyr	Val	Glu
		35					40					45			
Gln	Asp	Ser	Lys	Asn	Ser	Leu	Val	Lys	Val	Arg	Val	Glu	Val	Asn	Val
	50					55					60				
Asp	Tyr	Gly	Val	Ser	Ile	Pro	Glu	Lys	Thr	Glu	Glu	Ile	Gln	Gly	Cys
65					70					75					80
Ile	Val	Ser	Glu	Ile	Ser	Glu	Tyr	Thr	Gly	Leu	His	Val	Ala	Ala	Val
				85					90					95	
His	Val	Val	Val	Lys	Gly	Leu	Thr	His	Pro	Lys	Ala	Lys	Asp	Glu	Glu
			100					105					110		
Val	Pro	Ala	Ile	Glu	Val	Ile	Glu	Glu	Pro	Cys	Leu	Glu	Glu	Phe	Ser
		115					120					125			
Ser	Ala	Glu	Glu	Tyr	Leu	Glu	Glu	Val	Ser	Val	Ile	Gln	Thr	Glu	Glu
		130					135					140			

(2) INFORMATION POUR LA SEQ ID NO: 606:

(A) LONGUEUR: 99 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(592849..593145)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 606:

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 607:

(A) LONGUEUR: 260 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(593121..593900)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 607:

Glu Phe Met Ser Ser Leu Arg Ile Ala Arg Ser Cys Ser Phe Lys Gln

```

1           5           10           15
Lys Thr Leu Leu Ala Ala Leu Val Phe Phe Gly Leu Gly Ala Ser Gln
20           25           30
Val Cys Ala Thr Pro Ser Asn Ser Arg Glu Ile Ala Trp Tyr Val Asp
35           40           45
Tyr Gln Glu Ala Arg Asp Glu Ser Arg Glu Lys Asp Leu Pro Met Leu
50           55           60
Leu Phe Phe Ser Gly Ser Asp Trp Asn Gly Ser Cys Met Lys Ile Arg
65           70           75           80
Asp Glu Val Leu Ser Ser Ser Asp Phe Ile Ser Ala Val Ala Asp Gln
85           90           95
Phe Val Cys Val Val Val Asp Phe Pro Arg His Thr Glu Leu Arg Asp
100          105          110
Pro Leu Ile Asn Glu Gln Asn Glu Asp Leu Lys Asn Arg Leu Tyr Val
115          120          125
Asn Thr Phe Pro Ser Leu Val Leu Leu Ser Pro Glu Glu Arg Ala Ile
130          135          140
Tyr Lys Ile Glu Ser Phe Gly Asn Glu Asn Gly Ser Asn Leu Gly Glu
145          150          155          160
Ser Leu Cys Arg Val Ile Ala Asn Asp Gln Glu Leu Glu Gln Val Phe
165          170          175
Pro Leu Ile Pro Thr Leu Ser Ser Val Ala Leu Arg Lys Tyr Tyr Gln
180          185          190
Leu Ala Glu Glu Leu Ser Arg Lys Asp Phe Met Ala Thr Ala Leu Glu
195          200          205
Gln Gly Val Leu Cys Asp Asp Ser Phe Phe Leu Ser Glu Lys Phe Arg
210          215          220
Gln Leu Val Glu Ala Gly Arg Met Asp Ser Glu Glu Cys Arg Ala Val
225          230          235          240
Lys Asn Arg Leu Leu Glu Leu Asp Pro Glu Asn Glu Gln Ser Arg Ile
245          250          255
Ser Gln Trp Leu
260

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(2) INFORMATIONS POUR LA SEQ ID NO: 608:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 481 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 594195..595637

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 608:

```

Met Asn Thr Ala Ile Asp Leu Phe Leu Tyr Asn Thr Leu Ser Arg Glu
1           5           10           15
Lys Glu Arg Phe Leu Pro Val Asn Asp Pro Val Lys Leu Tyr Thr Cys
20           25           30
Gly Pro Thr Val Tyr Asp Tyr Ala His Ile Gly Asn Phe Arg Thr Tyr
35           40           45
Ile Phe Glu Asp Leu Leu Lys Arg Val Leu Leu Phe Leu Gly Tyr Ser
50           55           60
Val Tyr His Val Met Asn Ile Thr Asp Val Asp Asp Lys Thr Leu Ala
65           70           75           80

```

Gly Ala Arg Lys Lys Gly Cys Ser Leu Glu Lys Tyr Cys Gln Pro Tyr
 85 90 95
 Ile His Ala Phe Phe Ala Asp Leu Glu Thr Leu His Ile Leu Lys Ala
 100 105 110
 Asp Ala Tyr Pro His Ala Thr His Tyr Ile Pro Gln Met Ile Glu Ala
 115 120 125
 Ile Gln Gln Leu Ile Asn Gln Gly Val Ala Tyr Ile Gly Gln Asp Gln
 130 135 140
 Ser Val Tyr Phe Ser Ile Ser Gln Phe Pro Asn Tyr Gly Ala Leu Ser
 145 150 155 160
 His Leu Asn Leu Glu Glu Leu Arg Asn Ser Ala Arg Ile Asp Ala Asp
 165 170 175
 Glu Tyr Asp Lys Asp Asn Leu Cys Asp Phe Val Leu Trp Lys Ala Tyr
 180 185 190
 Asp Pro Asp Arg Asp Gly Glu Ile Phe Trp Glu Ser Pro Phe Gly Lys
 195 200 205
 Gly Arg Pro Gly Trp His Leu Glu Cys Ser Ile Met Ser Met Ser Leu
 210 215 220
 Leu Gly Gln Ser Leu Asp Ile His Ala Gly Gly Val Asp Asn Ile Phe
 225 230 235 240
 Pro His His Glu Asn Glu Ile Ala Gln Ser Glu Ser Leu Thr His Lys
 245 250 255
 Pro Phe Val Arg Tyr Trp Leu His Ser His His Leu Leu Val Asp Arg
 260 265 270
 Lys Lys Met Ser Lys Ser Leu Gly Asn Phe Phe Thr Leu Arg Asp Leu
 275 280 285
 Leu Asp Gln Gly Phe Ser Gly Glu Glu Val Arg Tyr Leu Leu Leu Gln
 290 295 300
 Gly His Tyr Arg Thr Gln Leu Asn Phe Thr Gln Glu Gly Leu His Ala
 305 310 315 320
 Ser Arg Gln Ser Leu Lys Arg Leu Arg Asp Phe Ile Cys Arg Leu Glu
 325 330 335
 Asp Pro Ser Tyr Pro Asp Asp Ile Ile His Pro Glu Val Ala Thr Ala
 340 345 350
 Cys Gln Ser Phe Leu Glu Thr Phe Ile Thr Ser Leu Thr Asn Asp Leu
 355 360 365
 Asn Ile Ser Ser Ser Leu Ala Ala Leu Phe Asp Phe Ile Arg Lys Ile
 370 375 380
 Asn Ser Ser Ile Asp Gln His Thr Gly Ile Gln Thr Glu Thr Asp Ser
 385 390 395 400
 Ser Val Phe Ser Lys Gln Asp Ala Gln His Ile Leu Ala Leu Leu Arg
 405 410 415
 Lys Ile Asp Gln Val Leu Gly Val Leu Pro Phe Ser Gln Pro Asp Ile
 420 425 430
 Pro Glu Glu Val Leu Leu Leu Val Glu Gln Arg Glu Ala Ala Arg Lys
 435 440 445
 Val Lys Asn Trp Gln Glu Ala Asp Arg Leu Arg Asp Glu Ile Leu Ser
 450 455 460
 Arg Gly Phe Ala Ile Glu Asp Gly Lys Thr Gly Met Lys Val Lys Lys
 465 470 475 480
 Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 609:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 161 acides aminés
- (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(595640..596122)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 609:

Asn	Phe	Arg	Asn	Thr	Asn	Ile	Ser	Pro	Glu	Lys	Thr	Tyr	Val	His	Ala
1				5					10					15	
Ser	Arg	Gly	Glu	Leu	Ile	Ala	Leu	Leu	Phe	Asp	Glu	Leu	Val	Cys	Asp
		20					25						30		
Lys	Leu	Ile	Ala	Pro	His	His	Ile	Thr	Asp	His	Pro	Leu	Glu	Thr	Thr
		35				40						45			
Pro	Leu	Cys	Lys	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Thr	Leu	Val	Glu	Arg
	50				55					60					
Phe	Glu	Ser	Phe	Cys	Leu	Gly	Lys	Glu	Leu	Cys	Asn	Ala	Tyr	Ser	Glu
65				70						75				80	
Leu	Asn	Asp	Pro	Leu	Gln	Gln	Arg	Lys	Leu	Leu	Glu	Glu	Gln	Met	Arg
			85					90					95		
Lys	Lys	Ala	Leu	Asn	Pro	Asp	Ser	Glu	Tyr	His	Pro	Ile	Asp	Glu	Glu
		100				105						110			
Phe	Leu	Glu	Ala	Leu	Cys	Gln	Gly	Met	Pro	Pro	Ala	Gly	Gly	Phe	Gly
		115				120						125			
Ile	Gly	Ile	Asp	Arg	Leu	Val	Met	Met	Leu	Thr	Asp	Ala	Ala	Ser	Ile
	130				135						140				
Arg	Asp	Val	Leu	Phe	Phe	Pro	Val	Met	Arg	Arg	Ile	Glu	Ala	Lys	Lys
145					150				155						160
Asp															

(2) INFORMATIONS POUR LA SEQ ID NO: 610:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 237 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(596154..596864)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 610:

Glu	Ile	Ala	Lys	Pro	Phe	Arg	Lys	Glu	Thr	Pro	Lys	Val	Arg	Phe	Ala
1				5				10						15	
Gly	Arg	Leu	Val	Leu	Phe	Arg	Ser	Met	Gly	Lys	Asn	Ala	Phe	Gly	Gln
		20					25					30			
Ile	Leu	Asp	Asn	Asp	Ala	Lys	Ile	Gln	Val	Met	Phe	Asn	Arg	Asp	Phe
	35					40					45				
Ser	Ala	Val	Ala	Gly	Leu	Ala	Ala	Asp	Ala	Gly	Ile	Ser	Pro	Ile	Lys
	50				55					60					
Phe	Ile	Glu	Lys	Lys	Leu	Asp	Leu	Gly	Asp	Ile	Leu	Gly	Leu	Glu	Gly
65				70					75					80	
Tyr	Leu	Phe	Phe	Thr	His	Ser	Gly	Glu	Leu	Thr	Val	Leu	Val	Glu	Thr
			85					90						95	

Val Thr Leu Leu Cys Lys Ser Leu Ile Ser Leu Pro Asp Lys His Ala
 100 105 110
 Gly Leu Ala Asp Lys Glu Ile Arg Tyr Arg Lys Arg Trp Ala Asp Leu
 115 120 125
 Ile Ser Ser Glu Asp Val Arg Lys Thr Phe Leu Thr Arg Ser Arg Ile
 130 135 140
 Leu Lys Leu Ile Arg Glu Tyr Met Asp Gln Gln Ser Phe Leu Glu Val
 145 150 155 160
 Glu Thr Pro Ile Leu Gln Thr Val Tyr Gly Gly Ala Glu Ala Thr Pro
 165 170 175
 Phe Val Thr Thr Leu Gln Gly Leu His Ala Glu Met Phe Leu Arg Ile
 180 185 190
 Ser Leu Glu Ile Ala Leu Lys Lys Leu Leu Val Gly Gly Met Ser Arg
 195 200 205
 Val Tyr Glu Ile Gly Lys Val Phe Arg Asn Glu Gly Ile Asp Arg Thr
 210 215 220
 His Asn Pro Glu Phe Thr Met Ile Glu Ala Ala Ser Met
 225 230 235

(2) INFORMATIONS POUR LA SEQ ID NO: 611:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 150 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(597282..597731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 611:

Gly Ala Cys Ser Ser His Val Trp Arg Ser Gln Leu Leu Val Leu Leu
 1 5 10 15
 Gln Asn Val Val Leu Arg Val Arg Arg Arg Ser Asn Arg Val Ala Glu
 20 25 30
 Thr Gly Ile His Trp Met Ser Tyr Gln Asp Ala Leu Asn Lys Ala Lys
 35 40 45
 Gln Glu Gly Lys His Val Ala Val Phe Phe Thr Gly Ser Asp Trp Cys
 50 55 60
 Ile Trp Cys Met Arg Met Gln Asp Gln Ile Leu Gln Thr Ala Ala Phe
 65 70 75 80
 Ser Glu Phe Asp Lys Gln Tyr Leu Cys Met Val Glu Ile Asp Phe Pro
 85 90 95
 His Asn Lys Glu Gln Thr Ala Glu Gln Lys Glu Gln Asn Arg His Leu
 100 105 110
 Lys Ser Leu Tyr Ser Val Asp Gly Phe Pro Thr Leu Val Phe Leu Asp
 115 120 125
 Ser Glu Gly Xaa Glu Val Ala Lys Met Gly Phe Glu Pro Gly Gly Gly
 130 135 140
 Gly His Met Phe Ile Asp
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 612:

- (i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 762 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 598524..600809

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 612:

Lys	Arg	Phe	Ser	Ile	Lys	Lys	Arg	Phe	Met	Asp	Pro	Thr	His	Gln	Pro	1	5	10	15
Phe	Arg	Leu	Tyr	Ala	Glu	Val	Ile	Val	Asn	Ala	Asn	Ile	Asn	Lys	Ile	20	25	30	
Leu	Asp	Tyr	Gly	Ile	Pro	Ala	Glu	Leu	Glu	Asn	Leu	Val	Thr	Val	Gly	35	40	45	
Ser	Val	Val	Lys	Val	Pro	Leu	Gln	Arg	Lys	Leu	Thr	Asn	Asp	Lys	Tyr	50	55	60	
Lys	Ile	Ala	Ile	Val	Leu	Lys	Ile	Lys	Ser	Ser	Ser	Asp	Phe	Val	His	65	70	75	80
Val	Ile	Gln	Pro	Ile	Leu	Asp	Ile	Ser	Tyr	Glu	Gly	Ile	Thr	Leu	Pro	85	90	95	
Gln	Asp	Leu	Ile	Asp	Leu	Ile	Phe	Trp	Ile	Ser	Gln	Tyr	Tyr	Phe	Cys	100	105	110	
Pro	Leu	Gly	Ser	Ala	Val	Ser	Leu	Phe	Leu	Pro	Thr	Val	Tyr	Ala	Gln	115	120	125	
Thr	His	Ser	Thr	Lys	His	Gln	Asn	Asn	Val	Phe	Leu	Gly	Gln	Asn	Ala	130	135	140	
Glu	Arg	Thr	Gln	Glu	Ile	Leu	Lys	Thr	Leu	Asp	Asn	Pro	Gln	Gln	Ile	145	150	155	160
Ala	Val	Leu	Arg	Lys	Leu	Leu	Lys	Thr	Thr	Lys	Pro	Leu	Thr	Pro	Pro	165	170	175	
Glu	Leu	Met	Arg	Lys	Thr	Glu	Val	Ser	Ala	Lys	Thr	Leu	Asp	Ala	Leu	180	185	190	
Val	Lys	Gln	Lys	Phe	Ile	Arg	Ile	Val	Asp	Ser	Ala	Asp	Leu	Glu	Ile	195	200	205	
Gln	Asp	Glu	Gln	Leu	His	Tyr	Phe	Leu	Pro	Glu	Thr	Pro	Thr	Leu	Asn	210	215	220	
Gln	Glu	Gln	Leu	Asp	Ala	Ile	Asn	Thr	Ile	Ser	Gln	Ser	Leu	Val	Ala	225	230	235	240
Glu	Gln	Phe	Gln	Thr	Cys	Leu	Leu	Phe	Gly	Val	Thr	Gly	Ser	Gly	Lys	245	250	255	
Thr	Glu	Val	Tyr	Leu	Gln	Val	Ile	Arg	Lys	Ala	Arg	Ala	Leu	Gly	Lys	260	265	270	
Ser	Val	Ile	Leu	Leu	Val	Pro	Glu	Val	Ala	Leu	Thr	Ile	Gln	Thr	Leu	275	280	285	
Ser	Phe	Phe	Lys	Met	His	Phe	Gly	Ser	Glu	Val	Gly	Val	Leu	His	Tyr	290	295	300	
Lys	Leu	Ser	Asp	Ser	Glu	Arg	Thr	Gln	Thr	Trp	His	Lys	Ala	Ser	Arg	305	310	315	320
Gly	Leu	Ile	Asn	Ile	Ile	Ile	Gly	Pro	Arg	Ser	Ala	Ile	Phe	Cys	Pro	325	330	335	
Ile	Gln	Asn	Leu	Gly	Leu	Ile	Ile	Val	Asp	Glu	Glu	His	Asp	Ser	Ala	340	345	350	
Tyr	Lys	Gln	Ser	Asp	Leu	Pro	Pro	Phe	Tyr	Gln	Ala	Arg	Asp	Val	Ala	355	360	365	
Val	Met	Arg	Gly	Lys	Met	Thr	Asn	Ala	Thr	Val	Ile	Leu	Gly	Ser	Ala	370	375	380	

(viii) POSITION DANS LE GENOME: complement(600734..601876)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 613:

Gly	Lys	Trp	Val	Leu	Lys	Glu	Ala	Leu	Ser	Ile	Asp	Phe	Ile	Thr	Asn	1	5	10	15
Asp	Phe	Leu	Gly	Phe	Ser	Arg	Leu	Asp	Ser	Leu	Val	His	Ala	Val	Glu	20	25	30	
Ala	Arg	Tyr	Arg	Leu	Tyr	Cys	Arg	Asp	Lys	Pro	His	Ala	Gln	Leu	Gly	35	40	45	
Tyr	Gly	Gly	Ser	Arg	Ala	Ile	Leu	Gly	Ser	Ser	Ser	Leu	Leu	Asp	Gly	50	55	60	
Val	Glu	His	Gln	Ile	Ala	His	Phe	His	Gly	Ala	Pro	Glu	Ala	Leu	Ile	65	70	75	80
Leu	Pro	Ser	Gly	Phe	Val	Ala	Asn	Thr	Ala	Ile	Cys	Ala	His	Leu	Ser	85	90	95	
Ser	Val	Ala	Asp	Tyr	Val	Leu	Trp	Asp	Glu	Gln	Val	His	Ile	Ser	Val	100	105	110	
Ser	Tyr	Asn	Leu	Ser	Val	Phe	Leu	Ser	Gly	Trp	His	Gln	Ser	Phe	Arg	115	120	125	
His	Asn	Asp	Leu	Asp	His	Leu	Glu	Ser	Leu	Leu	Glu	Ser	Cys	Gln	Gln	130	135	140	
Arg	Gly	Phe	Gln	Arg	Val	Phe	Ile	Leu	Val	Cys	Ser	Val	Tyr	Ser	Phe	145	150	155	160
Lys	Gly	Ser	Phe	Ala	Pro	Leu	Glu	Gln	Ile	Val	Ala	Leu	Ser	His	Gln	165	170	175	
Tyr	His	Ala	Gln	Leu	Ile	Val	Asp	Glu	Ala	His	Ala	Val	Gly	Leu	Phe	180	185	190	
Gly	Asp	Ala	Gly	Lys	Gly	Phe	Cys	Ala	Ser	Leu	Gly	Tyr	Glu	Asn	Phe	195	200	205	
Tyr	Ser	Val	Leu	Val	Thr	Phe	Ser	Lys	Ala	Leu	Gly	Ser	Ala	Gly	Ala	210	215	220	
Ala	Trp	Leu	Ser	Ser	Cys	Asp	Arg	Lys	Gln	Asp	Leu	Ile	Lys	Glu	Pro	225	230	235	240
Met	Val	Ser	Leu	Ser	Thr	Gly	Ile	Pro	Pro	Tyr	Leu	Leu	Val	Ser	Ile	245	250	255	
Gln	Val	Ala	Tyr	Glu	Phe	Leu	Ser	Gln	Glu	Gly	Glu	Leu	Ala	Arg	Thr	260	265	270	
Arg	Leu	Arg	Arg	Ile	Arg	Asp	Tyr	Phe	Ala	Gln	Lys	Ile	Ser	Trp	Ala	275	280	285	
Ala	Ala	Gly	Phe	Val	Gln	Pro	Leu	Ser	Leu	Pro	Gly	Ile	Ser	Glu	Gln	290	295	300	
Glu	Leu	Tyr	Gln	Lys	Leu	Val	Ala	Thr	Gly	Ile	Arg	Val	Gly	Val	Ala	305	310	315	320
Cys	Pro	Pro	Thr	Gly	Lys	Val	Leu	Arg	Ala	Asn	Leu	His	Ala	Phe	Asn	325	330	335	
Thr	Glu	Gln	Glu	Val	Asp	Ile	Leu	Val	Ser	Leu	Leu	Ala	Thr	Glu	Gln	340	345	350	
Val	Thr	Tyr	Gln	Lys	Asn	Val	Val	Thr	Gly	Ser	Thr	Ser	Thr	Met	Gln	355	360	365	
Arg	Thr	Leu	Glu	Asp	Asn	Phe	Ala	Ala	Ala	Asn	Ala	Ser				370	375	380	

(2) INFORMATIONS POUR LA SEQ ID NO: 614:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 538 acides aminés

(B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(601910..603523)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 614:

Glu	Met	Arg	Asp	Asn	Arg	Asn	Thr	Ala	Arg	Ser	Lys	Arg	Gly	Lys	Leu
1				5					10					15	
Arg	Ser	Glu	Lys	Thr	Val	Leu	Arg	Ser	Phe	Leu	Lys	Leu	Cys	Ala	Glu
		20						25					30		
Met	Thr	Thr	Ala	Thr	Val	Phe	Trp	Asp	Glu	Gln	Leu	Gly	Lys	Leu	Ser
		35					40					45			
Tyr	Asn	Gln	Val	Tyr	Lys	Ala	Val	Cys	Ala	Leu	Ala	Thr	Arg	Leu	Ala
	50					55					60				
Asn	Tyr	Pro	Asp	Gln	His	Ile	Gly	Ile	Met	Met	Pro	Ala	Ser	Ala	Gly
65					70				75						80
Ala	Tyr	Ile	Ala	Tyr	Phe	Ala	Thr	Leu	Leu	Ser	Gly	Lys	Ile	Pro	Val
				85				90						95	
Met	Ile	Asn	Trp	Ser	Gln	Gly	Leu	Arg	Glu	Val	Thr	Ala	Cys	Ala	Asn
		100						105					110		
Leu	Val	Gly	Val	Thr	His	Val	Ile	Thr	Ala	Lys	Pro	Leu	Met	Gln	Lys
		115					120					125			
Leu	Ala	Gln	Thr	His	Gly	Glu	Asp	Ala	Glu	Tyr	Pro	Phe	Ser	Leu	Xaa
	130					135					140				
Phe	Leu	Asp	Glu	Val	Arg	Lys	Glu	Leu	Ser	Phe	Leu	Glu	Lys	Cys	Arg
145					150					155					160
Val	Gly	Ile	Cys	Met	Ser	Ile	Pro	Phe	Glu	Trp	Met	Met	Arg	Trp	Phe
				165					170					175	
Gly	Val	Phe	Asp	Lys	Asp	Pro	Glu	Asp	Val	Ala	Val	Ile	Leu	Phe	Thr
		180						185					190		
Ser	Gly	Thr	Glu	Lys	Leu	Pro	Lys	Gly	Val	Pro	Leu	Thr	Asn	Ala	Ser
		195					200					205			
Leu	Leu	Ala	Asn	Gln	Arg	Ala	Cys	Phe	Asp	Cys	Phe	Ser	Pro	Lys	Glu
	210					215					220				
Asp	Asp	Ala	Met	Ile	Ser	Phe	Leu	Pro	Pro	Phe	His	Ala	Tyr	Gly	Phe
225					230					235					240
Asn	Ser	Cys	Thr	Leu	Phe	Pro	Leu	Leu	Ser	Gly	Ile	Pro	Val	Val	Phe
				245					250					255	
Ala	Tyr	Asn	Pro	Leu	Tyr	Ala	Lys	Lys	Ile	Val	Glu	Met	Ile	Asp	Glu
		260						265					270		
Ala	Lys	Val	Thr	Leu	Leu	Gly	Ser	Thr	Pro	Val	Phe	Leu	Ser	Tyr	Ile
		275					280					285			
Ile	Asn	Ala	Ala	Lys	Lys	Ser	Glu	Thr	Thr	Leu	Pro	Ser	Leu	Arg	Phe
	290					295					300				
Val	Val	Val	Gly	Gly	Asp	Val	Phe	Lys	His	Ser	Leu	Tyr	Gln	Glu	Ala
305					310					315					320
Leu	Lys	Thr	Phe	Pro	His	Val	Gln	Leu	Arg	Gln	Gly	Tyr	Gly	Thr	Thr
				325					330					335	
Glu	Cys	Ser	Pro	Val	Ile	Thr	Ile	Asn	Thr	Val	Asn	Ser	Pro	Lys	His
			340					345					350		
Glu	Ser	Cys	Val	Gly	Met	Pro	Val	Arg	Gly	Met	Glu	Val	Leu	Ile	Val
		355					360					365			
Ser	Glu	Glu	Thr	Lys	Val	Pro	Val	Ser	Thr	Gly	Val	Thr	Gly	Leu	Val
	370					375					380				
Leu	Thr	Arg	Gly	Thr	Ser	Leu	Phe	Lys	Gly	Tyr	Leu	Gly	Glu	Asp	Phe

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385                               390                               395                               400
Gly His Gly Phe Ile Glu Leu Ala Gly Glu Thr Trp Tyr Val Thr Gly
                               405                               410
Asp Leu Gly Tyr Val Asp Arg His Gly Glu Leu Phe Leu Lys Gly Arg
                               420                               425                               430
Leu Ser Arg Phe Val Lys Ile Gly Ala Glu Met Val Ser Leu Glu Ala
                               435                               440                               445
Met Glu Ser Ile Ile Met Glu Gly Cys Gly Gln Asn Ala Ala Asp His
                               450                               455                               460
Pro Leu Val Val Cys Gly Leu Pro Gly Glu Lys Glu Arg Leu Cys Leu
465                               470                               475
Phe Thr Ile Phe Pro Thr Ser Val Ser Glu Val Asn Asp Ile Leu Lys
                               485                               490                               495
Asn Ser Lys Thr Ser Asn Leu Leu Lys Ile Ser Tyr His His Gln Val
                               500                               505                               510
Glu Ala Ile Pro Met Leu Gly Thr Gly Lys Pro Asp Tyr Cys Ser Leu
                               515                               520                               525
Asn Ala Leu Ala Lys Arg Leu Phe Ser Glu
530                               535

```

(2) INFORMATIONS POUR LA SEQ ID NO: 615:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 88 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(603531..603794)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 615:

```

Leu Arg His Arg Ile Trp Gly Ser Ser Phe Ser Arg Tyr Arg Thr Gly
1                               5                               10                               15
Ser Thr Pro Lys Leu Gly Lys Val Phe Lys Glu Ala Val Lys Ala Leu
                               20                               25                               30
Leu Arg Cys Gly Ile Phe Phe Met Pro Lys Arg Glu Val Arg Val Ser
                               35                               40                               45
Val Cys Pro Ala Asp Tyr Ser Val Leu Lys Gln Phe Pro Thr Lys Gln
                               50                               55                               60
Glu Phe Asn Thr Phe Leu Ser Asp Trp Phe Asn Gln Glu Gly Gly Glu
65                               70                               75                               80
Thr Pro Leu Glu Val Pro Tyr Ala
                               85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 616:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 219 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(603757..604413)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 616:

```

Ser His Asp Ile Phe Leu Ile Ile Asn Glu Lys Asn Ser Ser Phe Gln
1      5      10      15
Asn Ala Asn Leu Leu Ile Trp Ile Trp Lys Tyr Cys Thr Leu Trp Cys
20      25      30
Lys Asn Asn Phe Asn Lys Pro Arg Gly Ser Met Lys Ile Gly Phe Trp
35      40      45
Arg Arg Leu Tyr Glu Val Cys Tyr Thr Ser Leu Ile Gly Cys Ala Leu
50      55      60
Lys Leu Arg Tyr Arg Val Leu Val Glu Gly Ile Glu Ser Ile Asn Gln
65      70      75      80
Asn Ser Gln Lys Gly Ala Leu Phe Leu Ser Asn His Val Ala Glu Ile
85      90      95
Asp Pro Val Ile Leu Glu His Val Phe Trp Leu Lys Phe His Val Arg
100     105     110
Pro Ile Ala Val Asp Tyr Leu Phe Asn Asn Pro Val Val Lys Trp Phe
115     120     125
Leu Asp Ser Val Arg Ala Ile Pro Val Pro Ser Val Val Pro Gly Arg
130     135     140
Asp Asp Lys Arg Leu Leu Glu Arg Ile Glu Arg Phe Tyr Val Cys Val
145     150     155     160
Thr Gln Ala Leu Asp Arg Lys Glu Ser Leu Leu Leu Tyr Pro Ser Gly
165     170     175
Arg Leu Ser Arg Asn Gly Lys Glu Glu Ile Val Asn Gln Gln Ala Ala
180     185     190
Tyr Thr Ile Leu His Arg Ala Lys Glu Cys Asp Val Phe Leu Val Lys
195     200     205
Thr Gln Asp Leu Gly Lys Phe Phe Thr Leu
210     215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 617:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 354 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 604549..605610

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 617:

```

Val Ile Val Thr Ser Leu Gln Pro Ala Glu Lys Leu Met Phe Ser Leu
1      5      10      15
Leu Asn Asp Cys Gln Lys Ala Ala Glu Thr Val Val Met Gln Ala Met
20      25      30
Leu Ser Leu Met Arg Tyr Arg Lys Ala His Lys Phe Ile Pro Phe Trp
35      40      45
Lys Lys Pro Asp Gln Thr Tyr Val Thr Pro Ala Asp Tyr Ala Ile Gln
50      55      60
Tyr Tyr Phe Tyr Gln Lys Leu Thr Ser Leu Phe Pro His Ile Pro Leu
65      70      75      80
Val Gly Glu Glu Thr Leu Asn Pro Ala Thr Asp His Pro Arg Ile Pro

```

Ser Lys Ala Met Thr Tyr Lys Ala Leu Leu Ser Ser Thr Glu Thr Gly
 65 70 75 80
 Gly Gly Lys Ser Val Ile Phe Leu Pro Lys Gly Met Thr Ser Pro Thr
 85 90 95
 Glu Gly Met Leu Arg Ala Phe Gly Gln Ala Val Asn Ser Leu Gln Gly
 100 105 110
 Lys Tyr Ile Ala Ala Glu Asp Val Gly Val Ser Val Gln Asp Val Met
 115 120 125
 Ile Ile Arg Glu Glu Thr Pro Tyr Val Cys Gly Leu Val Thr Val Ser
 130 135 140
 Gly Asp Pro Ser Ile Tyr Thr Ala His Gly Val Phe Leu Cys Ile Gln
 145 150 155 160
 Glu Thr Ala Asp Tyr Leu Trp Lys Thr Asp Ile Arg Gly Lys Arg Val
 165 170 175
 Ala Val Gln Gly Leu Gly Ala Val Gly Arg Lys Leu Val His Glu Leu
 180 185 190
 Phe Phe Ala Gly Ala Glu Leu Ile Val Tyr Asp Thr Arg Lys Asp Leu
 195 200 205
 Leu Asp Glu Val Val Thr Leu Tyr Gly Ala Gln Val Asp Glu Asn Ile
 210 215 220
 Ile Ser Ser Asp Cys Asp Ile Leu Cys Pro Cys Ala Leu Gly Gly Ile
 225 230 235 240
 Ile Asn Ser Met Ser Ile Asp Gln Leu Arg Cys Arg Ala Ile Val Gly
 245 250 255
 Ala Thr Asn Asn Gln Leu Glu Asn Pro Ala Ile Gly Arg Glu Leu Val
 260 265 270
 Ala Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Leu Ala Asn Ala Gly Gly
 275 280 285
 Leu Leu Asn Val Ala Gly Ser Val Gly Arg Ala Tyr Ser Pro Lys Glu
 290 295 300
 Val Leu Ser Lys Val Glu Gly Leu Pro Lys Ile Leu Arg Lys Leu Tyr
 305 310 315 320
 Glu Gln Gly Ala Lys Glu Asn Arg Asp Thr Gly Thr Leu Ala Asp Ala
 325 330 335
 Ile Val Glu Glu Arg Leu Ala Val Tyr Ala
 340 345

(2) INFORMATIONS POUR LA SEQ ID NO: 619:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 217 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 606843..607493

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 619:

Asn Thr Leu Ile Glu Ser Asp Leu Met Ser Lys Thr Pro Leu Ser Ile
 1 5 10 15
 Ala His Pro Trp His Gly Pro Val Leu Thr Arg Asp Asp Tyr Glu Ser
 20 25 30
 Leu Cys Cys Tyr Ile Glu Ile Thr Pro Ala Asp Ser Val Lys Phe Glu
 35 40 45
 Leu Asp Lys Glu Thr Gly Ile Leu Lys Val Asp Arg Pro Gln Lys Phe

50		55		60
Ser Asn Phe Cys Pro Cys Leu Tyr Gly Leu Leu Pro Lys Thr Tyr Cys				
65		70		80
Gly Asp Leu Ser Gly Glu Tyr Ser Gly Gln Ser Asn Arg Glu Asn				
	85		90	95
Ile Lys Gly Asp Gly Asp Pro Leu Asp Ile Cys Val Leu Thr Glu Lys				
	100		105	110
Asn Ile Thr Gln Gly Asn Ile Leu Leu Gln Ala Arg Pro Ile Gly Gly				
	115		120	125
Ile Arg Ile Leu Asp Ser Glu Glu Ala Asp Asp Lys Ile Ile Ala Val				
	130		135	140
Leu Glu Asp Asp Leu Val Tyr Gly Asn Ile Glu Asp Ile Ser Glu Cys				
145		150		160
Pro Gly Thr Val Leu Asp Met Ile Gln His Tyr Phe Leu Thr Tyr Lys				
	165		170	175
Ala Thr Pro Glu Ser Leu Ile Gln Ala Lys Pro Ala Lys Ile Glu Ile				
	180		185	190
Val Gly Leu Tyr Gly Lys Lys Glu Ala Gln Lys Val Ile Arg Leu Ala				
	195		200	205
His Glu Asp Tyr Cys Asn Leu Phe Met				
210		215		

(2) INFORMATIONS POUR LA SEQ ID NO: 620:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 346 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(608031..609068)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 620:

Ser Phe Tyr Tyr Leu Cys Ser Cys Ser Arg Lys Glu Gly Asn Ser Tyr				
1	5	10	15	
Val Arg Trp Asp Gln Asp Thr Leu Pro Ala Asp Ser His Arg Cys Gly				
	20	25	30	
Val Ile Ile Gly Ser Gly Met Gly Gly Leu Arg Thr Leu Asp Glu Gly				
	35	40	45	
Ile Glu Lys Leu Ser Ala Gly Asn Arg Lys Leu Ser Pro Phe Phe Ile				
	50	55	60	
Pro Tyr Ile Ile Thr Asn Met Ala Pro Ala Leu Ile Ala Met Asp Tyr				
65		70	75	80
Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ala				
	85	90	95	
Asn Tyr Cys Ile Asp Ala Ala Tyr Gln His Leu Ile Glu Gly Arg Ala				
	100	105	110	
Asp Val Ile Val Cys Gly Gly Thr Glu Ala Ala Ile Asn Arg Val Gly				
	115	120	125	
Leu Ala Gly Phe Ile Ala Asn Arg Ala Leu Ser Glu Arg Asn Asp Ala				
	130	135	140	
Pro Glu Gln Ala Ser Arg Pro Trp Asp Arg Asp Arg Asp Gly Phe Val				
145		150	155	160
Leu Gly Glu Gly Ala Gly Ile Leu Val Leu Glu Thr Leu Asp Asn Ala				
	165	170	175	

Leu Lys Arg Gly Ala Pro Ile Phe Ala Glu Val Leu Gly Thr Tyr Lys
 180 185 190
 Thr Cys Asp Ala Phe His Ile Thr Ala Pro Arg Asp Asp Gly Glu Gly
 195 200 205
 Ile Thr Ala Cys Ile Leu Gly Ala Leu Asn Lys Ala Gly Ile Pro Lys
 210 215 220
 Glu Arg Val Asn Tyr Ile Asn Ala His Gly Thr Ser Thr Pro Leu Gly
 225 230 235 240
 Asp Leu Ser Glu Val Leu Ala Leu Lys Lys Ala Phe Gly Ser His Val
 245 250 255
 Lys Asn Leu Arg Leu Asn Ser Thr Lys Ser Leu Ile Gly His Cys Leu
 260 265 270
 Gly Ala Ala Gly Gly Val Glu Ala Val Ala Thr Ile Gln Ala Ile Gln
 275 280 285
 Thr Gly Lys Leu His Pro Thr Ile Asn Val Glu Asn Pro Ile Ala Glu
 290 295 300
 Ile Glu Glu Phe Asp Val Val Ala Asn Lys Ala Gln Asp Trp Asp Val
 305 310 315 320
 Asp Val Ala Met Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Thr
 325 330 335
 Ile Leu Phe Ser Arg Tyr Glu Pro Ser Leu
 340 345

(2) INFORMATIONS POUR LA SEQ ID NO: 621:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(609296..609652)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 621:

Met Asp Ser Phe Cys Leu Asn Leu Leu Lys Val Ile Val Lys Ala Ile
 1 5 10 15
 Asp Asn Lys Lys Gly Arg Asn Pro Val Val Leu Asp Val Gln Asn Ile
 20 25 30
 Ser Gln Leu Thr Asp Tyr Phe Val Phe Val Glu Gly Asn Val Gly Val
 35 40 45
 His Ile Lys Ala Ile Ala Asp Thr Ile Ile Glu Glu Leu Lys Lys Leu
 50 55 60
 Lys Val Tyr Pro Leu Asn Val Glu Gly Leu Ser His Ser Asp Trp Val
 65 70 75 80
 Val Ile Asp Tyr Gly Phe Ile Val Ile His Leu Phe Val Ser Xaa Xaa
 85 90 95
 Arg Glu Gln Tyr Cys Leu Glu Glu Leu Trp Lys Asp Gly Ala Ile Ile
 100 105 110
 Thr Ser Asp Cys Leu Ala Ser
 115

(2) INFORMATIONS POUR LA SEQ ID NO: 622:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 584 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(610109..611860)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 622:

Cys	Ile	Ala	Arg	Ala	Asn	Phe	Asp	Tyr	Gln	Leu	Phe	Phe	Leu	Ser	Arg	1	5	10	15
Leu	Thr	Leu	Thr	Asn	Ser	Tyr	His	Met	Asp	Ile	Pro	Glu	Gln	Gly	Ser	20	25	30	
Asn	Thr	Pro	Glu	Val	Glu	Gln	Ala	Ala	Cys	Cys	Asn	Gln	Glu	Ala	Ala	35	40	45	
Glu	Asn	Asp	Arg	Ala	Lys	Asp	Lys	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Ala	50	55	60	
Glu	Ala	Val	Gln	Ser	Cys	Glu	Ser	Met	Glu	Ala	Phe	Glu	Gln	Val	Val	65	70	75	80
Ala	Glu	Arg	Ser	Ser	Ile	Glu	Glu	Lys	Ile	Leu	Phe	Ala	Leu	Glu	Gln	85	90	95	
Met	Gly	Ala	Leu	Leu	Lys	Gly	Ala	Asp	Gln	Asn	Ser	Asp	Leu	Lys	Leu	100	105	110	
Phe	Trp	Asn	Val	Arg	Lys	Phe	Cys	Leu	Pro	Leu	Phe	Gln	Gln	Leu	Glu	115	120	125	
Asp	Pro	Val	Gln	Arg	Ala	Asn	Leu	Trp	Gly	Arg	Tyr	Thr	Glu	Leu	Thr	130	135	140	
Arg	Glu	Gly	Arg	Tyr	Ile	Lys	Thr	Leu	Gln	Asp	Glu	Glu	Gly	Ala	Phe	145	150	155	160
Leu	Val	Gly	Gln	Ile	Glu	Leu	Ala	Ile	Ser	Cys	Leu	Glu	Ser	Gly	Val	165	170	175	
Gln	Gly	Phe	Phe	Ser	Lys	Thr	Glu	Lys	Glu	Glu	Ile	Ser	Glu	Glu	Asp	180	185	190	
Arg	Ala	Ala	Leu	Glu	Ile	Pro	Ser	Leu	Ser	Ala	His	Lys	Asp	Phe	Tyr	195	200	205	
Leu	Ser	Thr	His	Ala	Asp	Leu	Arg	Trp	Leu	Gly	Ser	Phe	Ser	Ser	Gln	210	215	220	
Ile	Ile	Asn	Leu	Arg	Lys	Glu	Leu	Met	Asn	Ile	Ser	Met	Arg	Met	Arg	225	230	235	240
Leu	Lys	Ser	Gln	Phe	Phe	Gln	Lys	Leu	Ser	Val	Leu	Gly	Asn	Lys	Val	245	250	255	
Phe	Pro	Arg	Arg	Lys	Glu	Leu	Thr	Glu	Lys	Val	Ser	Glu	Leu	Phe	Ala	260	265	270	
Gln	Asp	Val	Glu	Ala	Phe	Val	Glu	Arg	Tyr	Phe	Ser	Arg	Ala	Ser	Arg	275	280	285	
Glu	Ser	Leu	Lys	Lys	Ser	Val	Phe	Phe	Leu	Arg	Lys	Glu	Ile	Lys	Arg	290	295	300	
Leu	Gln	Gln	Ala	Ala	Lys	Tyr	Leu	Ser	Ile	Ser	Ser	Gly	Val	Phe	Ser	305	310	315	320
Ser	Thr	Arg	Leu	Gly	Leu	Ser	Gln	Cys	Trp	Asp	Gln	Leu	Lys	Gly	Leu	325	330	335	
Glu	Lys	Glu	Ile	Arg	Gln	Glu	Gln	Ser	Arg	Leu	Ala	Ala	Thr	Ser	Ala	340	345	350	
Glu	Asn	Met	Lys	Glu	Val	Gln	Gly	Arg	Leu	Asp	Gln	Val	Glu	Val	Leu	355	360	365	
Leu	Gln	Glu	Asn	Glu	Glu	Val	His	Lys	Ile	Arg	Lys	Glu	Ile	Glu	Ala	370	375	380	

130 135 140
 Pro Ser Leu His Pro His Phe Phe Ser Ala Val Glu Ile Ala His Ala
 145 150 155 160
 Ala Gln Ile Ser Gly Ile Ser Thr Glu Gln Ala Leu Glu Arg Leu Trp
 165 170 175
 Glu Ala Gly Gln Arg Thr Ile Pro Gly Gly Gly Ala Glu Ile Leu Ser
 180 185 190
 Glu Arg Ile Arg Lys Gln Ile Ser Pro Lys Lys Met Gly Pro Asp Gly
 195 200 205
 Trp Ile Gln Phe His Lys Leu Ala His Arg Leu Gly Phe Arg Ser Thr
 210 215 220
 Ala Thr Met Met Phe Gly His Val Glu Ser Pro Glu Asp Ile Leu Leu
 225 230 235 240
 His Leu Gln Thr Leu Arg Asp Ala Gln Asp Glu Asn Pro Gly Phe Phe
 245 250 255
 Ser Phe Ile Pro Trp Ser Tyr Lys Pro Asn Asn Thr Ala Leu Gly Arg
 260 265 270
 Arg Val Pro His Gln Ala Ser Pro Glu Leu Tyr Tyr Arg Ile Leu Ala
 275 280 285
 Val Ala Arg Ile Phe Leu Asp Asn Phe Asp His Ile Ala Ala Ser Trp
 290 295 300
 Phe Gly Glu Gly Lys Glu Glu Gly Val Lys Gly Leu Phe Tyr Gly Ala
 305 310 315 320
 Asp Asp Phe Gly Gly Thr Ile Leu Asp Glu Ser Val His Lys Cys Thr
 325 330 335
 Gly Trp Asp Leu Gln Ser Ser Glu Lys Glu Ile Cys Ala Met Leu Leu
 340 345 350
 Gln Ala Gly Phe Thr Pro Val Glu Arg Asp Thr Phe Tyr Arg Pro Leu
 355 360 365
 Ser Leu Ala Arg
 370

(2) INFORMATIONS POUR LA SEQ ID NO: 624:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 220 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(612938..613597)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 624:

Ser Pro His Ser Arg Arg Arg Asp Arg Phe Leu Phe Pro Tyr Phe Ser
 1 5 10 15
 Ile Arg Ser Ala Ile Trp Ala Phe Ser Arg Phe Cys Ile Ala Gly Xaa
 20 25 30
 Leu Thr Leu Glu Ala Gln Glu Arg Gly Ile Ser Ala Leu Tyr Gln Glu
 35 40 45
 Leu Glu Leu Leu Asp Pro Val Tyr Ala Ala Thr Ile Thr Lys His Asp
 50 55 60
 Lys Asn Lys Ile Ile Arg Ala Leu Glu Ile Ile Arg Lys Thr Gly Ser
 65 70 75 80
 Lys Val Ser Ser Tyr Ala Trp Gln Ser Thr Val Asn Glu Ser Lys Glu
 85 90 95


```

Tyr His Cys Arg Gly Trp Leu Leu Ser Pro Asp Pro Glu Leu Leu Arg
      100      105      110
His Asn Ile Leu Glu Arg Cys Asp Gln Met Leu Glu Glu Gly Leu Leu
      115      120      125
Asp Glu Val Gln Ala Leu Leu Ala Ala Gly Ile Lys Gly Asn Ser Ser
      130      135      140
Ala Ser Arg Ala Ile Gly Tyr Arg Glu Trp Ile Glu Phe Leu Asp Leu
145      150      155      160
Gly Ser Pro Pro Asp Leu Phe Glu Ile Thr Lys Gln Lys Phe Ile Thr
      165      170      175
Asn Thr Trp Arg Tyr Thr Lys Lys Gln Arg Thr Trp Phe Lys Arg Tyr
      180      185      190
Ser Leu Phe Arg Glu Leu Arg Pro Met Gly Met Thr Leu Asp Asp Met
      195      200      205
Ala Lys Lys Ile Ala Gln Asp Tyr Phe Leu Cys Gly
      210      215      220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 625:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 68 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(613692..613895)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 625:

```

Gln Lys Ser Phe Ser Lys Met Phe Lys Arg Thr Val Ile Leu Leu Ala
1      5      10      15
Gly Pro Thr Gly Ser Gly Lys Thr Ala Val Ser Leu Lys Leu Ala Pro
      20      25      30
Leu Val Asp Gly Glu Ile Ile Ser Val Asp Ser Met Gln Val Tyr Gln
      35      40      45
Gly Met Asp Ile Gly Thr Ala Lys Val Ser Leu Ala Asp Arg Lys Arg
      50      55      60
Phe Arg Ile Thr
65

```

(2) INFORMATIONS POUR LA SEQ ID NO: 626:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 310 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 614315..615244

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 626:

```

Ser Asn Asp Glu Ile Leu Asp Gly Arg Ser Leu Tyr Leu Leu Ser Ser

```

```

1              5              10              15
Asn Lys Gly Phe Ser Leu Phe Phe Tyr Leu Lys Lys Gln Phe Phe Leu
20              25              30
Asp Ser Ser Arg Cys Thr Leu Glu Val Ile Leu Pro Pro Arg Ser Pro
35              40              45
Ser Phe Leu Val His Ile Trp Arg Leu Phe Phe Ala Lys Gly Pro Asn
50              55              60
Tyr Ser Leu Pro Tyr Ala Phe Leu Cys Ile Phe Val Ser Val Leu Val
65              70              75              80
Phe Leu Pro Ile Gly Leu Trp Leu Thr Leu Pro Ser Phe Leu Asn Phe
85              90              95
Lys His Ser Leu Thr Pro Ile Lys Thr Leu Phe Leu Thr Cys Thr Glu
100              105              110
Pro Pro Cys Leu Pro Glu Pro Phe Phe Ser Asp Ile Leu His Leu Ser
115              120              125
Ala Asp Ser Pro Pro Ala Leu Gln Thr Phe Ser Thr Lys Ser Ala Glu
130              135              140
His Phe Leu Asn Glu Leu Gly Val Phe Ser Phe Ile Ser Ile Glu Lys
145              150              155              160
Val Pro Asp His Lys Gly Leu Asp Ile Ser Tyr Ala Leu His Thr Pro
165              170              175
Leu Ala Phe Leu Gly Asn Gln Thr His Thr Phe Ile Gly Tyr Glu Gly
180              185              190
Gln Thr Phe Pro Ala Leu Pro Phe Phe Gln Ser Leu Glu Leu Pro Thr
195              200              205
Val Phe Phe Ser Gln Gln Ala Leu Ser Gln Thr Arg Ile Pro His Gln
210              215              220
Thr Leu Ser Ile Val Thr Ser Leu Ile Asp Gln Leu Gln Met Asp Pro
225              230              235              240
Pro Ser Ile Ile Asp Leu Ser Gln Ile Asp His Tyr Pro Gly Glu Phe
245              250              255
Val Val Ser Leu Ser Ser Gly Thr Leu Leu Arg Phe Arg Lys Asp Ser
260              265              270
Phe Leu Pro Gly Ile Gln His Tyr Gln Gln Ala Leu Ser Leu Gly Ala
275              280              285
Phe Ser Pro Gln Gln Ala Val Ile Cys Asp Leu Arg Cys Glu Asp Tyr
290              295              300
Leu Leu Leu Lys Arg Lys
305              310

```

(2) INFORMATIONS POUR LA SEQ ID NO: 627:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 93 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 615405..615683

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 627:

```

Met Glu Asp Phe Ala Ala Tyr Ile Val Lys Asn Leu Val Thr Asp Pro
1              5              10              15
Asn Ala Val Glu Ile Arg Ser Ser Glu Asp Lys Ala Ser Ala Thr Leu
20              25              30

```

Lys Leu Glu Ile His Ala Ala Ser Glu Asp Ile Gly Lys Ile Ile Gly
 35 40 45
 Arg Lys Gly Gln Thr Ile Gln Ala Leu Arg Thr Ile Leu Lys Arg Val
 50 55 60
 Gly Ala Arg Leu Gln Lys Lys Ile Leu Val Glu Leu Ala Gln Pro Glu
 65 70 75 80
 Asn Gly Ser Leu Thr Asp Glu Glu Val Leu Ser Leu Asp
 85 90

(2) INFORMATIONS POUR LA SEQ ID NO: 628:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 616 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(615864..617711)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 628:

Arg Arg Ser Arg Ala Ser Ser Gly Phe Phe Glu Arg Phe Ala Leu Lys
 1 5 10 15
 Thr Gln Gln Ile Cys Trp Tyr Asn Gly Tyr Cys Pro Arg Leu Arg Ser
 20 25 30
 Cys Leu Gln Gly His Thr Phe Gly Leu Asp Ser Ser Cys Asp Leu His
 35 40 45
 Ile Leu Ser Tyr Tyr Gln Glu Gly Trp Arg Leu Tyr Phe Thr Ala Lys
 50 55 60
 Tyr Gln Asp Val Val Tyr Ala Asp Ile Glu Val Gln Leu Val Gly Met
 65 70 75 80
 His Asn Val Leu Asn Ala Ala Ala Ala Met Gly Ile Ala Leu Ser Leu
 85 90 95
 Gly Ile Asp Glu Gly Ala Ile Arg Asn Ala Phe Arg Gly Phe Ser Gly
 100 105 110
 Val Gln Arg Arg Leu Gln Arg Lys Asn Ser Ser Glu Thr Phe Leu Phe
 115 120 125
 Leu Glu Asp Tyr Ala His His Pro Ser Glu Ile Ser Cys Thr Leu Arg
 130 135 140
 Ala Val Arg Thr Ala Val Gly Gln Arg Arg Ile Leu Ala Ile Cys Gln
 145 150 155 160
 Pro His Arg Phe Ser Arg Leu Arg Glu Cys Ile Asp Ser Phe Pro Ser
 165 170 175
 Ala Phe Lys Asp Ala Asp Glu Val Leu Leu Thr Glu Val Tyr Ser Ala
 180 185 190
 Gly Glu Glu Ala Glu Asp Ile Ser Tyr Gln Glu Leu Ala Glu Ala Ile
 195 200 205
 Ser Gln Glu Ser Ile Val Lys Cys Thr His Ile Pro Phe His Glu Leu
 210 215 220
 Gln Arg His Leu Glu Gln Ser Ile Arg Val His Asp Val Cys Val Ser
 225 230 235 240
 Leu Gly Ala Gly Asn Ile Val Asn Leu Gly Glu Lys Leu Arg Asp Phe
 245 250 255
 Glu Pro Gln Lys Leu His Leu Gly Ile Cys Gly Gly Lys Ser Cys
 260 265 270
 Glu His Glu Ile Ser Val Leu Ser Ala Lys Asn Ile Ala Lys His Leu

Ser Asn His Cys Ile Ser Leu Phe Val Asn Leu Tyr Arg Leu Met Met
 1 5 10 15
 Lys Ser Leu Phe Tyr His Phe Ile Gly Ile Gly Gly Ile Gly Met Ser
 20 25 30
 Ala Leu Ala His Val Leu Leu Asp Arg Gly Tyr Ser Val Ser Gly Ser
 35 40 45
 Asp Leu Ser Glu Gly Lys Val Val Glu Lys Leu Lys Asn Lys Gly Ala
 50 55 60
 Glu Phe Phe Leu Gly Asn Gln Glu Glu His Ile Pro Glu Gly Ala Val
 65 70 75 80
 Val Val Tyr Ser Ser Ser Ile Ser Lys Glu Asn Pro Glu Phe Leu Ser
 85 90 95
 Ala Lys Ser Arg Gly Asn Arg Val Val His Arg Ala Glu Leu Leu Ala
 100 105 110
 Glu Leu Ala Gln Asp Gln Ile Ser Ile Phe Val Thr Gly Ser His Gly
 115 120 125
 Lys Thr Thr Val Ser Ser Leu Ile Thr Ala Ile Leu Gln Glu Ala Lys
 130 135 140
 Lys Asn Pro Ser Phe Val Ile Gly Gly Leu Asn Gln Glu Gly Ile Asn
 145 150 155 160
 Gly Gly Ser Gly Ser Glu Tyr Phe Val Ala Glu Ala Asp Glu Ser Asp
 165 170 175
 Gly Ser Ile Arg Cys Tyr Thr Pro Glu Phe Ser Val Ile Thr Asn Ile
 180 185 190
 Asp Asp Glu His Leu Ser Asn Phe Glu Gly Asp Arg Glu Leu Leu Leu
 195 200 205
 Ala Ser Leu Lys Asp Leu His Ser Arg Leu Ser Arg Ser Val Gly Ile
 210 215 220
 Met Asp Ile Val Leu Ala Cys Val His Ala Cys Lys Gly Ile Leu Leu
 225 230 235 240
 Asp Trp Thr Leu Leu Val Ile Tyr Ile Phe Tyr Leu Ile Ile Lys Lys
 245 250 255
 Asp Gly Asp Cys Thr Leu Gln Gln Ser Ile Lys Met
 260 265

(2) INFORMATIONS POUR LA SEQ ID NO: 630:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 325 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(618361..619335)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 630:

Met Lys Lys Ile Asn Lys Ile Val Leu Ala Val Gly Gly Thr Gly Gly
 1 5 10 15
 His Ile Ile Pro Ala Leu Ala Ala Arg Glu Thr Phe Ile His Glu Asp
 20 25 30
 Ile Glu Val Leu Leu Leu Gly Lys Gly Leu Ala His Phe Leu Gly Asp
 35 40 45
 Asp Ser Glu Ile Ala Tyr Cys Asp Ile Pro Ser Gly Ser Pro Phe Ser
 50 55 60
 Leu Arg Val Asn Arg Met Phe Ser Gly Ala Lys Gln Leu Tyr Lys Gly

65					70					75				80	
Tyr	Val	Ala	Ala	Leu	Gln	Lys	Ile	Arg	Asp	Phe	Thr	Pro	Asp	Leu	Ala
				85					90					95	
Ile	Gly	Phe	Gly	Ser	Tyr	His	Ser	Leu	Pro	Ala	Met	Leu	Ala	Ser	Ile
			100					105					110		
Arg	Ser	Arg	Ile	Pro	Leu	Phe	Leu	His	Glu	Gln	Asn	Ile	Val	Pro	Gly
		115					120					125			
Lys	Val	Asn	Lys	Leu	Phe	Ser	Arg	Phe	Ala	Lys	Gly	Val	Gly	Met	Ser
	130					135					140				
Phe	Ala	Ala	Ala	Gly	Glu	His	Phe	His	Cys	Arg	Ala	Glu	Glu	Val	Phe
145					150					155					160
Leu	Pro	Ile	Arg	Lys	Leu	Ser	Glu	Gln	Ile	Val	Phe	Pro	Gly	Ala	Ser
				165					170					175	
Pro	Val	Ile	Cys	Val	Val	Gly	Gly	Ser	Gln	Gly	Ala	Lys	Ile	Leu	Asn
			180					185					190		
Asp	Val	Val	Pro	Lys	Ala	Leu	Ala	Arg	Ile	Arg	Glu	Ser	Tyr	Ser	Asn
	195						200					205			
Leu	Tyr	Val	His	His	Ile	Val	Gly	Pro	Lys	Gly	Asp	Leu	Gln	Ala	Val
	210					215					220				
Ser	Gln	Val	Tyr	Gln	Asp	Ala	Gly	Ile	Asn	His	Thr	Val	Thr	Ala	Phe
225					230					235					240
Asp	His	Asn	Met	Leu	Gly	Val	Leu	Gln	Ala	Ser	Asp	Leu	Val	Ile	Ser
				245					250					255	
Arg	Ser	Gly	Ala	Thr	Met	Leu	Asn	Glu	Leu	Leu	Trp	Val	Gln	Val	Pro
			260					265					270		
Ala	Ile	Leu	Ile	Pro	Tyr	Pro	Gly	Ala	Tyr	Gly	His	Gln	Glu	Val	Asn
	275						280					285			
Ala	Lys	Phe	Phe	Thr	His	Thr	Val	Gly	Gly	Gly	Thr	Met	Ile	Leu	Gln
	290					295					300				
Lys	Tyr	Leu	Thr	Glu	Glu	Ser	Leu	Ser	Lys	Gln	Val	Leu	Leu	Cys	Phe
305					310					315					320
Arg	Ser	Cys	Asn	Gln											
				325											

(2) INFORMATIONS POUR LA SEQ ID NO: 631:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 390 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(619247..620416)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 631:

Ile	Ser	Gly	Ile	Ile	Met	Lys	Trp	Phe	Leu	Ile	Ser	Cys	Leu	Leu	Gly
1				5				10					15		
Ile	Phe	Ser	Leu	Gly	Leu	Ile	Met	Val	Phe	Asp	Thr	Ser	Ser	Ala	Glu
			20					25					30		
Val	Leu	Asp	Arg	Ala	Leu	Ser	Cys	Ser	Thr	His	Lys	Ala	Leu	Ile	Arg
		35					40					45			
Gln	Ile	Thr	Tyr	Leu	Gly	Leu	Gly	Leu	Gly	Ile	Ala	Ser	Phe	Val	Tyr
	50					55					60				
Ile	Leu	Gly	Trp	Lys	Asp	Phe	Leu	Lys	Met	Ser	Pro	Met	Leu	Leu	Ile
65					70					75					80

Gly Ile Asn Asn Arg Ala Thr Lys Ala Thr Asn Arg Leu Lys Leu Leu
 20 25 30
 35 40 45
 Arg Ile Glu Gly Phe Val Val Lys His Ser Ile Ala Thr His Gly Thr
 50 55 60
 Lys Tyr Leu Thr Asn Ser Glu Gly Cys Lys Val Asn Cys Pro Thr Pro
 65 70 75 80
 Ser Gln Arg Leu Ala Pro Phe Leu Gln Thr Pro Ile Pro Gly Ile Arg
 85 90 95
 Thr Lys Thr Arg Val Ile Pro Thr Lys Ile Ser Asn Ile Gly Leu Ile
 100 105 110
 Phe Lys Lys Ser Phe His Pro Lys Met Tyr Thr Asn Glu Ala Ile Pro
 115 120 125
 Ser Pro Asn Pro Arg
 130

(2) INFORMATIONS POUR LA SEQ ID NO: 633:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 255 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(620420..621184)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 633:

Ala Phe Gly Trp Asp Gly Arg Gly Ser Phe Met Asn Arg Arg Asn Thr
 1 5 10 15
 Met Ile Val Ala Thr Thr Val Asn Ala Val Leu Leu Ala Val Leu Phe
 20 25 30
 Met Thr Ala Arg His Ser Glu Gln Glu Ile Glu Tyr Pro Gln Lys Ile
 35 40 45
 Ala Pro Ile Lys Ile Leu Glu Pro Val Pro Val Val Asp Lys Ala Pro
 50 55 60
 Glu Lys Leu Glu Lys Lys Pro Glu Val Ile Ala Lys Pro Ser Gln Val
 65 70 75 80
 Val Arg Asn Pro Val Val Ser Lys Ala Glu Leu Ala Ala Gln Phe Ala
 85 90 95
 Asp Lys Asn Pro Lys Thr Glu Lys Glu Ser Ser Gly Gly Ser Lys Lys
 100 105 110
 Ile Ser Ser Thr Pro Val Glu Ser Thr Thr Pro Val Ala Pro Glu Ile
 115 120 125
 Ser Val Val Asn Ala Lys Val Val Glu Lys Thr Pro Glu Lys Glu Glu
 130 135 140
 Phe Ser Thr Val Ile Val Lys Lys Gly Asp Phe Leu Glu Arg Ile Ala
 145 150 155 160
 Arg Ser Asn His Thr Thr Val Ser Ala Leu Met Gln Leu Asn Asp Leu
 165 170 175
 Ser Ser Thr Gln Leu Gln Ile Gly Gln Val Leu Arg Val Pro Lys Thr
 180 185 190
 Asn Lys Thr Glu Lys Asp Leu Gln Val Lys Thr Pro Asn Pro Glu Asp
 195 200 205
 Tyr Tyr Val Val Lys Glu Gly Asp Ser Pro Trp Ala Ile Ala Leu Ser
 210 215 220

Asn Gly Ile Arg Leu Asp Glu Leu Leu Lys Leu Asn Gly Leu Asp Glu
 225 230 235 240
 Gln Lys Ala Arg Arg Leu Arg Pro Gly Asp Arg Leu Arg Ile Arg
 245 250 255

(2) INFORMATIONS POUR LA SEQ ID NO: 634:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 179 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(621154..621690)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 634:

Asn His Trp Tyr Leu His Asp Lys Tyr Asn Tyr Cys Cys Ala Tyr Leu
 1 5 10 15
 Leu Ala Lys Ile Glu Phe Pro Ile Ser Glu Thr Ser Phe Ile Glu Ala
 20 25 30
 Val Ala Thr Phe Asn Lys Pro Pro His Arg Met Glu Tyr Leu Gly Gln
 35 40 45
 Lys Gln Gly Ile His Tyr Ile Asn Asp Ser Lys Ala Thr Thr Val Ser
 50 55 60
 Ala Thr Glu Thr Ala Leu Leu Gly Val Gly Asn Gln Ala Ile Val Ile
 65 70 75 80
 Leu Gly Gly Arg Asn Lys Gly Cys Thr Phe Ser Ser Leu Leu Pro Ala
 85 90 95
 Leu Arg Lys Ala Ala Lys Ser Val Val Ala Met Gly Glu Cys Ala Gln
 100 105 110
 Glu Ile Ala Arg Asp Leu Glu Glu Phe Pro Val Thr Val Val Lys Asn
 115 120 125
 Leu Ser Glu Ala Leu Leu Cys Ala Glu Glu Gln Ala Val Pro Gly Asp
 130 135 140
 Val Ile Val Leu Ser Pro Ala Cys Ala Ser Phe Asp Gln Phe Arg Ser
 145 150 155 160
 Tyr Glu Glu Arg Gly Ala Met Phe Lys His Leu Val Gly Met Glu Glu
 165 170 175
 Val Leu Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 635:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 242 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(621674..622399)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 635:

Met Gly Leu Glu Arg Val Val Val Ile Gly Leu Gly Val Ser Gly Arg
 1 5 10 15
 Ser Ile Xaa Xaa Phe Leu Ala Gln Lys Gly Val Cys Val Leu Gly Val
 20 25 30
 Asp Lys Ser Leu His Ala Leu Gln Asn Cys Pro Tyr Ile Xaa Lys Asn
 35 40 45
 Ile Trp Arg Thr Lys Ser Ser Leu His Arg Trp Ile Met Leu Ser Ser
 50 55 60
 Pro Gly Val Ser Lys Glu His Pro Trp Val Gln Ala Ala Ile Ala Ser
 65 70 75 80
 His Ile Pro Val Met Thr Asp Ile Gln Leu Ala Phe Gln Thr Glu Lys
 85 90 95
 Phe Thr Glu Arg Glu Ser Leu Ala Ile Thr Gly Thr Thr Gly Lys Thr
 100 105 110
 Thr Thr Ile Leu Phe Leu Glu Tyr Leu Phe Lys Arg Ser Gly Ile Pro
 115 120 125
 Ala Phe Ala Met Gly Asn Val Gly Ile Pro Ile Leu Asp Gly Met Gln
 130 135 140
 Asn Pro Gly Val Arg Ile Val Glu Ile Ser Ser Phe Gln Leu Ala Asp
 145 150 155 160
 Gln Glu Lys Ser Tyr Pro Val Leu Ser Gly Gly Met Ile Leu Asn Ile
 165 170 175
 Ser Asp Asn His Leu Asp Tyr His Gly Asn Phe Ser Glu Tyr Phe Gln
 180 185 190
 Ala Lys Gln Asn Leu Ala Leu Cys Met Arg Asn Pro Asp Asp Leu Trp
 195 200 205
 Val Gly Asp Glu Arg Phe Tyr Gly His Leu Tyr Leu Glu Glu Val Gln
 210 215 220
 Lys Tyr Met Arg Leu Leu Asp Lys Glu Ser Ala Leu Lys Pro Leu Val
 225 230 235 240
 Leu Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 636:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 351 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(622414..623466)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 636:

Arg Glu Phe Leu Ile Arg Ala Ser His Asn Lys Thr Arg Lys Gln Met
 1 5 10 15
 Leu Pro Leu Thr Tyr Val Val Lys Ala Phe Ser Ile Gly Leu Phe Phe
 20 25 30
 Ser Leu Phe Leu Met Lys Pro Leu Ile Ser Trp Leu Lys Lys Gln Gly
 35 40 45
 Phe Gln Asp His Ile His Lys Asp His Cys Glu Lys Leu Glu Glu Leu
 50 55 60
 His Lys Asp Lys Ala Tyr Ile Pro Thr Ala Gly Gly Ile Val Phe Val
 65 70 75 80


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Phe Ala Ser Val Leu Ala Val Leu Leu Leu Phe Pro Ile Gln Leu Trp
      85                      90                      95
Ser Thr Trp Phe Cys Ile Gly Thr Ile Leu Leu Trp Gly Ala Leu Gly
      100                    105                    110
Trp Cys Asp Asp Gln Ile Lys Asn Arg Arg Arg Val Gly His Gly Leu
      115                    120                    125
Ser Ala Lys His Lys Phe Leu Ile Gln Asn Cys Leu Ala Ala Gly Val
      130                    135                    140
Val Leu Pro Ile Met Phe Ala Tyr Lys Glu Ser Phe Leu Ser Phe His
      145                    150                    155                    160
Leu Pro Phe Leu Gly Ile Val Ser Leu Pro His His Trp Trp Ser Tyr
      165                    170                    175
Leu Leu Ser Phe Ala Ile Ala Thr Leu Ala Ile Val Gly Thr Ser Asn
      180                    185                    190
Ser Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ala Gly Ala Met
      195                    200                    205
Val Ile Ala Cys Leu Gly Met Leu Val Val Ala Cys Thr Asn Gly Ala
      210                    215                    220
Pro Trp Ala Phe Ile Cys Cys Val Leu Leu Ala Thr Leu Ala Gly Ser
      225                    230                    235                    240
Cys Leu Gly Phe Leu Arg Tyr Asn Lys Ser Pro Ala Arg Val Phe Met
      245                    250                    255
Gly Asp Thr Gly Ser Leu Phe Leu Gly Ala Met Leu Gly Met Cys Ala
      260                    265                    270
Val Leu Leu Arg Ala Glu Phe Leu Leu Leu Phe Met Gly Gly Ile Phe
      275                    280                    285
Val Leu Glu Ser Leu Ser Val Ile Val Gln Val Gly Ser Tyr Lys Leu
      290                    295                    300
Arg Lys Lys Arg Val Phe Leu Cys Ala Pro Leu His His His Tyr Glu
      305                    310                    315                    320
Tyr Lys Gly Leu Ser Glu Lys Ala Val Val Arg Asn Phe Leu Ile Val
      325                    330                    335
Glu Leu Ile Cys Val Val Val Gly Ile Ile Ala Val Phe Val Asp
      340                    345                    350

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(2) INFORMATIONS POUR LA SEQ ID NO: 637:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(623570..624178)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 637:

```

Asn Gly Arg Phe Leu Leu Ser Ser Asp Ser Phe Arg Arg Val Leu Ile
1      5                      10                      15
Ser Ala Pro Asp Gly Asp Ile Glu Leu Pro Ala Val Phe Pro Tyr Ser
      20                    25                    30
Pro Ala Tyr Met Asn Phe Ile Ile Ala Val Ala Leu Ala Trp Ile Thr
      35                    40                    45
Asn Val Pro Met Asp Arg Leu Glu Gln Val Ser Gln Ser Leu Phe Leu
      50                    55                    60
Pro Ala Met Arg Phe Glu Gln Gln Glu His Asn Gly Ile Arg Val Ile

```

Ser Leu Leu Leu Glu Arg Cys Gly Leu Gln Leu Ile Pro Lys Asp Ser
 210 215 220
 Ser Trp Phe Gln Phe Phe Ala Lys Lys Asn Ser Ala Ala Glu Arg Phe
 225 230 235 240
 Ser Phe Ser Met Ser Asn Glu Thr Ala Asp Phe Tyr Tyr Arg Ala Ile
 245 250 255
 His Ser Glu Glu Ser Leu Leu Val Leu Leu Met Gly Thr Leu Ser Cys
 260 265 270
 Leu Pro Tyr Phe Arg Ile Leu Gln Arg Ile
 275 280

(2) INFORMATIONS POUR LA SEQ ID NO: 639:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 440 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 625346..626665

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 639:

Pro Leu Gln Glu Tyr Pro Ala Met Pro His Asp Asn Asn Glu Met His
 1 5 10 15
 Arg Asn Thr Ile His Gln Leu Phe Thr Gly Leu Asp Lys Ala Tyr Gln
 20 25 30
 Ile Val Lys Gly Phe Tyr Gly Pro Ala Tyr Ser Ser Ser Ser Lys Asp
 35 40 45
 Phe Phe Lys Gly Arg Gly Tyr His Ile Leu Ser Arg Ile Glu Leu Ser
 50 55 60
 Asp Pro Phe Glu Arg Ile Gly Val Tyr Phe Ala Arg Ser Leu Ala Lys
 65 70 75 80
 Arg Ile His Lys Arg His Ala Asp Gly Val Ile Ser Ser Val Ile Leu
 85 90 95
 Leu Arg Ala Phe Leu Lys Ala Ser Ile Pro Phe Ile Asp Gln Gly Leu
 100 105 110
 Ser Pro Arg Leu Leu Ala Ser Ala Leu Ala Ser Gln Lys Glu Ala Val
 115 120 125
 Cys Ala Tyr Leu His Ser His Ser Phe Leu Leu Lys Asp Ala Ser Lys
 130 135 140
 Val Leu Gly Leu Ile Arg Ser His Leu Pro Asp Pro Leu Ile Gly Glu
 145 150 155 160
 Ala Phe Ala Glu Ala Val Ala Tyr Thr Gly His Glu Gly Ala Val Ala
 165 170 175
 Leu Ser Gln Arg Ser Gly Ser Thr Leu His Leu Val Lys Gly Ile Gln
 180 185 190
 Thr Gln Lys Gly Tyr Arg Met Pro Ser Phe Phe Pro His Asp Ser Phe
 195 200 205
 His Glu Asn Pro Ile Val Ala Pro Lys Ile Phe Val Thr Asp Gln Lys
 210 215 220
 Ile His Cys Leu Phe Pro Phe Leu Pro Leu Leu Lys Lys Phe Ser Glu
 225 230 235 240
 Glu Gln Thr Pro Leu Ile Ile Phe Cys Lys Glu Ile Ala Pro Asp Pro
 245 250 255
 Leu Ala Thr Cys Ile Ala Asn Arg Ile Ala Gly Leu Leu Asp Val Leu

(2) INFORMATION POUR LA SEQ ID NO: 640:

(A) LONGUEUR: 129 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 626514..626900

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 640:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 641:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 300 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 626954..627853

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 641:

Ile	Gly	Phe	Ser	Ile	Asn	His	Arg	Phe	Ser	Met	Pro	Asn	Lys	Pro	Ser
1				5					10					15	
His	Ala	Phe	Arg	Leu	Ile	His	Cys	Ser	Asp	Ile	His	Phe	Cys	Val	Leu
			20					25					30		
Pro	Lys	Asn	Pro	Phe	Gln	Cys	Phe	Asn	Lys	Arg	Phe	Lys	Gly	Leu	Leu
		35					40					45			
Arg	Gln	Leu	Ile	Gly	Gly	Val	Ser	Phe	Gln	Ala	Phe	Ala	Ile	Ser	Gln
	50					55					60				
Arg	Phe	Pro	Gln	Leu	Val	Lys	Gln	Leu	Glu	Ala	Asp	Ser	Val	Cys	Val
65					70				75					80	
Thr	Gly	Asp	Met	Thr	Ile	Thr	Ala	Leu	Asp	Thr	Glu	Phe	Arg	Phe	Ala
			85						90				95		
Lys	Glu	Phe	Leu	Ser	Arg	Val	Glu	Ser	Val	Ala	Pro	Val	Tyr	Ile	Val
		100						105					110		
Pro	Gly	Asn	His	Asp	Val	Xaa	Thr	His	Arg	Ala	Leu	Lys	Lys	Gln	Thr
		115					120					125			
Phe	Tyr	Ser	Tyr	Phe	Pro	Asn	Lys	Glu	Leu	Gln	Thr	His	Arg	Ile	Ala
	130					135					140				
Phe	Lys	Lys	Leu	Thr	Pro	Thr	Trp	Trp	Leu	Val	Leu	Leu	Asp	Cys	Ser
145					150				155					160	
Cys	Phe	Asn	Gly	Trp	Tyr	Thr	Ala	Asn	Gly	Glu	Val	Thr	Asp	Ser	Gln
			165					170					175		
Leu	Leu	Ala	Leu	Glu	Gln	Phe	Leu	Ser	Ser	Leu	Pro	Ala	Ser	Glu	His
		180						185					190		
Val	Ile	Val	Ala	Asn	His	Tyr	Pro	Leu	Ser	Pro	Thr	Thr	Arg	Pro	Ala
		195					200					205			
His	Asp	Leu	Leu	Asn	Tyr	Ala	Pro	Leu	Lys	Ser	Leu	Leu	Met	Asn	Ser
	210					215					220				
Pro	Ser	Val	Arg	Leu	Tyr	Leu	His	Gly	His	Asp	His	Tyr	Val	Glu	Leu
225					230					235				240	
Asp	His	Leu	Pro	Pro	Leu	Val	Val	Asn	Ser	Gly	Ser	Leu	Thr	Leu	Pro
			245					250					255		
Ser	Asn	Ala	Arg	Phe	His	Ile	Ile	Asp	Leu	His	Pro	Glu	Gly	Gly	Tyr
		260						265				270			
Gln	Ile	Ala	Thr	Ala	Ala	Leu	Thr	Asn	Leu	Lys	Glu	Thr	Ser	Thr	Pro
		275					280					285			
Leu	Thr	Ile	Ser	Ile	Glu	Glu	Asn	Thr	Ile	Ser	Leu				
	290					295					300				

(2) INFORMATIONS POUR LA SEQ ID NO: 642:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 101 acides aminés
 (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 627822..628124

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 642:

```

Pro Phe Leu Ser Lys Lys Ile Pro Ser Leu Tyr Lys Ser Ser Ala Leu
1      5      10      15
Asn Leu Arg Ile Thr Asn Leu Glu Gly Leu Pro Met Lys Glu Lys Lys
20      25      30
Val Leu Glu Leu Ser Pro Glu Ala Thr Leu Leu Lys Lys Leu Arg Asp
35      40      45
Arg Ala Ile Ser Gln Gln Glu Thr Gln Lys Arg Lys Ala Trp Val Glu
50      55      60
Lys Leu Ala Ala Met Pro Glu Ser Thr Arg Asp Tyr Leu Glu Pro Gln
65      70      75      80
Ala His Leu Glu Pro Ser Gln Leu Phe Arg Lys Val Ala Glu Arg Leu
85      90      95
Leu Glu Glu Gly Ala
100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 643:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 190 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(628146..628715)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 643:

```

Met Val Arg Val Ser Thr Ser Glu Phe Arg Val Gly Leu Arg Val Glu
1      5      10      15
Ile Asp Gly Gln Pro Tyr Val Ile Leu Gln Asn Asp Phe Val Lys Pro
20      25      30
Gly Lys Gly Gln Ala Phe Asn Arg Ile Lys Val Lys Asn Phe Leu Thr
35      40      45
Gly Arg Val Ile Glu Lys Thr Phe Lys Ser Gly Glu Ser Ile Glu Thr
50      55      60
Ala Asp Val Arg Glu Gln Met Arg Leu Leu Tyr Thr Asp Gln Glu
65      70      75      80
Gly Ala Thr Phe Met Asp Asp Glu Thr Phe Glu Gln Glu Leu Ile Phe
85      90      95
Trp Asp Lys Leu Glu Asn Val Arg Gln Trp Leu Leu Glu Asp Thr Ile
100      105      110
Tyr Thr Leu Val Leu Tyr Asn Gly Asp Val Ile Ser Val Glu Pro Pro
115      120      125
Ile Phe Met Glu Leu Thr Ile Ala Glu Thr Ala Pro Gly Val Arg Gly
130      135      140
Asp Thr Ala Ser Gly Arg Val Leu Lys Pro Ala Thr Thr Asn Thr Gly
145      150      155      160

```

Ala Lys Ile Met Val Pro Ile Phe Ile Glu Glu Gly Glu Val Val Lys
 165 170 175
 Val Asp Thr Arg Thr Gly Ser Tyr Glu Ser Arg Val Ser Lys
 180 185 190

(2) INFORMATIONS POUR LA SEQ ID NO: 644:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 290 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 628932..629801

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 644:

Phe Met Thr His Gln His Lys Lys Ile Ser Glu Glu Thr Ile Ala Cys
 1 5 10 15
 Asp Met Leu Glu Arg Tyr Thr Gly Ser Thr Ile Gln Glu Phe Gln Pro
 20 25 30
 Tyr Leu Leu Leu Thr Asn Phe Gly Tyr Tyr Val Asp Val Phe Ala Glu
 35 40 45
 Ile Tyr Gln Val Pro Val Ser Arg Gly Ser Met Phe Ser Ala Ala His
 50 55 60
 Ala Pro Gln Ile His Thr Ser Ile Ile Asp Phe Lys Leu Gly Ser Pro
 65 70 75 80
 Gly Ala Ala Leu Thr Val Asp Leu Cys Ser Phe Leu Pro Asn Ala Thr
 85 90 95
 Ala Ala Ile Met Leu Gly Met Cys Gly Gly Leu Arg Ser His Tyr Gln
 100 105 110
 Ile Gly Asp Tyr Phe Val Pro Val Ala Ser Ile Arg Lys Asp Gly Thr
 115 120 125
 Ser Asp Ala Tyr Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val
 130 135 140
 Val Gln Lys Met Ile Thr Asn Ile Leu Glu Ala Lys Asn Leu Pro Tyr
 145 150 155 160
 His Ile Gly Ile Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn
 165 170 175
 Lys Glu Phe Arg Arg Lys Leu Tyr Glu Asn Lys Ala Gln Thr Val Glu
 180 185 190
 Met Glu Cys Ala Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro
 195 200 205
 Leu Gly Ala Leu Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Asp Gly
 210 215 220
 Ile Lys Thr Lys Glu Ser Ser Ser Ala Val Leu Asn Ser His Thr Lys
 225 230 235 240
 Glu His Ile Leu Thr Gly Val Glu Val Phe Ala Ser Leu Gln Lys Lys
 245 250 255
 Ser Gly Pro Gly Ile Lys Lys Thr Lys Gly Leu Pro His Met Glu Phe
 260 265 270
 Gly Gln Ala Asp Asp Ser Leu Ser Glu Gln Thr Gly Val Ser Asp Gly
 275 280 285
 Asp Phe
 290

Lys Phe Leu Ala Ser Pro Arg Arg Lys Val Phe Arg Ser Ser Ala Val
1 5 10 15

130 135 140
 Phe Asp Ala Lys Val Tyr Cys Leu Ala Gly Asp Gly Cys Phe Met Glu
 145 150 155 160
 Gly Val Ser His Glu Ala Cys Ser Phe Ala Gly Ser Leu Gly Leu Asp
 165 170 175
 Asn Leu Val Leu Ile Tyr Asp Tyr Asn Glu Ile Ile Leu Asp Gly Thr
 180 185 190
 Leu His Asp Val Ser Ile Glu Asp Thr Lys Gln Arg Phe Leu Ala Tyr
 195 200 205
 Gly Trp Asp Val Phe Glu Thr Asp Gly His Asp Phe Glu Ser Leu His
 210 215 220
 Gln Val Phe Thr Gln Ile Lys Lys Ser Gln Cys Lys Pro Thr Leu Ile
 225 230 235 240
 Ile Ala His Thr Ile Ile Gly His Gly Ser Pro Lys Glu Gly Thr Asn
 245 250 255
 Lys Ala His Gly Ser Pro Leu Gly Glu Asp Gly Val Ala Gln Thr Lys
 260 265 270
 Ser Phe Trp His Leu Pro Glu Glu Lys Phe Phe Val Leu Arg Gln
 275 280 285

(2) INFORMATIONS POUR LA SEQ ID NO: 648:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 150 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 637635..638084

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 648:

Met Leu Ser Asn Thr Leu Arg Ser Asn Phe Leu Lys Phe Tyr Ala Asn
 1 5 10 15
 Arg Asn His Thr Pro Val Ala Ser Ser Pro Val Phe Pro His Asn Asp
 20 25 30
 Pro Ser Ile Leu Phe Thr Asn Ala Gly Met Asn Gln Phe Lys Asn Ile
 35 40 45
 Phe Leu Gly Lys Glu Gln Thr Ser Tyr Thr Arg Ala Thr Thr Ser Gln
 50 55 60
 Lys Cys Ile Arg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly
 65 70 75 80
 His Thr Ser Arg His Leu Thr Phe Phe Glu Met Leu Gly Asn Phe Ser
 85 90 95
 Phe Gly Asp Tyr Phe Lys Gln Asp Ala Ile Ser Phe Ala Trp Glu Val
 100 105 110
 Ser Leu Ser Val Phe Asn Phe Asp Pro Asp Phe Ile Tyr Ala Thr Val
 115 120 125
 His Glu Lys Asp Asp Glu Xaa Ser Leu Phe Gly Lys Asn Ile Phe Arg
 130 135 140
 Gln Thr Glu Phe Phe Val
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 649:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 724 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 638036..640207

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 649:

Xaa	Phe	Ala	Leu	Trp	Glu	Lys	Tyr	Leu	Pro	Thr	Asp	Arg	Ile	Phe	Arg
1			5					10					15		
Leu	Thr	Asp	Lys	Asp	Asn	Phe	Trp	Ser	Met	Ala	Asp	Thr	Gly	Pro	Cys
			20					25					30		
Gly	Phe	Cys	Ser	Glu	Leu	Leu	Phe	Asp	Arg	Gly	Glu	Lys	Phe	Gly	Lys
		35					40					45			
Ala	Ala	Ser	Pro	Leu	Glu	Asp	Val	Asp	Gly	Glu	Arg	Phe	Leu	Glu	Tyr
	50					55					60				
Trp	Asn	Leu	Val	Phe	Met	Glu	Phe	Asn	Arg	Thr	Ser	Asp	Gly	Thr	Leu
65					70					75					80
Leu	Ala	Leu	Gln	Lys	Lys	Cys	Val	Asp	Thr	Gly	Ala	Gly	Leu	Glu	Arg
				85				90					95		
Leu	Val	Ser	Leu	Leu	Ala	Glu	Thr	Lys	Thr	Val	Phe	Glu	Ala	Asp	Val
		100						105					110		
Leu	Arg	His	Leu	Ile	Ser	Lys	Ile	Glu	Asn	Leu	Ser	Gly	Thr	Thr	Tyr
		115				120						125			
Ser	Pro	Thr	Glu	Ala	Lys	Gly	Ala	Ala	Phe	Arg	Val	Ile	Ala	Asp	His
	130					135					140				
Ile	Arg	Ser	Leu	Ser	Phe	Ala	Ile	Ala	Asp	Gly	Leu	Leu	Pro	Gly	Asn
145					150					155					160
Thr	Glu	Arg	Gly	Tyr	Val	Leu	Arg	Lys	Ile	Leu	Arg	Arg	Ala	Val	Asn
				165				170						175	
Tyr	Gly	Lys	Arg	Leu	Gly	Phe	Asn	Arg	Pro	Phe	Leu	Ala	Asp	Val	Val
		180					185						190		
Pro	Ser	Leu	Val	Asp	Val	Met	Gly	Glu	Ala	Tyr	Pro	Glu	Leu	Ser	Ala
		195				200						205			
Ser	Val	Thr	Gln	Ile	Gln	Glu	Val	Leu	Thr	Thr	Glu	Glu	Glu	His	Phe
	210					215					220				
Phe	Lys	Thr	Leu	Gln	Arg	Gly	Gly	Asn	Leu	Leu	Gln	Gln	Val	Val	Lys
225				230						235					240
Ser	Ser	Ala	Ser	Ser	Ala	Lys	Ile	Ser	Gly	Glu	Asp	Ala	Phe	Lys	Leu
				245				250						255	
Lys	Asp	Thr	Tyr	Gly	Leu	Pro	Ile	Asp	Glu	Ile	Ala	Leu	Leu	Ala	Lys
		260						265					270		
Asp	Tyr	Asn	Tyr	Ala	Ile	Asp	Met	Asp	Thr	Phe	Glu	Lys	Leu	Glu	Val
		275				280						285			
Glu	Ala	Lys	Glu	Arg	Ser	Arg	Lys	Asn	Thr	Lys	Lys	Thr	Lys	Asn	Asp
	290					295					300				
Ser	Asp	Ser	Val	Phe	Gln	Asp	Leu	Asp	Pro	Thr	Asn	Thr	Ser	Glu	Phe
305					310					315					320
Ile	Gly	Tyr	Asp	Thr	Leu	Ser	Cys	Asp	Thr	Phe	Ile	Glu	Gly	Ile	Ile
				325				330						335	
Lys	Tyr	Asn	Glu	Ile	Ala	Ser	Ser	Leu	Glu	Glu	Gly	Asp	Glu	Gly	Ala
		340						345					350		
Ile	Ile	Leu	Arg	Thr	Thr	Pro	Phe	Tyr	Ala	Glu	Lys	Gly	Gly	Gln	Ile
		355				360						365			
Gly	Asp	Ser	Gly	Glu	Ile	Phe	Cys	Glu	Ser	Gly	Thr	Phe	Leu	Val	Ser

(2) INFORMATION POUR LA SEQ ID NO: 650:

(A) LONGUEUR: 1084 acides aminés

(A) LONGUEUR: 1004 ac.
(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 640221..643472

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 650:

Gln Asn Phe Lys Thr Met Asp Phe Asp Pro Thr Ser Ile Asp Phe Ser
 1 5 10 15
 Ser Phe Pro Leu Leu Lys Asp Thr Lys Leu Pro Ser Leu Val Glu Asn
 20 25 30
 Leu His Ser Gly Ala Arg Ser Phe Val Ile Ala Lys Leu Phe Lys Glu
 35 40 45
 Leu Lys Arg Ser Ile Val Val Ile Thr Thr Pro Ala Lys Leu Asp Asp
 50 55 60
 Leu Phe Glu Asp Leu Thr Thr Leu Leu Ala Glu Ser Pro Leu Glu Phe
 65 70 75 80
 Pro Ala Ser Glu Ile Asp Leu Ser Pro Lys Leu Val Asn Val Asp Ala
 85 90 95
 Val Gly Lys Arg Asp His Ile Leu Tyr Ser Leu Gln Lys Gln Ser Ala
 100 105 110
 Pro Val Ile Cys Val Thr Thr Leu Lys Ala Leu Leu Glu Arg Thr Pro
 115 120 125
 Ser Pro Glu Ser Met Ile Arg Asp His Leu Glu Leu Arg Val Gly Glu
 130 135 140
 Glu Leu Asp Pro Asp Thr Leu Leu Asp Leu Cys Lys Ser Leu Gly Tyr
 145 150 155 160
 Arg His Glu Ala Leu Ala Arg Glu Lys Gly Asp Phe Ala Phe Arg Gly
 165 170 175
 Gly Ile Val Asp Ile Phe Pro Leu Ser Ser Pro Glu Pro Phe Arg Ile
 180 185 190
 Glu Phe Trp Gly Asp Arg Val Ser Ser Ile Arg Ser Tyr Asn Pro Ser
 195 200 205
 Asp Gln Leu Ser Thr Gly Lys Leu Ser Gln Ile Thr Ile Ser Pro Ala
 210 215 220
 Thr Ala Ile Ile Pro Thr Asp Lys Leu Ser Tyr Ser Leu Leu Asp Tyr
 225 230 235 240
 Phe Lys Ala Phe Pro Leu Cys Ile Phe Asp Gly Leu Ser Ser Leu Glu
 245 250 255
 Asp Asn Phe Ser Asp Ile Ala Gly Ile Leu Ala Ser Leu Pro Lys Arg
 260 265 270
 Phe Met Pro Ile Gln Asp Leu Cys Gln Arg Ile Leu Lys Glu Phe Thr
 275 280 285
 Pro Leu Phe Phe Glu Glu Lys Thr Phe Pro Asn Leu Ile Ser His Lys
 290 295 300
 Asp Thr Gly Phe Ser Ile Glu Ala Phe His Lys Lys Ile Ser Val Gln
 305 310 315 320
 Arg Val Ser Leu Pro Phe Ile Tyr Pro Pro Ala Leu Ile Glu Thr Ser
 325 330 335
 Gly Glu Gln Asn Pro Leu Leu Ala Phe Leu Lys Thr Phe Gln Asp Phe
 340 345 350
 Cys Ala Gly Arg Thr Leu Ser Leu Ala Leu Tyr Cys Ser Asn Thr Lys
 355 360 365
 Ser Leu Lys Glu Ala His Asp Leu Ala Ala Ala Cys Ile Pro Asn Thr
 370 375 380
 Gln Ile Tyr Asp His Pro Thr Thr Leu Ser Ser Ser Phe Ala Leu Val
 385 390 395 400
 Glu Ala Gly Phe Ala Ala Val Ser Leu Ser Glu Phe Ala Ala Ser Lys
 405 410 415
 Val Leu Arg Arg Gln Lys Gln Arg Asn Tyr Phe Ser Thr Thr Glu
 420 425 430
 Glu Val Tyr Ile Pro Val Pro Gly Glu Thr Val Val His Leu His Asn
 435 440 445
 Gly Ile Gly Lys Phe Ile Gly Ile Glu Lys Lys Pro Asn His Leu Asn

450 455 460
 Ile Glu Thr Asp Tyr Leu Val Leu Glu Tyr Ala Asp Lys Ala Arg Leu
 465 470 475 480
 Tyr Val Pro Ser Asp Gln Ala Tyr Leu Ile Ser Arg Tyr Val Gly Ala
 485 490 495
 Ser Glu Lys Ala Pro Asp Leu His His Leu Asn Gly Ala Lys Trp Arg
 500 505 510
 Arg Ser Arg Glu Leu Ser Glu Asn Ser Val Ile Leu Tyr Ala Glu Lys
 515 520 525
 Leu Ile Gln Met Glu Ala Gln Arg Ser Thr Ala Asn Ser Phe Ile Tyr
 530 535 540
 Pro Pro His Gly Glu Glu Val Ile Lys Phe Ala Glu Ser Phe Pro Tyr
 545 550 555 560
 Glu Glu Thr Pro Asp Gln Leu Lys Ala Ile Asp Gln Ile Tyr Ala Asp
 565 570 575
 Met Met Ser Asp Lys Leu Met Asp Arg Leu Ile Cys Gly Asp Ala Gly
 580 585 590
 Phe Gly Lys Thr Glu Ile Ile Met Arg Ala Ala Val Lys Ala Val Cys
 595 600 605
 Asp Gly His Lys Gln Val Ile Val Met Val Pro Thr Thr Ile Leu Ala
 610 615 620
 Asn Gln His Phe Glu Thr Phe Ser Gln Arg Met Ala Gly Leu Pro Ile
 625 630 635 640
 Thr Ile Gly Leu Leu Ser Arg Phe Ser Gln Gly Lys Thr Met Lys Lys
 645 650 655
 Thr Leu Glu Asp Ile Ala Gln Gly Arg Ile Asp Ile Leu Ile Gly Thr
 660 665 670
 His Lys Val Ile Asn Lys Ala Ile Glu Phe His Asn Pro Gly Leu Leu
 675 680 685
 Ile Ile Asp Glu Glu Gln Arg Phe Gly Val Lys Ala Lys Asp Ser Leu
 690 695 700
 Lys Glu Arg Phe Pro Thr Ile Asp Cys Leu Thr Val Ser Ala Thr Pro
 705 710 715 720
 Ile Pro Arg Thr Leu Tyr Leu Ser Leu Ser Gly Ala Arg Asp Leu Ser
 725 730 735
 Leu Ile Thr Met Pro Pro Leu Asp Arg Leu Pro Val Ser Thr Phe Val
 740 745 750
 Met Glu His Ser Glu Glu Thr Leu Ser Ala Ala Ile Arg His Glu Leu
 755 760 765
 Leu Arg Gly Gly Gln Val Tyr Val Ile His Asn Arg Ile Glu Ser Ile
 770 775 780
 Phe Arg Leu Gly Glu Thr Ile Arg Thr Leu Ile Pro Glu Ala Arg Ile
 785 790 795 800
 Gly Val Ala His Gly Gln Met His Ala Asp Glu Leu Ala Ser Ile Phe
 805 810 815
 Tyr Lys Phe Lys Thr Gln Gln Thr Asn Val Leu Val Ala Thr Ala Leu
 820 825 830
 Ile Glu Asn Gly Ile Asp Ile Pro Asn Ala Asn Thr Ile Leu Ile Asp
 835 840 845
 His Ala Asp Lys Phe Gly Met Ala Asp Leu Tyr Gln Met Lys Gly Arg
 850 855 860
 Val Gly Arg Trp Asn Lys Lys Ala Tyr Cys Tyr Xaa Leu Val Pro His
 865 870 875 880
 Leu Asp Arg Leu Ser Gly Pro Thr Ser Lys Arg Leu Glu Ala Leu Asn
 885 890 895
 Lys Gln Glu Tyr Gly Gly Gly Met Lys Ile Ala Leu His Asp Leu Glu
 900 905 910
 Ile Arg Gly Ala Gly Asn Ile Leu Gly Thr Asp Gln Ser Gly His Ile
 915 920 925

```

Ser Ala Val Gly Phe Asn Leu Tyr Cys Lys Leu Leu Lys Lys Ala Val
  930          935          940
Ala Ala Leu Lys His Lys Gln Lys Pro Met Leu Phe His Asp Asp Ile
945          950          955          960
Lys Ile Glu Phe Pro Tyr His Ala Arg Ile Pro Glu Asp Tyr Ile Asp
          965          970          975
Leu Ala Ser Met Arg Ile Glu Phe Tyr Gln Lys Ile Gly Asn Ala Glu
          980          985          990
Ser Glu Glu Glu Leu Glu Ala Ile Glu Glu Glu Leu Arg Asp Arg Phe
          995          1000          1005
Gly Pro Ser Pro Glu Ala Ile Ser Trp Leu Phe Ala Leu Ala Arg Ile
1010          1015          1020
Arg Leu Ile Ala Gln Glu Tyr His Leu Ser Ser Ile Lys Gly Thr Gly
1025          1030          1035          1040
Asn Ala Leu Tyr Ile Gln Gln Tyr His Asp Lys Asp Lys Gln Ile Gln
          1045          1050          1055
Lys Thr Leu Pro Tyr Ser Leu Ser Pro Thr Pro Glu Leu Leu Val Lys
          1060          1065          1070
Glu Val Gln Glu Ser Val Glu Lys Ala Phe Pro Lys
          1075          1080

```

(2) INFORMATIONS POUR LA SEQ ID NO: 651:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(640220..640627)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 651:

```

Ser Arg Ile Ile Asp Ser Gly Glu Gly Val Leu Ser Asn Lys Ala Phe
1          5          10          15
Ser Val Val Thr Gln Ile Thr Gly Ala Leu Cys Phe Cys Arg Glu Tyr
20          25          30
Arg Ile Trp Ser Leu Phe Pro Thr Ala Ser Thr Phe Thr Ser Leu Gly
35          40          45
Asp Lys Ser Ile Ser Glu Ala Gly Asn Ser Arg Gly Asp Ser Ala Asn
50          55          60
Arg Val Val Lys Ser Ser Asn Lys Ser Ser Ser Phe Ala Gly Val Val
65          70          75          80
Ile Thr Thr Ile Glu Arg Leu Ser Ser Leu Asn Ser Phe Ala Met Thr
85          90          95
Lys Asp Leu Ala Pro Glu Trp Arg Phe Ser Thr Lys Asp Gly Ser Phe
100          105          110
Val Ser Phe Asn Lys Gly Lys Leu Glu Lys Ser Met Leu Val Gly Ser
115          120          125
Lys Ser Ile Val Leu Lys Phe Cys
130          135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 652:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 643485..644495

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 652:

```

Arg Met Pro Met Thr Gly Phe Tyr Glu Thr Ile Ser Pro Arg Asp Gln
1          5          10          15
Gln Arg Pro Pro Ile Trp Phe Leu Arg Gln Val Gly Arg Tyr Ile Pro
20          25          30
Gln Tyr Gln Glu Leu Lys Arg Asn Arg Ser Leu Lys Asp Phe Phe Leu
35          40          45
Asp Thr Glu Ser Ile Val Glu Ala Thr Leu Leu Gly Pro Ser Leu Leu
50          55          60
Gly Val Asp Ala Ala Ile Val Phe Ala Asp Ile Leu Ser Ile Leu Glu
65          70          75
Gly Phe Ser Val Asp Tyr Arg Phe Ala Pro Gly Pro Glu Val Ser Tyr
85          90          95
Ser Pro His Glu Pro Leu Ile Phe Thr Lys Asp Pro Gln Glu Thr Phe
100         105         110
Ser Phe Leu Leu Glu Ala Ile Gln Gln Leu Thr Lys Arg Leu Thr Val
115         120         125
Pro Leu Ile Ala Phe Ala Ala Ser Pro Phe Thr Leu Ala Ser Tyr Leu
130         135         140
Ile Glu Gly Gly Ala Ser Arg Asp Tyr Pro Lys Thr Ile Ala Phe Leu
145         150         155
Tyr Gln Tyr Pro Asp Arg Phe Lys Ala Leu Leu Asp Glu Ile Thr Leu
165         170         175
Gly Thr Ala Thr Tyr Leu Gln Met Gln Val Gln Ala Gly Ala Ala Ala
180         185         190
Ile Gln Leu Phe Glu Ser Ser Ser Leu Arg Leu Pro Pro His Leu Phe
195         200         205
Ala Lys Tyr Val Val Ala Pro Asn Thr Lys Leu Ile Arg Gln Ile Lys
210         215         220
Gln Thr Gly Asn Pro Pro Ile Ser Leu Phe Cys Arg Cys Phe Tyr Gln
225         230         235
Glu Phe Leu Ser Leu Tyr Ala Ile Gly Ala Asp Thr Leu His Pro Asp
245         250         255
Tyr His Val Glu Leu Pro Glu Val Tyr Arg Gln Ile His Ser Pro Gly
260         265         270
Ser Ile Gln Gly Asn Phe Asp Pro Ala Leu Leu Leu Leu Pro Gln Asp
275         280         285
Ala Leu Ile Ala His Leu Glu Ala Tyr Leu Ala Pro Leu Lys Gln Gln
290         295         300
Ser His Tyr Ile Phe Asn Leu Gly His Gly Ile Leu Pro Gln Thr Pro
305         310         315
Ile Glu Asn Val Gln Ala Val Val Ser Cys Leu Thr Ser Ile Ser Thr
325         330         335
Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 653:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 320 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 644471..645430

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 653:

Met	Phe	Asn	Ile	Asn	Phe	Asn	Phe	Leu	Lys	Gly	Leu	His	Gln	Pro	Ala	1	5	10	15
Pro	Arg	Tyr	Thr	Ser	Tyr	Pro	Thr	Ile	Val	Asp	Trp	Glu	Ser	Ser	Ser	20	25	30	
Asp	Tyr	Gly	Tyr	Thr	Ala	Leu	Glu	Arg	Leu	Ala	Gln	Glu	Gln	Asp	Pro	35	40	45	
Leu	Ser	Leu	Tyr	Phe	His	Ile	Pro	Phe	Cys	Gln	Ser	Met	Cys	Leu	Tyr	50	55	60	
Cys	Gly	Cys	Thr	Val	Val	Leu	Asn	Arg	Lys	Ala	Glu	Ile	Val	Asp	His	65	70	75	80
Tyr	Ile	Glu	Thr	Leu	Ile	Gln	Glu	Met	Arg	Leu	Ala	Phe	Ser	Leu	Leu	85	90	95	
Gly	Gly	Lys	Lys	Pro	Val	Ser	Arg	Ile	His	Phe	Gly	Gly	Gly	Thr	Pro	100	105	110	
Ser	Arg	Leu	Ser	Arg	Ala	Gln	Phe	Glu	Arg	Leu	Phe	Thr	His	Ile	His	115	120	125	
Arg	Phe	Phe	Asp	Leu	Ser	Asn	Ile	Glu	Glu	Leu	Ala	Ile	Glu	Phe	Asp	130	135	140	
Pro	Arg	Ser	Leu	Arg	Glu	Asp	Ala	Asp	Lys	Pro	Leu	Phe	Leu	His	Asn	145	150	155	160
Leu	Gly	Phe	Asn	Arg	Val	Ser	Leu	Gly	Ile	Gln	Asp	Thr	Gln	Trp	Glu	165	170	175	
Val	Gln	Glu	Ala	Val	Arg	Arg	Arg	Gln	Ser	Tyr	Glu	Glu	Ser	Leu	Leu	180	185	190	
Ala	Tyr	Gln	Leu	Phe	Arg	Asp	Leu	Lys	Phe	Thr	Gly	Ile	Asn	Ile	Asp	195	200	205	
Leu	Ile	Tyr	Gly	Leu	Pro	Lys	Gln	Thr	Gln	Ser	Ser	Phe	Lys	Gln	Thr	210	215	220	
Ile	Glu	His	Ile	Leu	Asp	Met	Arg	Pro	Asp	Arg	Leu	Ala	Leu	Phe	Ser	225	230	235	240
Phe	Ala	His	Val	Pro	Trp	Ala	Lys	Pro	His	Gln	Lys	Ala	Leu	Arg	Thr	245	250	255	
Lys	Asp	Leu	Pro	Ser	Met	Glu	Glu	Lys	Phe	Ala	Ile	Tyr	Ser	Gln	Ser	260	265	270	
Arg	His	Thr	Leu	Ile	Gln	Glu	Gly	Tyr	Gln	Ala	Ile	Gly	Leu	Asp	His	275	280	285	
Phe	Ser	Leu	Pro	Asp	Asp	Pro	Leu	Thr	Ile	Ala	Leu	Lys	Asn	Lys	Thr	290	295	300	
Leu	Ile	Arg	Asn	Phe	Gln	Gly	Thr	Leu	Phe	Leu	Leu	Lys	Lys	Ile	Phe	305	310	315	320

(2) INFORMATIONS POUR LA SEQ ID NO: 654:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 149 acides aminés
 (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 645394..645840

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 654:

```

Phe Pro Arg Tyr Ser Leu Pro Pro Glu Glu Asp Leu Leu Gly Phe Gly
1      5      10
Ile Ser Ala Thr Ser Phe Ile Arg Gly Ile Tyr Leu Gln Asn Val Lys
20      25      30
Asp Leu Arg Glu Tyr Ser Glu Thr Ile Gln Ala Ser Lys Leu Ala Thr
35      40      45
Val Lys Gly Lys Ile Leu Ser Gln Asp Asp Lys Ile Arg Lys Trp Val
50      55      60
Ile His Thr Leu Met Cys Ser Phe Ser Leu Ser Lys Leu Glu Phe Glu
65      70      75      80
Gln Arg Phe His Glu Arg Phe Asp Arg Tyr Phe Ala Asp Ser Tyr Asp
85      90      95
Arg Leu Cys Gly Met Glu Ser Ala Gly Leu Ile Arg Gln Asp Ser Ser
100      105      110
Ser Leu Gln Val Thr Pro Leu Gly Glu Leu Phe Val Arg Val Ile Ala
115      120      125
Thr Ala Phe Asp His Tyr Phe Leu Lys Asn Ile Val Glu Lys Pro Leu
130      135      140
Phe Ser Lys Ser Ile
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 655:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 424 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 645840..647111

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 655:

```

Met Lys His Ala Leu Ile Val Gly Ser Gly Ile Ala Gly Leu Ser Ala
1      5      10
Ala Trp Trp Leu His Lys Arg Phe Pro His Val Gln Leu Ser Ile Leu
20      25      30
Glu Lys Glu Ser Arg Ser Gly Gly Leu Ile Val Thr Glu Lys Gln Gln
35      40      45
Gly Phe Ser Leu Asn Met Gly Pro Lys Gly Phe Val Leu Ala His Asp
50      55      60
Gly Gln His Thr Leu His Leu Ile Gln Ser Leu Gly Leu Ala Asp Glu
65      70      75      80
Leu Leu Tyr Ser Ser Pro Glu Ala Lys Asn Arg Phe Ile His Tyr Asn
85      90      95
Asn Lys Thr Arg Lys Val Ser Pro Trp Thr Ile Phe Lys Gln Asn Leu
100      105      110

```



```

Pro Leu Ser Phe Ala Lys Asp Phe Phe Ala Arg Pro Tyr Lys Gln Asp
      115                      120                      125
Ser Ser Val Glu Ala Phe Phe Lys Arg His Ser Ser Ser Lys Leu Arg
      130                      135                      140
Arg Asn Leu Leu Asn Pro Ile Ser Ile Ala Ile Arg Ala Gly His Ser
145                      150                      155                      160
His Ile Leu Ser Ala Gln Met Ala Tyr Pro Glu Leu Thr Arg Arg Glu
      165                      170                      175
Ala Gln Thr Gly Ser Leu Leu Arg Ser Tyr Leu Lys Asp Phe Pro Lys
      180                      185                      190
Glu Lys Arg Thr Gly Pro Tyr Leu Ala Thr Leu Arg Ser Gly Met Gly
      195                      200                      205
Met Leu Thr Gln Ala Leu His Asp Lys Leu Pro Ala Thr Trp Tyr Phe
      210                      215                      220
Ser Ala Pro Val Ser Lys Ile Arg Gln Leu Ala Asn Gly Lys Ile Ser
225                      230                      235                      240
Leu Ser Ser Pro Gln Gly Glu Ile Thr Gly Asp Met Leu Ile Tyr Ala
      245                      250                      255
Gly Ser Val His Asp Leu Pro Ser Cys Leu Glu Glu Ile Pro Glu Thr
      260                      265                      270
Lys Leu Ile Lys Gln Thr Thr Ser Ser Trp Asp Leu Ser Cys Val Ser
      275                      280                      285
Leu Gly Trp His Ala Ser Leu Pro Ile Pro His Gly Tyr Gly Met Leu
      290                      295                      300
Phe Ala Asp Thr Pro Pro Leu Leu Gly Ile Val Phe Asn Thr Glu Val
305                      310                      315                      320
Phe Pro Gln Pro Glu Arg Pro Asn Thr Ile Val Ser Leu Leu Leu Glu
      325                      330                      335
Gly Arg Trp His Gln Glu Glu Ala Tyr Ala Phe Ser Leu Ala Ala Ile
      340                      345                      350
Ser Glu Tyr Leu Gln Ile Tyr Thr Pro Pro Gln Ala Phe Ser Leu Phe
      355                      360                      365
Ser Pro Arg Glu Gly Leu Pro Gln His His Val Gly Phe Ile Gln Ser
      370                      375                      380
Arg Gln Arg Leu Leu Ser Lys Leu Pro His Asn Ile Lys Ile Val Gly
385                      390                      395                      400
Gln Asn Phe Ala Gly Pro Gly Leu Asn Arg Ala Thr Ala Ser Ala Tyr
      405                      410                      415
Lys Ala Ile Ala Ser Leu Leu Pro
      420

```

(2) INFORMATIONS POUR LA SEQ ID NO: 656:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 856 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(647109..649676)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 656:

```

Lys Ile Leu His Arg Ser Phe Gln Asn Gly Leu Leu Arg Cys Pro His
1           5           10           15
Asp Glu Lys Ser Leu Gln Ser Ser Leu Lys Arg Asn Lys Gln Val Phe

```

20 25 30
 Phe His Met Asn Ile Tyr Arg Phe Ile Ser Gly Ser Cys Ser Trp Phe
 35 40 45
 Leu Ile Gly Trp Gly Ile Cys Phe Gly Ala Asp Val Pro Leu Ser Phe
 50 55 60
 Gly His Gln Cys Ala Asp Val Arg Lys Ala Met Gln Glu Gly Lys Pro
 65 70 75 80
 Leu Leu Pro Ile Phe Asp Ala Phe Ile Arg Arg Ile Val Asn Asp Ser
 85 90 95
 Ser Ser Leu Ser Glu Lys Asp Trp Glu Thr Ala Thr Trp Leu Ile Cys
 100 105 110
 Glu Tyr Ile Arg Gly Ser Leu Lys Arg Gly Glu Gln Glu Leu Cys Ser
 115 120 125
 Glu Leu Val Lys Pro Leu Phe Ser Leu Ala Val Met Pro Pro Gln Ser
 130 135 140
 Lys Ala Arg Ile Lys Gln Val Trp Gln Val Leu Asn Pro Gln Gly Ala
 145 150 155 160
 Ser Leu Lys Asp Leu Val Arg Leu Leu Glu Ser Ser Gly Cys Ser Ser
 165 170 175
 Ser Pro Gln Asp His Leu Leu Leu Ser Leu Tyr Asn Met Thr Leu His
 180 185 190
 Ser Ser Tyr Glu Asn Lys Lys Ala Glu Ile Leu Phe Ala Arg Glu Gln
 195 200 205
 Lys Asn Tyr Gln Asp Ala Leu Arg Leu Cys Glu Glu Leu Gln Glu Asn
 210 215 220
 Leu Thr Ser Gly Leu Cys Ser Pro Leu Ser Thr Val Tyr Glu Val Glu
 225 230 235 240
 Gln Ala Phe Leu Lys Arg Ile Ser Leu Ala Ile Arg Trp Glu Gln Glu
 245 250 255
 Lys Glu Leu Gln Gly Ser Pro Ser Ile Glu Leu Leu Leu Ala Tyr Cys
 260 265 270
 Ser Ala Glu Glu Ser Tyr Ala Glu Ala Val Glu Gln Leu Ile Lys Lys
 275 280 285
 Ile Glu Leu Gly Ser Leu Asp Arg Ser Gln Glu Val Asp Ala Ile Leu
 290 295 300
 Phe Ala His Ala Leu Ser Lys Leu Pro Trp Glu Glu Thr Leu Gly Glu
 305 310 315 320
 His Glu Leu Glu Val Leu Ile Ser Gly Gly His Tyr Leu Thr Ser Ile
 325 330 335
 Tyr Ser Gln His Ala Tyr Phe Ser Leu Leu Glu Gln Tyr Phe Lys Lys
 340 345 350
 Ser Gln Ile Gln Glu Ile Ser Arg Leu Leu Asp Phe Gly Lys Thr Val
 355 360 365
 Phe Val Glu Thr His Lys Lys Tyr Pro Glu Tyr Leu Phe Phe Leu Gly
 370 375 380
 Lys Tyr Trp Phe Tyr Leu Arg Asp Phe Ser Arg Ala Glu Glu Ala Phe
 385 390 395 400
 Ser Ser Val Ile Arg Tyr Ala Asp Arg Leu Gly Val Ser Leu Ala Glu
 405 410 415
 Thr Tyr Glu Tyr Leu Gly Cys Leu Ala Cys Tyr Lys Gly His Tyr Ala
 420 425 430
 Ser Ala Lys Glu Phe Phe Leu Lys Ala Tyr Lys Gly Trp Gly Arg Glu
 435 440 445
 Asp Ala Gly Ile Gly Leu Tyr Leu Leu Ala Val Leu Glu Lys Asp Pro
 450 455 460
 Ile Leu Cys Gln Gln Val Arg Glu Gln Val Ser Leu Ser Phe Ser His
 465 470 475 480
 Gln Glu Phe Leu Lys Trp Met Asp Arg Asn Phe Leu Pro Glu Pro Gly
 485 490 495

```

Lys Glu Gly Ser Ser Phe Phe Lys Val Leu Gly Ser Ser Arg Xaa Leu
      500                      505                      510
Ser Glu Glu Glu Phe Tyr Gly Xaa Leu Leu Lys Glu Met Ile Ser Arg
      515                      520                      525
Xaa His Arg Glu Lys Leu Ser Cys Ser Pro Ile Gln Arg Leu Val Tyr
      530                      535                      540
Asp Gln Leu Asp Arg Glu Ile Gln Leu Arg Leu Thr Glu Thr Leu Ile
545      550                      555                      560
Gln Thr Glu Asp Leu Leu Val Arg Arg Lys Leu Ser Leu Trp Arg Ala
      565                      570                      575
Leu Tyr Glu Gly Ser Phe Val Ser Trp Gly Ser Ala His Gln Asn Gln
      580                      585                      590
Thr Leu Phe Glu Lys Ser Ile Leu Gln Cys Phe Ser Ala Leu Ser Gln
      595                      600                      605
Gln Asp Pro Ser Ala Ile Gln Gln Ile Ala Glu Ala Phe Ser Ser Gly
610      615                      620
Ala Ser Leu Trp Gln Ser Ser Leu Arg Met Val Trp Ala Val Ser His
625      630                      635                      640
Thr Ser Glu Asn Pro Ile Ser Lys Ala Tyr Ser Leu Gly Ile Ser Asp
      645                      650                      655
Arg Pro Trp Gly Asp Arg Leu Tyr Leu Leu Gln Tyr Ser Leu Glu Gln
      660                      665                      670
Tyr Leu Ser Gly Asp Thr Glu Leu Leu Glu Tyr Leu Thr Gln Phe Pro
      675                      680                      685
Glu Leu Phe Pro Asn Ser Pro Leu Leu Pro Leu Val Tyr Tyr Leu Gln
690      695                      700
Ala Arg Gly Glu Gly Asp Pro Ile Arg Lys Ile Ala Trp Leu Thr Lys
705      710                      715                      720
Ala Leu Glu Thr Phe Thr Glu Asn Ser Leu Leu Ala Lys Glu Met Lys
      725                      730                      735
Ala Trp Ala Pro Leu Tyr Tyr Leu Met Arg Met Asp Leu Ala Glu Thr
      740                      745                      750
Tyr Leu Tyr Leu Gly Asn Val Ser Lys Ser Asp Thr Leu Phe Glu Ala
      755                      760                      765
Ile Gln Glu Glu Trp Asp Ala Pro His His Pro Tyr Val Lys Leu Ile
770      775                      780
Asp Pro Pro His Ile Arg Val Ser Leu Glu Met Arg Trp Val Ser Gly
785      790                      795                      800
Leu Ala His Val Tyr Glu Ala Ile Gln Ala Thr Glu Gln Arg Asn Ala
      805                      810                      815
Leu Leu Ile Ser His Ile Glu Lys Arg Phe Phe Gln Thr Arg Pro Arg
      820                      825                      830
Gln Glu Tyr Ile Gly Lys Met Leu Thr Phe Thr Ser Ser Leu Cys Arg
      835                      840                      845
Glu Leu Leu Ala Asp Ala Ser Trp
850                      855

```

(2) INFORMATIONS POUR LA SEQ ID NO: 657:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 125 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 649970..650344

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 657:

Met	Ala	Leu	Lys	Asp	Thr	Ala	Lys	Lys	Met	Thr	Asp	Leu	Leu	Glu	Ser	15
1			5						10							
Ile	Gln	Gln	Asn	Leu	Leu	Lys	Ala	Glu	Lys	Gly	Asn	Lys	Ala	Ala	Ala	30
			20					25								
Gln	Arg	Val	Arg	Thr	Glu	Ser	Ile	Lys	Leu	Glu	Lys	Thr	Ala	Lys	Val	45
			35				40									
Tyr	Arg	Lys	Glu	Ser	Ile	Lys	Ala	Glu	Lys	Met	Gly	Leu	Met	Lys	Lys	60
			50			55										
Ser	Lys	Ala	Ala	Ala	Lys	Lys	Ala	Lys	Ala	Ala	Ala	Lys	Lys	Pro	Val	80
65					70				75							
Arg	Ala	Thr	Lys	Thr	Val	Ala	Lys	Lys	Ala	Cys	Thr	Lys	Arg	Thr	Cys	95
				85				90								
Ala	Thr	Lys	Ala	Lys	Val	Lys	Pro	Thr	Lys	Lys	Ala	Ala	Pro	Lys	Thr	110
			100				105									
Lys	Val	Lys	Thr	Ala	Lys	Lys	Thr	Arg	Ser	Thr	Lys	Lys				125
			115				120									

(2) INFORMATIONS POUR LA SEQ ID NO: 658:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 435 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 650418..651722

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 658:

Ser	Leu	Leu	Phe	Phe	Leu	Leu	Ser	Phe	Pro	Phe	Ser	Gln	Arg	Gln	Val	15
1			5					10								
Leu	Ala	Asn	Lys	Ser	Thr	Thr	Ser	His	Leu	Leu	Trp	Arg	Lys	Asn	Leu	30
			20				25									
Ser	Leu	Ser	Leu	Gly	Phe	Lys	Leu	Leu	Ser	Cys	Tyr	Arg	Asn	Cys	Lys	45
			35			40										
His	Phe	Gly	Val	Cys	Gly	Gly	Cys	Ser	Ser	Pro	Gln	Met	Glu	Tyr	Ala	60
			50		55											
Ser	Ser	Leu	Lys	Thr	Lys	Glu	Leu	Ala	Leu	His	Asn	Leu	Phe	Ala	Pro	80
65				70				75								
Leu	Ile	Pro	Ser	Gln	Asn	Ile	Leu	Pro	Val	Ile	Pro	Cys	Ser	Pro	Leu	95
			85			90										
Leu	Arg	Gly	Arg	Asn	Lys	Met	Glu	Phe	Ser	Phe	Tyr	Gln	Thr	Val	Asp	110
			100			105										
Gly	Glu	Lys	Thr	Leu	Gly	Phe	Ile	Ser	Pro	Ser	Lys	Pro	Lys	Lys	Gly	125
		115				120										
Ile	Pro	Ile	Thr	Glu	Cys	Leu	Met	Ile	Asp	Glu	Arg	Ala	Met	Asp	Ile	140
		130			135											
Leu	Asn	Ile	Thr	Arg	Ser	Trp	Trp	Thr	Ala	His	Pro	Asp	Leu	Ser	Ala	160
145				150				155								
Tyr	Tyr	Pro	Pro	Leu	Asn	Lys	Gly	Ser	Leu	Cys	Thr	Ile	Thr	Val	Arg	175
			165					170								
Val	Gly	Asn	Ile	Ser	Asn	Asp	Phe	Met	Ile	Ile	Leu	Thr	Thr	Ser	Gly	190
			180					185								

```

Arg Glu Glu Phe Ala Val Pro Leu Asn Ile Ile Gln Glu Trp Gln Gln
      195                200                205
Ser Leu Leu Asp Ser Gly Leu Pro Ile Thr Ser Ile Phe Trp Glu Glu
      210                215                220
Lys Leu Ser Ala Arg Asn Ser Pro Thr Thr Phe Arg Thr Thr His Leu
      225                230                235                240
Tyr Gly Ala Pro Phe Leu Lys Gln Gln Leu Ser Ile Asp Gly Arg Ser
      245                250                255
Ser Leu Phe His Ile Arg Pro Arg Ser Phe Phe Gln Pro Gln Ser Leu
      260                265                270
Gln Ala Glu Lys Ile Ile Gln Thr Ile Lys Glu Phe Ile Asp Pro Cys
      275                280                285
Gly Glu Glu Thr Leu Leu Asp Leu Tyr Cys Gly Ala Gly Thr Ile Gly
      290                295                300
Ile Leu Leu Ala Pro Tyr Val Lys Lys Ile Ile Gly Val Glu Leu Val
      305                310                315                320
Pro Asp Ala Val Ala Ser Ala Gln Glu Asn Ile Gln Leu Asn Ser Val
      325                330                335
Asp Met Glu Val Phe Leu Glu Asp Ala Lys Gln Phe Cys Lys Arg Asn
      340                345                350
Glu Asn Leu Pro Ser Pro Asp Ile Val Val Ile Asp Pro Pro Arg Cys
      355                360                365
Gly Met Gln Asn Lys Ala Leu Lys Tyr Leu Leu Arg Met Ala Pro Lys
      370                375                380
Lys Ile Val Tyr Val Ser Cys Asn Pro Leu Thr Gln Ile Gln Glu Cys
      385                390                395                400
Ser Val Leu Val Glu Gln Gly Tyr Gln Leu Arg His Met Gln Pro Ile
      405                410                415
Asp Gln Phe Pro His Thr Asn His Leu Glu Asn Ile Val Leu Leu Glu
      420                425                430
Arg Leu Ser
      435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 659:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 162 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 651686...652171

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 659:

```

Ser Phe Gly Lys Tyr Cys Ala Leu Arg Lys Ala Phe Leu Lys Gln Glu
1      5      10      15
Ser Leu Ile Pro Asn Ala Val Pro Ser Gly Lys Gly Leu Ile Pro Leu
      20      25      30
Ser Ser Cys Val Asn Leu Ser Phe Leu Thr Leu Ile Lys Gly Thr Ser
      35      40      45
Met Tyr Ser Arg Leu Phe Phe Ser Ile Leu Xaa Phe Leu Gly Cys Cys
      50      55      60
Pro Ala Leu Phe Ala Asp Thr Asp Ser Pro Gln Arg Ala Thr Phe Gly
      65      70      75      80
Gln Pro Ala Val Met Leu Gly Ile Ala Ile Val Phe Phe Tyr Phe Ile

```

(2) INFORMATION POUR LA SEQ ID NO: 660:

(A) LONGUEUR: 131 acides aminés

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 652516..652908

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 660:

(2) INFORMATION POUR LA SEQ ID NO: 661:

(A) LONGUEUR: 265 acides aminés

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 652799..653593

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 661:

```

Ile Leu Arg Ala Leu Phe Leu Leu Asn Leu Glu Ala Ile Tyr Lys Leu
1      5      10      15
Pro Phe Leu Leu Ile Lys Pro Ile Leu Ser Asp Trp Lys Gln Thr Met
      20      25      30
Asp Pro Gln Tyr Tyr Ser Asp Trp Glu Thr Phe His Leu Phe Asp Gln
      35      40      45
Val Ile Asp Asn Leu Ser Leu Asp Thr Asp Ser Ala Asn Lys Ala Tyr
      50      55      60
Ser Leu Ala Ser Tyr Pro Ala Glu Leu Pro Leu Ile Lys Phe Asn Val
65      70      75      80
Arg Ile Ala Thr Pro Ser Phe Val Asp Gln Ala Pro Asp Pro Thr Ile
      85      90      95
Pro Trp Gly Val Cys Ser Ser Tyr Ile Phe Ser Leu Lys Pro Gly Asp
      100      105      110
Lys Val Met Val Ser Gly Pro Tyr Gly Glu Ser Phe Met Lys Glu Asn
      115      120      125
Asn Arg Pro Val Ile Phe Leu Ile Gly Gly Ala Gly Ser Ser Phe Gly
      130      135      140
Arg Ser His Ile Leu Asp Leu Leu Leu Asn Lys His Ser Asp Arg Glu
145      150      155      160
Leu Thr Leu Trp Tyr Gly Ala Arg Ser Leu Lys Glu Asn Ile Tyr Gln
      165      170      175
Glu Glu Tyr Glu Lys Leu Glu Lys Glu Phe Pro Asn Phe His Tyr His
      180      185      190
Leu Val Leu Ser Gln Pro Leu Gln Glu Asp Leu Asp Gln Gly Trp Asp
      195      200      205
Lys Asn Asp Pro Ile Lys Thr Asn Phe Leu Phe Lys Ala Phe Glu Leu
      210      215      220
Gly Gln Leu Ser His Leu Pro Asn Pro Glu Asp Tyr Leu Tyr Tyr Val
225      230      235      240
Cys Gly Pro Ala Leu His Asn Ser Ser Ile Leu Thr Val Leu Asp Asn
      245      250      255
Tyr Gly Val Ser Ala Leu Leu Leu Phe
      260      265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 662:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 572 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 660136..661851

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 662:

```

Met Lys Arg Thr Pro Ala Pro Leu Ala Phe Arg Lys Ala Ala Ala Phe
1      5      10      15
Gly Ala Ile Pro Val Cys Cys Ala Val Leu Leu Ser Met Ile Ser Pro
      20      25      30
Ala Gln Asn Leu Pro Gln Phe Leu Ala Thr Arg Val Pro Met Val Val
      35      40      45
Met Asp Leu Gln Pro Pro Lys Ala Tyr Leu Gly Gly Ile Pro Phe Tyr

```

50 55 60
 Leu Leu Tyr Asp Gly Asn Ser Phe Ser Leu Lys Leu Leu Ile Gly Ala
 65 70 75 80
 Val Gly Thr Gly Leu Ile Phe Leu Ala Ile Leu Leu Cys Ala Ile Phe
 85 90 95
 Tyr Leu Ile Pro Lys Ser Phe Val Leu Lys Lys Lys Ala Leu Leu Asp
 100 105 110
 Asp Leu Leu Lys Phe Leu Lys Asn Lys Phe Tyr Ala Cys Trp Asn Ala
 115 120 125
 Cys Lys Lys Leu Leu Lys Asn Leu Val Asn Asn Lys Ser Tyr Val Pro
 130 135 140
 Glu Pro Ser Leu Arg Val Pro Ser Ser Pro Ser Val Ala Lys Lys Glu
 145 150 155 160
 Met Leu Lys Leu Pro Thr Pro Val Ile Ser Leu Pro Leu Glu Asn Lys
 165 170 175
 Asp Leu His Asp Asp Ser Ser Val Asn Arg Thr Ile Phe Leu Thr Pro
 180 185 190
 Pro His Pro Thr Lys Arg Thr Leu Ser Pro Gln Lys Arg Thr Asp Leu
 195 200 205
 Pro Asn Leu Leu Pro Lys Asp Ser Ala Ser Ala Pro Ala Gln Thr Ser
 210 215 220
 Tyr Lys Pro Leu Pro Thr Pro Ser Pro Phe Val Leu Ala Gly Asp Ala
 225 230 235 240
 Pro Asp Leu Pro Gln Tyr His Leu Leu Ser Lys Arg Asn Val Arg Arg
 245 250 255
 Pro Glu Ser Leu Leu Glu Glu Leu Lys Lys Lys Ala Ala Ile Leu Gln
 260 265 270
 Gln Thr Leu Ala Ser Phe Gly Ile Glu Ala Ala Ile Gly Asn Ile Cys
 275 280 285
 Ser Gly Pro Thr Leu Ala Ala Phe Glu Val Leu Pro Asn Thr Gly Val
 290 295 300
 Lys Val Gln Lys Ile Lys Ala Leu Glu Asn Asp Ile Ala Leu Asn Leu
 305 310 315 320
 Gln Ala Ser Ser Ile Arg Ile Ile Ala Pro Ile Pro Gly Lys Ala Ala
 325 330 335
 Val Gly Ile Glu Ile Pro Asn Pro Asp Pro Gln Pro Val Asn Phe Arg
 340 345 350
 Asp Leu Leu Glu Asp Tyr Gln Lys Gly Thr Gln Arg Leu Gln Val Pro
 355 360 365
 Leu Leu Leu Gly Arg Lys Ala Asn Gly Asp Asn Phe Trp Thr Asp Leu
 370 375 380
 Ala Thr Met Pro His Leu Ile Ile Ala Gly Thr Thr Gly Ser Gly Lys
 385 390 395 400
 Ser Val Cys Ile Asn Thr Ile Val Met Ser Leu Ile Met Thr Ser Pro
 405 410 415
 Pro Thr Asp Ile Lys Leu Val Ile Val Asp Pro Lys Lys Val Glu Leu
 420 425 430
 Thr Gly Tyr Ser Gln Leu Pro His Met Leu Thr Pro Val Ile Thr Glu
 435 440 445
 Ser Lys Glu Ala His Ser Ala Leu Ile Trp Leu Val Arg Glu Met Glu
 450 455 460
 Leu Arg Tyr Glu Ile Leu Arg Phe Leu Gly Leu Arg Asn Ile Gln Ser
 465 470 475 480
 Phe Asn Ser Arg Thr Arg Asn Val Asp Ile Glu Ala Ser Tyr Asp Lys
 485 490 495
 Glu Ile Pro Glu Lys Met Pro Phe Ile Val Gly Ile Ile Asp Glu Leu
 500 505 510
 Ser Asp Leu Leu Ser Ser Ser His Asp Ile Glu Thr Pro Ile Val
 515 520 525


```

Arg Leu Ala Gln Met Ala Arg Ala Val Gly Ile His Leu Ile Leu Ala
530                      535                      540
Thr Gln Arg Pro Ser Arg Asp Val Ile Thr Gly Ile Ile Lys Ala Asn
545                      550                      555                      560
Ser Leu Leu Glu Ser Pro Leu Lys Leu Pro Thr Lys
565                      570

```

(2) INFORMATIONS POUR LA SEQ ID NO: 663:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 181 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 661740..662282

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 663:

```

Ser Cys Arg Asn Pro Pro Asn Leu Ser Asn Thr Thr Pro Phe Ser Arg
1      5      10      15
Cys Asp His Arg Asn Asn Gln Ser Lys Phe Pro Ser Arg Ile Ala Phe
20     25     30
Lys Val Ala Asn Lys Val Asn Ser Gln Ile Ile Ile Asp Glu Pro Gly
35     40     45
Ala Glu Asn Leu Met Gly Asn Gly Asp Met Leu Val Val Ser Pro Gly
50     55     60
Ser Phe Ala Pro Val Arg Val Gln Gly Ala Tyr Ile Cys Asp Asp Asp
65     70     75     80
Ile Asn Lys Val Ile Lys Asp Leu Cys Ser Arg Phe Pro Cys Lys Tyr
85     90     95
Val Ile Pro Ser Phe Asn Thr Tyr Asp Asp Pro Gly Ser Met Asp Pro
100    105    110
Glu Asp Leu Asp Pro Leu Phe Asn Gln Ala Lys Thr Leu Val Leu Gln
115    120    125
Thr Gly Asn Ala Ser Thr Thr Phe Leu Gln Arg Lys Leu Lys Ile Gly
130    135    140
Tyr Ala Arg Ala Ala Ser Ile Ile Asp Gln Leu Glu Glu Ala Arg Ile
145    150    155    160
Val Gly Pro Ser Glu Gly Ala Lys Pro Arg Gln Ile Leu Val Gln Leu
165    170    175
Ser Asn Gln Asp Asp
180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 664:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 263 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 662286..663074

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 664:

```

Ser Met Glu Gly Phe Cys Pro Ile Ala Ser Gly Ser Lys Gly Asn Cys
1      5      10      15
Ala Tyr Leu Gly Thr Arg Ser Cys Lys Leu Leu Ile Asp Leu Gly Ile
20      25      30
Ser Lys Gln Ala Val Thr Glu Ala Leu His Ser Met Gly Ile His Pro
35      40      45
Glu Asp Ile Gln Gly Ile Phe Val Thr His Glu His Ser Asp His Ile
50      55      60
Ala Gly Leu Arg Ser Phe Ile Lys Thr Tyr Arg Thr Pro Ile Ile Cys
65      70      75      80
Asn Ile Glu Thr Ala Arg Ser Leu Arg Gln Leu Leu Asp Leu Cys Pro
85      90      95
Thr Phe Lys Ile Phe Thr Thr Gly His Arg Phe Ser Leu Glu Asp Leu
100     105     110
Arg Val Gln Thr Phe Asn Val Pro His Asp Ala Val Asp Pro Val Gly
115     120     125
Phe Ile Phe Gln Tyr Ser Gly Met Lys Leu Gly Phe Cys Thr Asp Leu
130     135     140
Gly Trp Val Thr Ser Trp Ile Thr His Leu Leu Cys Asp Cys Asp Tyr
145     150     155     160
Leu Leu Ile Glu Ser Asn His Asp Pro Glu Met Val Leu Arg Ser Ser
165     170     175
Arg Pro Glu Ser Cys Lys Gln Arg Ile Leu Ser Lys Gln Gly His Ile
180     185     190
Ser Asn Ala Glu Cys Gly Ala Leu Leu Gln Arg Val Leu Thr Pro Arg
195     200     205
Ile Lys Lys Ile Tyr Leu Ala His Leu Ser Leu Glu Cys Asn Thr Ala
210     215     220
Glu Gln Ala Leu Asn Thr Val Thr Ser Ala Ile Gln Glu Ile Thr Asp
225     230     235     240
Val His Pro Val Ile Ala Gln Ser Ser Gly Ile Thr Asp Pro Ile Phe
245     250     255
Phe Ser Ala Pro Ser Leu Val
260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 665:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 260 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 662951..663730

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 665:

```

Tyr Gly Arg Ala Ser Phe Glu Tyr Ser Asp Val Cys His Ser Arg Asp
1      5      10      15
His Arg Cys Ser Ser Arg Asn Cys Ser Lys Phe Trp His Tyr Arg Ser
20      25      30
Tyr Phe Leu Phe Cys Ser Glu Pro Cys Met Thr Thr Asn Ser Thr Gln
35      40      45

```

```

Asp Thr Leu Tyr Leu Ser Leu His Gly Gly Ile Asp Ser Ala Ile Pro
 50          55          60
Tyr Pro Val Arg Arg Val Glu Gln Leu Leu Gln Phe Ser Phe Leu Pro
 65          70          75          80
Glu Leu Gln Phe Gln Asn Ala Ala Val Lys Gln Arg Ile Gln Arg Leu
          85          90          95
Cys Tyr Arg Glu Glu Lys Arg Leu Ala Val Ser Ser Leu Ala Lys Trp
          100          105          110
Leu Gly Gln Leu His Lys Gln His Leu Arg Ala Pro Lys Asn Pro Pro
          115          120          125
Val Ala Ile Cys Trp Ile Asn Ser Tyr Val Gly Tyr Gly Val Phe Ala
          130          135          140
Arg Glu Ser Ile Pro Ala Trp Ser Tyr Ile Gly Glu Tyr Thr Gly Ile
 145          150          155          160
Leu Arg Arg Arg Gln Ala Leu Trp Leu Asp Glu Asn Asp Tyr Cys Phe
          165          170          175
Arg Tyr Pro Val Pro Arg Tyr Ser Phe Arg Tyr Phe Thr Ile Asp Ser
          180          185          190
Gly Met Gln Gly Asn Val Thr Arg Phe Ile Asn His Ser Asp Asn Pro
          195          200          205
Asn Leu Glu Ala Ile Gly Ala Phe Glu Asn Gly Ile Phe His Ile Ile
 210          215          220
Ile Arg Ala Ile Lys Asp Ile Leu Pro Gly Glu Glu Leu Cys Tyr His
 225          230          235          240
Tyr Gly Pro Leu Tyr Trp Lys His Arg Lys Lys Arg Glu Glu Phe Val
          245          250          255
Pro Gln Glu Glu
          260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 666:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 156 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(663745..664212)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 666:

```

Ile Gln Glu Thr Ser Ile Met Gln Leu Thr Ser Gln Ala Phe Ser Tyr
 1          5          10          15
Gly Arg Pro Ile Pro Lys Lys Tyr Ser Cys Gln Gly Val Gly Ile Ser
          20          25          30
Pro Pro Leu Ser Phe Ser Asp Val Pro Arg Glu Ala Lys Ser Leu Val
          35          40          45
Leu Ile Val Glu Asp Pro Asp Val Pro Pro Ser Val Arg Glu Asp Gly
 50          55          60
Leu Trp Ile His Trp Ile Val Tyr Asn Leu Ser Pro Val Val Ser Asn
 65          70          75          80
Leu Ala Glu Gly Ala Gln Ile Phe Ala Val Gln Gly Leu Asn Thr Ala
          85          90          95
Gly Glu Ile Gly Tyr Cys Pro Pro Cys Pro Pro Asp Ala Lys His Arg
          100          105          110
Tyr Tyr Phe Tyr Ala Tyr Ala Leu Asp Val Val Leu Ser Asp Glu Glu

```

Pro Val Ile Val Ala Val Val Cys Ser Ile Thr Met Met Val Leu Leu
 305 310 315 320
 Val Thr Gly Ala Tyr Asp Ser Gly Glu Leu Gly Val Leu Met Val Met
 325 330 335
 Asn Ala Phe Lys Ser Ser Leu Gly Met Leu Gly Gly Ser Val Val Leu
 340 345 350
 Ile Ser Met Ile Leu Phe Gly Tyr Thr Thr Ala Leu Ser Trp Phe Ala
 355 360 365
 Cys Ala Glu Lys Ser Leu Glu Tyr Met Ile Pro Gly Lys Arg Ala Asn
 370 375 380
 Leu Leu Leu Lys Ala Ile Tyr Ile Ala Ile Ile Pro Met Gly Gly Val
 385 390 395 400
 Leu Gly Met Gln Phe Ile Trp Ala Leu Ser Asp Leu Gly Phe Cys Gly
 405 410 415
 Met Val Ile Phe Asn Ser Ile Ser Leu Ile Ala Leu Phe Arg Glu Val
 420 425 430
 Ile Ala Thr Arg Tyr Glu Val Ala Leu Leu Arg Lys Glu Ala Gln Ala
 435 440 445
 Gln Ser Asp Pro Leu Arg Gln
 450 455

(2) INFORMATIONS POUR LA SEQ ID NO: 668:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 119 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(665727..666083)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 668:

Cys Leu Leu Leu Leu Ile Ser Leu Leu Leu Leu Trp Leu Trp Leu Arg
 1 5 10 15
 Gly Lys Leu Lys Ala His Tyr Arg Val Leu Glu Arg Ser Ile Leu Leu
 20 25 30
 His Leu Leu Gln Ala Leu Ala Glu Asp Pro Ala Leu Ile Ala Gly Met
 35 40 45
 Lys Lys Met Gln Gly Arg Asp Trp Val Trp Asn Ile Phe Ile Thr Glu
 50 55 60
 Leu Ser Lys Val Phe Ser Gln Ala Ala Ser Leu Gly Leu Ser Ala Leu
 65 70 75 80
 Gln Thr Phe Ala Ala Phe Ala Ser Thr Leu Gly Leu Asp Ser Gly Thr
 85 90 95
 Val Thr Ser Ile Val Asp Gly Glu Arg Trp Ala Glu Leu Ile Asp Val
 100 105 110
 Val Ile Gln Asn Pro Ala Ile
 115

(2) INFORMATIONS POUR LA SEQ ID NO: 669:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 214 acides aminés
- (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(665782..666423)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 669:

Tyr	Tyr	Lys	Phe	Ile	Phe	Asn	Phe	Gly	Arg	Phe	Met	Lys	Lys	Phe	Ile
1				5					10					15	
Tyr	Lys	Tyr	Ser	Phe	Gly	Ala	Leu	Leu	Leu	Leu	Ser	Gly	Leu	Ser	Gly
			20					25					30		
Leu	Ser	Ser	Cys	Cys	Ala	Asn	Ser	Tyr	Gly	Ser	Thr	Leu	Ala	Lys	Asn
		35					40					45			
Thr	Ala	Glu	Ile	Lys	Glu	Glu	Ser	Val	Ile	Leu	Arg	Glu	Lys	Pro	Asp
	50					55					60				
Ala	Gly	Cys	Lys	Lys	Lys	Ser	Ser	Cys	Tyr	Leu	Arg	Lys	Phe	Phe	Ser
65					70					75					80
Arg	Lys	Lys	Pro	Lys	Glu	Lys	Thr	Glu	Pro	Val	Leu	Pro	Asn	Phe	Lys
				85					90					95	
Ser	Tyr	Ala	Asp	Pro	Met	Thr	Asp	Ser	Glu	Arg	Lys	Asp	Leu	Ser	Phe
			100					105					110		
Val	Val	Ser	Ala	Ala	Ala	Asp	Lys	Ser	Ser	Ile	Ala	Leu	Ala	Met	Ala
		115					120					125			
Gln	Gly	Glu	Ile	Lys	Gly	Ala	Leu	Ser	Arg	Ile	Arg	Glu	Ile	His	Pro
	130					135					140				
Leu	Ala	Phe	Val	Thr	Ser	Cys	Arg	Arg	Ser	Cys	Phe	Asn	Cys	Trp	
145					150				155					160	
Asn	Glu	Lys	Asp	Ala	Arg	Thr	Gly	Leu	Gly	Leu	Glu	Tyr	Leu	Tyr	His
				165					170					175	
Arg	Ile	Lys	Gln	Ser	Phe	Phe	Ser	Ser	Ser	Ile	Phe	Arg	Ala	Phe	Ser
			180					185					190		
Val	Ala	Asp	Val	Cys	Arg	Val	Arg	Val	Asp	Leu	Arg	Ile	Arg	Leu	Gly
		195					200					205			
Asp	Arg	Tyr	Leu	Asn	Cys										
															210

(2) INFORMATIONS POUR LA SEQ ID NO: 670:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 429 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 666831..668117

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 670:

Cys	Pro	Cys	Phe	Leu	Ser	Thr	Ser	Thr	Ser	Arg	Asn	Val	Pro	Ser	Ser
1				5					10					15	
Thr	Thr	Lys	Ile	Gly	Ser	Glu	Val	Trp	Ile	Glu	Gln	Lys	Val	Arg	Gln
			20					25					30		
Tyr	Pro	Glu	Leu	Leu	Trp	Leu	Val	Glu	Pro	Ser	Ser	Thr	Gly	Ala	Ser
			35				40						45		

Leu Lys Ser Pro Ser Gly Ala Ile Phe Ser Pro Thr Leu Phe Gln Lys
 50 55 60
 Lys Val Pro Ala Phe Asp Ile Ala Val Arg Ser Leu Ile His Leu His
 65 70 75 80
 Leu Leu Ile Gln Gly Ser Arg Gln Ala Tyr Ala Gln Leu Ile Gln Leu
 85 90 95
 Gln Thr Ser Glu Ser Pro Leu Thr Phe Lys Gln Phe Leu Ala Leu His
 100 105 110
 Lys Gln Leu Thr Leu Phe Leu Asn Ser Pro Lys Glu Phe Tyr Asp Ser
 115 120 125
 Val Lys Val Leu Glu Thr Ala Ile Val Leu Arg His Leu Gly Cys Ser
 130 135 140
 Thr Lys Ala Val Ala Ala Phe Lys Pro Tyr Phe Ser Glu Met Gln Arg
 145 150 155 160
 Glu Thr Phe Tyr Thr Lys Ala Leu His Val Leu His Thr Phe Pro Glu
 165 170 175
 Leu Ser Pro Ser Phe Ala Arg Leu Ser Pro Glu Gln Lys Thr Leu Phe
 180 185 190
 Phe Ser Leu Arg Lys Leu Ala Asn Tyr Asp Glu Leu Leu Ser Leu Thr
 195 200 205
 Asn Thr Pro Ser Phe Gln Leu Leu Ser Ala Gly Arg Ser Gln Arg Ala
 210 215 220
 Leu Leu Ala Leu Asp Leu Tyr Leu Tyr Ala Leu Asp Ser Cys Gly Glu
 225 230 235 240
 Gln Gly Met Ser Ser Gln Phe His Thr Asn Phe Ala Pro Leu Gln Ser
 245 250 255
 Met Leu Gln Gln Tyr Ala Thr Val Glu Glu Ala Phe Ser Arg Tyr Phe
 260 265 270
 Thr Tyr Arg Ala Asn Arg Leu Gly Phe Asp Gly Ser Ser Arg Ser Glu
 275 280 285
 Met Ala Leu Val Arg Met Ala Thr Leu Met Asn Leu Ser Pro Ser Glu
 290 295 300
 Ala Ala Ile Leu Thr Thr Ser Phe Lys Thr Leu Pro Thr Glu Glu Ala
 305 310 315 320
 Asp Thr Leu Val Asn Ser Phe Tyr Thr Asn Lys Gly Asp Ser Leu Ala
 325 330 335
 Leu Ser Leu Arg Gly Leu Pro Thr Leu Val Ser Glu Leu Thr Arg Thr
 340 345 350
 Ala Arg Gly Asn Thr Asn Ala Glu Ala Arg Ser Gln Gln Ile Tyr Ala
 355 360 365
 Thr Thr Leu Ser Leu Val Ala Lys Ser Leu Lys Ala His Lys Glu Met
 370 375 380
 Leu Asn Lys Gln Ile Leu Ser Lys Glu Ile Val Leu Asp Phe Ser Glu
 385 390 395 400
 Thr Ala Ala Ser Cys Gln Gly Leu Asp Ile Phe Ser Glu Asn Val Ala
 405 410 415
 Val Gln Ile His Leu Asn Gly Thr Val Ser Ile His Leu
 420 425

(2) INFORMATIONS POUR LA SEQ ID NO: 671:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 668121..668375

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 671:

Ser	Lys	Lys	Thr	Pro	Asp	Leu	Ile	Arg	Arg	Ser	Ser	Phe	Ser	Thr	Pro
1				5					10				15		
Phe	Tyr	Ser	Phe	Pro	Ile	Arg	Glu	Asn	Asn	Asp	Ala	Ile	Ser	Lys	Ala
			20				25					30			
Val	Phe	Met	Pro	Glu	Ala	Pro	Lys	Leu	Gly	Pro	Leu	Ile	Pro	Ala	Arg
		35					40					45			
Ser	Gln	Ala	Ala	Ser	Ile	Leu	Gly	Ala	Val	Ile	Thr	Glu	Asn	Val	Ile
	50				55					60					
Gly	Arg	Gln	Lys	Ser	Lys	Asp	Arg	Arg	Leu	Thr	Pro	Ala	Ala	Thr	Leu
65					70				75						80
Ser	Ala	Ile	Cys	Ser											
					85										

(2) INFORMATIONS POUR LA SEQ ID NO: 672:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(668174..668470)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 672:

Ile	Pro	Cys	Ala	Ile	Lys	Lys	Leu	Leu	Ser	Thr	Ser	Gly	Gln	Phe	His
1				5					10					15	
Ala	Val	Val	Ala	Cys	Gly	Val	Leu	Ile	Gln	Gly	Glu	Thr	Ser	His	Tyr
			20				25						30		
Glu	His	Ile	Ala	Asp	Ser	Val	Ala	Ala	Gly	Val	Ser	Arg	Leu	Ser	Leu
		35					40					45			
Asp	Phe	Cys	Leu	Pro	Ile	Thr	Phe	Ser	Val	Ile	Thr	Ala	Pro	Asn	Met
	50				55					60					
Glu	Ala	Ala	Trp	Glu	Arg	Ala	Gly	Ile	Lys	Gly	Pro	Asn	Leu	Gly	Ala
65					70				75						80
Ser	Gly	Met	Lys	Thr	Ala	Leu	Glu	Met	Ala	Ser	Leu	Phe	Ser	Leu	Ile
				85					90					95	
Gly	Lys	Glu													

(2) INFORMATIONS POUR LA SEQ ID NO: 673:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 306 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(668616..669533)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 673:

```

Ser Gly Ser Asp Ser Glu Ser Phe Val Arg Pro Gly His Val Phe Pro
1      5      10      15
Leu Ile Ser Gln Pro Gly Gly Val Val Gln Arg Pro Gly His Thr Glu
20      25      30
Ala Ala Met Asp Leu Met Arg Leu Ala Gly Met Gln Pro Cys Gly Ile
35      40      45
Phe Ala Glu Leu Val Asn Pro Asp His Ser Met Met Arg Gln Gln Gln
50      55      60
Val Leu Ala Phe Ala Glu Gln His Asp Leu Thr Val Ile Thr Val Asp
65      70      75      80
Asp Leu Ile Thr Tyr Arg Tyr Thr Tyr Asp Ser Leu Val Thr Lys Ile
85      90      95
Ser Ser Ala Arg Leu Pro Thr Lys Tyr Gly Asp Phe Ser Ile Tyr Val
100      105      110
Tyr Glu Ser Ile Ile Asp Gly Thr Gln His Phe Ala Leu Val Lys Gly
115      120      125
Asp Ile His Glu Gln Glu Ala Val Pro Val Arg Val His Ser Glu Cys
130      135      140
Leu Thr Gly Asp Ile Leu Gly Ser Cys Arg Cys Asp Cys Gly Ala Gln
145      150      155      160
Leu Asp Met Ala Met Arg Tyr Ile Ala Glu Glu Gly Leu Gly Val Ile
165      170      175
Val Tyr Leu Arg Gly Gln Glu Gly Arg Gly Ile Gly Phe Gly His Lys
180      185      190
Ile Arg Ala Tyr Ala Leu Gln Asp Leu Gly Tyr Asp Thr Val Asp Ala
195      200      205
Asn Leu Gln Leu Gly Phe Pro Ile Asp Ala Arg Glu Tyr Gly Met Ala
210      215      220
Ala Gln Val Leu Lys Asp Leu Gln Leu Thr Ser Val Arg Leu Ile Thr
225      230      235      240
His Asn Pro Arg Lys Phe Phe Glu Leu Gln Arg Leu Gly Ile His Val
245      250      255
Leu Asp Arg Ile Ile Leu Pro Val Ser Ile Ser Thr Glu Asn Glu Gly
260      265      270
Tyr Leu Arg Thr Lys Lys Glu Arg Met Gly His Trp Leu Asp Leu Pro
275      280      285
Val Leu Asp Asp Val Glu Glu Glu Tyr Glu Thr Val Glu Arg Met Ser
290      295      300
Cys Arg
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 674:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 128 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(669485..669868)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 674:


```

Gly Ile Ala Ser Val Gln Gln Ala Ile Lys Asp Val Ala Glu Gly Lys
1           5           10           15
Phe Val Ile Val Ile Asp Ala Ala Ser Arg Glu Asn Glu Gly Asp Leu
           20           25           30
Ile Leu Ala Gly Glu Lys Val Ser Thr Glu Lys Met Ser Phe Leu Leu
           35           40           45
Ser His Thr Thr Gly Ile Val Cys Ala Ser Leu Ser Arg Glu Gln Ala
           50           55           60
Lys Ser Leu Asp Leu Pro Ala Met Val Gln Asp Asn Gln Cys Ala Phe
65           70           75           80
Lys Thr Ala Phe Thr Val Ser Val Asp Ala Ser Ser Gly Val Thr Thr
           85           90           95
Gly Val Ser Ala Ser Asp Arg Thr Arg Thr Val Gln Leu Leu Ala Asp
           100          105          110
Pro Ala Ala Thr Ala Ser Pro Leu Phe Asp Gln Gly Met Phe Ser Leu
           115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 675:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(669998..670780)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 675:

```

Lys Arg Arg Thr Arg Leu Gln Ala Ala Gly Ile Pro Val Tyr Val Gly
1           5           10           15
Val Gly Ser Gln Glu Ala Lys Thr Ser Leu Gln Pro Tyr Leu Tyr Gln
           20           25           30
Arg Glu Arg Gly Leu Pro Trp Val Val Met Lys Thr Ala Ala Ser Leu
           35           40           45
Asp Gly Gln Thr Ala Asp Arg Gly Gly Ser Ser Gln Trp Ile Ser Gly
           50           55           60
Glu Leu Ala Arg Ala Asp Val Gly Lys Leu Arg Ala Glu Ser Gln Ala
65           70           75           80
Ile Ile Val Gly Ala Arg Thr Val Cys Leu Asp Asn Pro Arg Leu Ser
           85           90           95
Ala Arg Phe Pro His Gly Asp Leu Tyr Glu Arg Gln Pro Leu Arg Val
           100          105          110
Val Val Asp Ser Arg Gly Thr Val Pro Leu Glu Ser Arg Val Phe Asp
           115          120          125
Leu Ser Ser Gly Ser Thr Leu Phe Ala Thr Thr Gln Gln Cys Pro Lys
           130          135          140
Glu Tyr Ile Gln Lys Leu Lys Asp Leu Gly Val Glu Val Trp Glu Ser
145          150          155          160
Ser Ser His Gln Val Asp Leu Lys Gly Leu Leu Arg Tyr Leu Ala Glu
           165          170          175
Arg Gly Cys Leu Gln Val Leu Val Glu Gly Gly Ala Gln Leu His Ser
           180          185          190
Ala Phe Trp Gln Gln Lys Leu Val Asn Ala Gly Val Ile Tyr Trp Gly
           195          200          205

```

Pro Lys Phe Leu Gly Asp Gln Gly Gln Pro Met Leu Arg Asp Leu Gln
 210 215 220
 Leu Ser Leu Val Thr Ala Glu His Val Arg Ile Thr Glu Thr Ser Leu
 225 230 235 240
 Val Arg Asp Ser Val Lys Thr Cys Phe Glu Cys Leu Glu Gln Glu Ser
 245 250 255
 Val Asp Lys Lys Gly
 260

(2) INFORMATIONS POUR LA SEQ ID NO: 676:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(670732..671241)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 676:

Arg Asn Xaa Xaa Xaa Leu Phe Phe Glu Asp Gly Phe Arg Thr Leu Leu
 1 5 10 15
 Val Pro Cys Val Leu Ile Val Tyr Pro Thr Ser Leu His Leu Phe Arg
 20 25 30
 Tyr Leu Ile Phe Gln Val Glu Tyr Met Glu Val Leu Ser Glu Gln Gln
 35 40 45
 Leu Phe Phe Met Arg Lys Ala Val Ala Leu Gly Glu Lys Gly Arg Ile
 50 55 60
 Phe Ala Pro Pro Asn Pro Trp Val Gly Cys Val Ile Val Lys Asn Gly
 65 70 75 80
 Cys Val Ile Gly Glu Gly Trp His Gln Gly Ile Gly Ser Pro His Ala
 85 90 95
 Glu Val Cys Ala Val Gln Asp Gln Lys Cys Ser Leu Glu Gly Ala Glu
 100 105 110
 Val Tyr Val Thr Leu Glu Pro Cys Cys His Phe Gly Arg Thr Pro Pro
 115 120 125
 Cys Val Asp Leu Leu Ile Lys Ser Lys Val Ala Ala Val Tyr Val Gly
 130 135 140
 Leu Leu Asp Pro Asp Pro Arg Val Cys Lys Lys Gly Val Pro Val Cys
 145 150 155 160
 Lys Gln Gln Gly Phe Pro Phe Met Leu Gly
 165 170

(2) INFORMATIONS POUR LA SEQ ID NO: 677:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 422 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 671182..672447

(2) INFORMATIONS POUR LA SEQ ID NO: 678:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 180 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 672692..673231

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 678:

Pro	Leu	Met	Glu	Lys	Ser	Tyr	Ser	Gln	Leu	Gly	Ser	Val	Gly	Phe	Phe	1	5	10	15
Ile	Pro	Ala	Val	Ser	Glu	Ala	Gln	Ala	Ala	Trp	Ala	Tyr	Ile	Glu	Leu	20	25	30	
Thr	His	Arg	Asn	Met	Leu	Gln	Glu	Lys	Lys	Glu	Ile	Glu	Thr	Asn	Pro	35	40	45	
Glu	Gln	Glu	Arg	Ile	Glu	Leu	Ala	Val	Leu	Tyr	Ala	Asn	Gln	Gly	Phe	50	55	60	
Gln	Glu	Pro	Leu	Ile	Ser	Gln	Met	Leu	Asp	Phe	Val	Cys	Ser	Asp	Ser	65	70	75	80
Ser	Leu	Leu	Leu	Ser	Thr	Met	Leu	Arg	Glu	Glu	Leu	His	Ile	Gln	Leu	85	90	95	
Glu	Asp	Tyr	Pro	His	Pro	Leu	Lys	Gln	Gly	Asn	Val	Lys	Ala	Leu	Gly	100	105	110	
Gly	Ile	Leu	Gly	Leu	Leu	Leu	Phe	Ala	Pro	Ile	Thr	Leu	Ala	Val	Ser	115	120	125	
Tyr	Thr	Ile	Ala	Ala	Ile	Leu	Ala	Ser	Phe	Met	Ile	Gly	Val	Leu	Phe	130	135	140	
Ala	Val	Lys	Thr	Arg	Leu	Ile	Lys	Asn	Ala	Ile	Thr	Pro	Ala	Ile	Val	145	150	155	160
Trp	Gly	Val	Gly	Met	Phe	Ile	Thr	Ala	Ile	Ser	Leu	Cys	Cys	Ser	Leu	165	170	175	
Ile	Arg	Leu	Phe													180			

(2) INFORMATIONS POUR LA SEQ ID NO: 679:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 453 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 673204..674562

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 679:

Pro	Leu	Leu	Leu	Phe	Asp	Pro	Ile	Ile	Leu	Val	His	Thr	Leu	Ser	Arg	1	5	10	15
Trp	Pro	Met	Ser	Pro	Gln	Leu	Phe	Ser	Ser	Pro	Phe	Ser	Arg	Glu	Leu	20	25	30	
Leu	Ser	Asp	Phe	Phe	Glu	Ser	Gly	Met	Ala	Glu	Glu	Asn	Ser	Pro	Leu				

35 40 45
 Leu Ser Gln Lys Asn Arg Arg Leu Ser Gln Asn Leu Thr Leu Lys Ser
 50 55 60
 Ala Tyr Ile Ser Leu Ala Leu Tyr Leu Gly Ser Leu Leu Ser His Trp
 65 70 75 80
 Ile Gly Tyr Gln Ala Leu Ser Ser Leu Leu Leu Ile Leu Thr Phe Phe
 85 90 95
 Leu Ala Gly Thr Pro Ala Leu Ile Lys Ser Phe Glu Asp Ile Leu Asp
 100 105 110
 Arg Thr Val Asn Ile Asp Ile Leu Met Thr Ser Ala Ala Phe Gly Ser
 115 120 125
 Ile Phe Ile Gly Gly Ala Leu Gly Gly Ala Leu Leu Leu Val Leu Phe
 130 135 140
 Ala Ile Ser Glu Ser Leu Gly Ala Met Val Ser Gly Lys Ala Lys Ser
 145 150 155 160
 Thr Leu Ala Ser Leu Lys His Leu Ala Pro Thr Val Ala Trp Val Val
 165 170 175
 Gln Gln Asp Gly Ser Leu Gln Lys Val Leu Val Gln Asn Val Lys Ile
 180 185 190
 Gly Glu Ile Ile Arg Val Lys Ser Gly Glu Val Val Pro Leu Asp Gly
 195 200 205
 Lys Ile Ile His Gly Ala Ser Ser Ile Asn Leu Met His Leu Thr Gly
 210 215 220
 Glu Lys Ile Pro Lys Ser Cys Gly Ile Gly Asp Thr Ile Pro Ala Gly
 225 230 235 240
 Ala His Asn Leu Glu Gly Ser Phe Asp Leu Gln Val Leu Arg Ile Gly
 245 250 255
 Ala Glu Ser Thr Ile Ala His Ile Ile Asn Leu Val Val Gln Ala Gln
 260 265 270
 Ser Ser Lys Pro Lys Leu Gln Gln Arg Leu Asp Arg Tyr Ser Ser Thr
 275 280 285
 Tyr Ala Leu Thr Ile Phe Ala Ile Ser Ala Cys Ile Ala Ile Gly Gly
 290 295 300
 Ser Leu Phe Thr Thr Leu Pro Phe Leu Gly Pro Asp Gly Ala Phe Tyr
 305 310 315 320
 Arg Ala Leu Ala Phe Leu Ile Ala Ala Ser Pro Cys Ala Leu Ile Ile
 325 330 335
 Ala Ile Pro Ile Ala Tyr Leu Ser Ala Ile Asn Ala Cys Ala Lys His
 340 345 350
 Gly Val Leu Leu Lys Gly Gly Val Val Leu Asp Arg Leu Val Ser Cys
 355 360 365
 Asn Ser Val Val Met Asp Lys Thr Gly Thr Leu Thr Thr Gly Asp Leu
 370 375 380
 Thr Cys Ser Gly Cys Glu Asp Phe Gly Pro Glu Ser Pro Leu Phe Tyr
 385 390 395 400
 Ser Cys Val Leu Ala Met Glu Gln Ser Ser Ser His Pro Ile Ala Gln
 405 410 415
 Ala Ile Val Asn Tyr Leu Thr Glu Lys Gln Val Arg Ser Leu Pro Ala
 420 425 430
 Thr Gln Cys Thr Thr Ile Pro Gly Glu Gly Val Arg Glu Asn Leu Thr
 435 440 445
 Glu Asn Lys Pro Leu
 450

(2) INFORMATIONS POUR LA SEQ ID NO: 680:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 207 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 674612..675232

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 680:

Thr	Ala	Ser	Arg	Thr	Pro	Gln	Gln	Ala	Gln	Glu	Arg	Gly	Asp	Thr	Cys
1				5					10					15	
Ser	Ile	Ala	Cys	Leu	Gly	Lys	Arg	Val	Ser	Leu	Phe	Tyr	Phe	Arg	Asp
		20						25					30		
Val	Pro	Arg	His	Asp	Ala	Ala	Asn	Ile	Val	Ser	Tyr	Leu	Lys	Lys	Asn
		35					40					45			
Gly	Tyr	Pro	Val	Cys	Met	Leu	Thr	Gly	Asp	His	Arg	Ile	Ser	Ala	Glu
	50					55				60					
Asn	Thr	Ala	Arg	Leu	Leu	Gly	Ile	Asp	Glu	Val	Phe	Tyr	Asp	Leu	Thr
65					70					75					80
Pro	Asp	Asn	Lys	Leu	Ser	Lys	Ile	Gln	Glu	Leu	Ala	Lys	Ser	Arg	Gln
			85						90					95	
Ile	Met	Met	Ile	Gly	Asp	Gly	Ile	Asn	Asp	Ala	Pro	Ala	Leu	Ala	Gln
			100					105					110		
Ala	Thr	Val	Gly	Ile	Ala	Met	Gly	Glu	Ala	Gly	Ser	Ala	Thr	Ala	Ile
		115					120					125			
Glu	Ala	Ala	Asp	Val	Val	Leu	Leu	Asn	Gln	Gly	Leu	Ser	Ser	Leu	Pro
	130					135					140				
Trp	Leu	Ile	Asp	Lys	Ala	Lys	Lys	Thr	Arg	Arg	Ile	Val	Ser	Gln	Asn
145					150					155					160
Leu	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Leu	Phe	Ile	Ser	Gly	Pro	Ala	Ser
			165						170					175	
Met	Gly	Val	Ile	Pro	Leu	Trp	Leu	Ala	Val	Ile	Leu	His	Glu	Gly	Gly
		180						185					190		
Thr	Val	Ile	Val	Gly	Leu	Asn	Ala	Leu	Arg	Leu	Leu	Lys	Asn	Thr	
		195					200						205		

(2) INFORMATIONS POUR LA SEQ ID NO: 681:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 379 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 675327..676463

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 681:

Met	Lys	Lys	Thr	Lys	Tyr	Leu	Arg	Gln	Val	Asn	Leu	Trp	Val	Phe	Val
1				5					10					15	
Val	Ile	Ile	Leu	Leu	Met	Ser	Ile	Ser	Val	Ile	Val	Ile	Ser	Ser	Gln
		20						25					30		
Asp	Pro	Ser	Ser	Met	Leu	Val	His	Thr	Ser	Arg	Gly	Leu	Phe	Ser	Ala
		35					40					45			
Lys	Ser	Lys	Lys	Gln	Leu	Asp	His	Phe	Ala	Leu	Gly	Trp	Cys	Ala	Tyr

50 55 60
 Phe Ile Cys Leu Tyr Val Asp Tyr His Gln Phe Lys Arg Trp Ala Trp
 65 70 75 80
 Val Leu Tyr Ser Leu Ile Leu Phe Ser Leu Ile Gly Leu Phe Phe Val
 85 90 95
 Pro Ala Val Gln Asn Val His Arg Trp Tyr Arg Ile Pro Ile Ile Asn
 100 105 110
 Leu Ser Val Gln Pro Ser Glu Tyr Ala Lys Leu Ala Val Ile Met
 115 120 125
 Leu Ser Tyr Ile Leu Glu Met Arg Lys Ala Arg Ile Ser Ser Lys Thr
 130 135 140
 Thr Ala Phe Val Ala Cys Ile Ile Val Gly Ile Pro Phe Leu Leu Ile
 145 150 155 160
 Leu Lys Glu Pro Asp Leu Gly Thr Ala Leu Val Leu Cys Pro Ile Ala
 165 170 175
 Leu Thr Ile Phe Tyr Leu Gly Asn Ile Tyr Pro Pro Leu Val Lys Val
 180 185 190
 Cys Ser Val Leu Val Ala Leu Gly Met Phe Cys Ser Leu Leu Ile Phe
 195 200 205
 Ser Gly Ile Ile Pro His Asp Lys Val Lys Pro Tyr Ala Leu Lys Val
 210 215 220
 Leu Lys Glu Tyr Gln Tyr Glu Arg Leu Ser Pro Ser Asn His His Gln
 225 230 235 240
 Arg Ala Ser Leu Ile Ser Ile Gly Val Gly Gly Leu Lys Gly Gln Gly
 245 250 255
 Trp Lys Ser Gly Glu Phe Ala Gly Arg Gly Trp Leu Pro Tyr Gly Tyr
 260 265 270
 Thr Asp Ser Val Phe Pro Ala Ile Gly Glu Glu Phe Gly Leu Leu Gly
 275 280 285
 Leu Leu Phe Val Leu Trp Leu Phe Tyr Asn Leu Val Cys Phe Gly Cys
 290 295 300
 Arg Thr Val Ala Val Ala Val Asp Asp Phe Gly Arg Phe Leu Ala Gly
 305 310 315 320
 Gly Val Thr Val His Leu Val Met His Val Leu Ile Asn Val Ser Met
 325 330 335
 Met Ser Gly Leu Leu Pro Ile Thr Gly Val Pro Leu Val Leu Ile Ser
 340 345 350
 Tyr Gly Gly Ser Ser Val Ile Ser Thr Met Ala Ser Leu Gly Ile Leu
 355 360 365
 Gln Ser Ile Tyr Ser Arg Arg Phe Ala Lys Tyr
 370 375

(2) INFORMATIONS POUR LA SEQ ID NO: 682:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(676476..677003)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 682:

Ala Arg Thr Glu Ser Thr Asn Thr Thr Ala Lys Glu Gly Leu Ser Leu
 1 5 10 15

```

Trp Asp Pro Tyr Ala Leu Thr Val Ile Thr Thr Arg Glu Gln Thr Ala
      20      25      30
Gly Arg Gly Lys Phe Gly Arg Val Trp His Ser Thr Asp Gln Asp Leu
      35      40      45
Leu Ala Ser Phe Cys Phe Phe Leu Ser Val Asn Asn Val Asp Ser Ala
      50      55      60
Leu Leu Phe Arg Ile Gly Thr Glu Ala Val Met Arg Leu Gly Glu Ser
      65      70      75      80
Leu Gly Ile Gln Glu Ala Val Met Lys Trp Pro Asn Asp Val Leu Val
      85      90      95
Gln Gly Gln Lys Leu Ser Gly Val Leu Cys Glu Thr Ile Pro Val Lys
      100     105     110
Thr Gly Thr Cys Val Ile Ile Gly Ile Gly Val Asn Gly Asn Val Gly
      115     120     125
Ala Asp Glu Leu Leu Gly Ile Asn Gln Pro Ala Thr Ser Leu Gln Glu
      130     135     140
Leu Ile Gly Arg Pro Val Asp Met Glu Glu Gln Leu Lys Arg Leu Thr
      145     150     155     160
Lys Glu Ile Lys His Leu Ile Gln Thr Leu Pro Leu Trp Gly Arg Glu
      165     170     175

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(2) INFORMATIONS POUR LA SEQ ID NO: 683:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 241 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(677700..678422)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 683:

```

Met Ala Lys Val Arg Leu Asn Lys Phe Leu Ala Ser Ala Gly Val Ala
1      5      10      15
Ser Arg Arg Lys Cys Asp Glu Ile Ile Phe Ala Gly Ser Val Thr Val
      20      25      30
Asn Gly Arg Val Ala Thr Gly Pro Phe Val Thr Val Asp Glu Glu Phe
      35      40      45
Asp Ser Val Glu Val Gly Gly Gln Arg Ile Gly Ala Glu Lys Lys Val
      50      55      60
Tyr Phe Met Val His Lys Pro Leu Gly Tyr Leu Cys Ser Ser Glu Arg
      65      70      75      80
Lys Phe Pro Gly Ser Lys Leu Val Ile Asp Leu Leu Ser His Cys Pro
      85      90      95
Tyr Arg Leu Phe Thr Val Gly Arg Leu Asp Lys Glu Thr Ser Gly Leu
      100     105     110
Ile Leu Val Thr Asn Asp Gly Glu Phe Ala Asn Arg Val Ile His Pro
      115     120     125
Ser Phe Gly Ile Thr Lys Glu Tyr Leu Leu Lys Val Ser Arg Asp Val
      130     135     140
Thr Ala Arg Asp Leu Glu Thr Leu Met Ala Gly Thr Val Ile Asp Gly
      145     150     155     160
Lys Val Val Arg Pro Val Ser Val Lys Lys Val Arg Arg Gly Thr Ile
      165     170     175
Lys Ile Ile Val Asn Glu Gly Lys Lys His Glu Ile Arg Leu Phe Ala

```

Glu Ala Ala Gly Leu Gln Leu Leu Glu Leu Lys Arg Ile Arg Ile Gly
 180 185 190
 Ser Leu Val Leu Gly Gly Leu Pro Tyr Gly Lys Tyr Arg Glu Leu Thr
 195 200 205
 Asp Ser Glu Leu Asp Ser Cys Leu Ser Gly Lys Ser Val Ala Leu Val
 210 215 220
 225 230 235 240
 Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 684:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 678717..679508

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 684:

Met Thr Leu Leu Ile Leu Leu Arg His Gly Gln Ser Val Trp Asn Gln
 1 5 10 15
 Lys Asn Leu Phe Thr Gly Trp Val Asp Ile Pro Leu Ser Gln Gln Gly
 20 25 30
 Ile Gln Glu Ala Ile Ala Ala Gly Glu Ser Ile Lys His Leu Pro Ile
 35 40 45
 Asp Cys Ile Phe Thr Ser Thr Leu Val Arg Ser Leu Met Thr Ala Leu
 50 55 60
 Leu Ala Met Thr Asn His Ser Ser Gln Lys Val Pro Tyr Ile Val His
 65 70 75 80
 Glu Glu Arg Pro Asp Met Ser Arg Ile His Ser Gln Lys Glu Met Glu
 85 90 95
 Gln Met Ile Pro Leu Phe Gln Ser Ser Ala Leu Asn Glu Arg Met Tyr
 100 105 110
 Gly Glu Leu Gln Gly Lys Asn Lys Gln Glu Val Ala Val Gln Phe Gly
 115 120 125
 Glu Glu Gln Val Lys Leu Trp Arg Arg Ser Tyr Arg Ile Ala Pro Pro
 130 135 140
 Gln Gly Glu Ser Leu Phe Asp Thr Gly Gln Arg Thr Leu Pro Tyr Phe
 145 150 155 160
 Gln Glu Arg Ile Phe Pro Leu Leu Gln Gln Gly Lys Asn Ile Phe Ile
 165 170 175
 Ser Ala His Gly Asn Ser Leu Arg Ser Leu Ile Met Asp Leu Glu Lys
 180 185 190
 Leu Ser Glu Glu Gln Val Leu Ser Leu Glu Leu Pro Thr Gly Gln Pro
 195 200 205
 Ile Val Tyr Glu Trp Thr Gly Gln Lys Phe Thr Lys His Ala Pro Ser
 210 215 220
 Leu Gly Lys Gln Pro Thr Ser His Pro Ser Phe Arg Asn Gly Glu Arg
 225 230 235 240
 Gly Phe Ser Thr Leu Arg Arg Arg Ile Phe Val Gln Arg Lys Tyr Leu
 245 250 255
 His Ser Asp Phe Thr Ser Arg Ser
 260

(2) INFORMATIONS POUR LA SEQ ID NO: 685:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 382 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 679357..680502

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 685:

Arg	Asp	Lys	Asn	Ser	Arg	Asn	Thr	Leu	Leu	Leu	Leu	Val	Asn	Asn	Gln
1				5					10					15	
Gln	Ala	Ile	Pro	Pro	Ser	Glu	Met	Val	Lys	Glu	Ala	Phe	Gln	Arg	Tyr
			20					25					30		
Ala	Asp	Val	Phe	Ser	Tyr	Ser	Ala	Asn	Thr	Ser	Ile	Leu	Thr	Leu	Gln
		35					40					45			
Ala	Glu	Ala	Glu	Ala	Ser	Ala	Arg	Lys	Leu	Thr	Gly	Cys	Gln	Glu	Lys
	50					55					60				
Ala	Phe	Thr	Phe	His	Phe	Ile	Leu	His	Tyr	Pro	Asn	Val	Thr	Ala	Ile
65					70					75					80
Ile	Val	Ala	Ala	Leu	Leu	Glu	Asn	Gln	Asn	Ala	Phe	Gln	Gly	Arg	Asn
				85				90						95	
His	Leu	Leu	Val	Pro	Ser	Cys	Glu	Gln	Gln	Phe	Ile	Ile	Asn	Ala	Leu
			100					105					110		
Cys	Arg	Arg	Gln	Asn	Leu	Gly	Thr	Thr	Tyr	Asp	Trp	Val	Thr	Ser	Lys
		115					120						125		
Asn	Gly	Arg	Val	Lys	Glu	Ser	Asp	Leu	Ala	Glu	Ala	Leu	Ser	Pro	Arg
	130					135					140				
Thr	Leu	Leu	Phe	Ser	Ile	Ser	Ala	Ala	Asn	Gly	Met	Thr	Gly	Phe	Leu
145					150					155					160
Glu	Ala	Ile	Pro	Glu	Leu	Ala	Ala	Leu	Cys	Lys	Glu	Arg	Gly	Val	Ile
				165					170					175	
Phe	His	Ile	Asp	Leu	Ser	Asp	Ile	Leu	Gly	Arg	Cys	Ala	Leu	Pro	Ala
			180					185					190		
Glu	Leu	Tyr	Gln	Ala	Asp	Ile	Leu	Thr	Phe	Ser	Ser	Gln	Ser	Leu	Gly
		195					200					205			
Gly	Ile	Gly	Pro	Ser	Gly	Ala	Met	Phe	Ile	Ser	Pro	Ala	Leu	Thr	Lys
	210					215						220			
Tyr	Phe	Ser	Leu	Trp	Leu	Pro	Ser	Asn	Pro	Gln	Val	Pro	Thr	Cys	Leu
225					230					235					240
Ser	Ser	Leu	Ala	Ala	Phe	Ser	Leu	Ala	Cys	Gln	Glu	Arg	Thr	Thr	Ala
				245					250					255	
Phe	Ser	Ser	Leu	Val	Leu	Ser	Ala	Ile	Ser	Ser	Arg	Ala	Ala	Leu	Lys
			260					265					270		
Gln	Ala	Leu	Ser	Ala	Ile	Pro	Gln	Val	Glu	Phe	Leu	Leu	Glu	Asp	Ser
		275					280					285			
Ala	Pro	Arg	Leu	Pro	Asn	Val	Ala	Val	Phe	Ala	Ile	Pro	Gly	Ile	Pro
	290					295					300				
Ala	Glu	Ser	Leu	Gly	Phe	Phe	Leu	Ser	Gln	Lys	Asn	Ile	Phe	Val	Gly
305					310					315					320
Leu	Gly	Tyr	Glu	Arg	Phe	Gln	Pro	Leu	Ser	Gln	Ile	Leu	Gln	Ser	Ser
				325					330					335	
Gly	Ile	Ser	Pro	Phe	Leu	Cys	His	Ser	Ala	Leu	His	Val	Ser	Phe	Thr

340 345 350
 Glu Arg Thr Pro Thr Thr His Phe Ser Ala Leu Ala Thr Ala Leu Gln
 355 360 365
 Glu Gly Ile Ser His Leu Gln Pro Leu Val Thr Gln Ser Leu
 370 375 380

(2) INFORMATIONS POUR LA SEQ ID NO: 686:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 234 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 680579..681280

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 686:

Thr Trp Arg Thr Leu Ser His Asp Gln Glu Asp Glu Glu Ile Gln Leu 15
 1 5 10
 Val Ile Gly Lys Gln Gly His Leu Leu Met Gly Asn Thr Leu Leu Phe 30
 20 25
 Tyr Trp Leu Val Asp Lys Thr Asn Gly Ile Ile Arg Glu Ala Lys Phe 45
 35 40
 Gln Tyr Phe Gly His Pro Tyr Leu Leu Val Leu Ala Glu Ala Thr Cys 60
 50 55
 Ser Leu Val Ile Gly Lys Thr Phe Ala Glu Ala Tyr Lys Ile Thr Ile 80
 65 70 75
 Asn Asp Leu Asp Gln Glu Val Arg Gly His Ala Asn Pro Ser Ile Phe 95
 85 90
 Leu Glu Asp Leu Ser Pro Leu Tyr His Leu Val Ile Asp Ala Leu Asp 110
 100 105
 Ile Ala Ile Glu Gln Cys Val Asp Ile Pro Val Asn Asp Ser Pro Phe 125
 115 120
 Pro Phe Lys Asp Ala Leu Ser Gln Leu Ser Glu Gly Asn Pro Tyr Ser 140
 130 135
 Thr Glu Glu Trp Gly Ala Leu Ser His Asp Glu Gln Leu Ser Ala Leu 160
 145 150 155
 Asn Thr Met Met Lys Glu Lys Ile Ala Pro Leu Val Ala Val Asp Ser 175
 165 170
 Gly Asp Val Arg Ile Val His Phe Glu Gly Leu Thr Val Thr Ile Ala 190
 180 185
 Tyr Ser Gly Asn Cys Ser Ser Cys Leu Ser Ser Val Gly Ser Thr Leu 205
 195 200
 Asn Ser Ile Gly Gln Leu Phe Arg Ala His Val Tyr Pro Leu Leu Glu 220
 210 215
 Ile Lys Val Asp Glu Gln Ser Leu Leu Phe 230
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 687:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 340 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 681539..682558

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 687:

the 1990s, the number of people in the world who are illiterate has increased from 1.2 billion to 1.5 billion. The number of illiterate people in the world is expected to increase to 1.7 billion by the year 2015. The number of illiterate people in the world is expected to increase to 1.7 billion by the year 2015.

(2) INFORMATION POUR LA SEQ ID NO: 688:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 178 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 682554..683087

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 688:

Glu	His	Lys	His	Leu	Glu	Asp	Tyr	Val	Ala	Ser	Pro	His	Leu	Arg	Ser	
1			5					10						15		
Leu	Ala	Cys	Leu	Asp	Asn	Ser	Gln	Leu	Pro	Ile	Glu	Thr	Pro	Leu	Phe	
		20					25						30			
Glu	Gln	Lys	Ala	Leu	Ser	His	Glu	Leu	Leu	Ser	Leu	Ile	Gln	Val	Phe	
		35				40						45				
Arg	Lys	Leu	Ser	Val	His	Leu	Leu	Ser	Glu	Ile	Glu	Lys	Leu	Ser	Gln	
	50				55					60						
Lys	Leu	Lys	Pro	Glu	Leu	Leu	Glu	Leu	Ala	Val	Leu	Val	Cys	Glu	Lys	
	65			70				75					80			
Phe	Leu	Tyr	Arg	Lys	Leu	Ala	Cys	Thr	Glu	Glu	Leu	Ala	Leu	Leu	Ile	
			85					90					95			
Ser	Ala	Ala	Leu	Gln	His	His	Leu	Ala	Thr	Tyr	Ala	Val	Ser	Pro	Ile	
		100					105					110				
Lys	Ile	Gly	Leu	His	Pro	Glu	Asp	Leu	Ser	Asn	Leu	Ser	Lys	Trp	Leu	
	115					120				125						
Ile	Leu	His	Asp	Val	Pro	Leu	Leu	Lys	Asn	Ile	Glu	Phe	Ile	Ala	Asp	
	130					135				140						
Pro	Leu	Cys	Lys	Lys	Ala	Ser	Tyr	Lys	Ile	Glu	Leu	Pro	Ser	Gly	Ile	
	145			150					155					160		
Leu	Arg	Gln	Asp	Ile	Gly	Glu	Glu	Leu	Ser	His	Leu	Leu	Ser	Val	Leu	
			165					170						175		

Thr Pro

(2) INFORMATIONS POUR LA SEQ ID NO: 689:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 434 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 683164..684465

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 689:

Met	Thr	His	Leu	Gln	Glu	Glu	Thr	Leu	Leu	Ile	His	Gln	Trp	Arg	Pro	
1			5					10						15		
Tyr	Arg	Glu	Cys	Gly	Ile	Leu	Ser	Arg	Ile	Ser	Gly	Ser	Leu	Leu	Glu	
		20					25						30			
Ala	Gln	Gly	Leu	Ser	Ala	Cys	Leu	Gly	Glu	Leu	Cys	Gln	Ile	Ser	Leu	
	35					40					45					
Ser	Arg	Ser	Asp	Pro	Ile	Leu	Ala	Glu	Val	Ile	Gly	Ile	His	Asn	Arg	
	50				55					60						
Thr	Thr	Leu	Leu	Leu	Ala	Leu	Thr	Pro	Ile	Tyr	Tyr	Leu	Ala	Ile	Gly	
	65				70				75					80		

Ala Glu Val Val Pro Leu Arg Arg Pro Ala Ser Leu Pro Leu Ser Asn
 85 90 95
 His Leu Leu Gly Arg Val Leu Asp Gly Phe Gly Asn Pro Leu Asp Gly
 100 105 110
 Gly Ser Gln Leu Pro Lys Thr Asn Leu Ser Pro Leu Phe Ser Ser Pro
 115 120 125
 Ser Ser Pro Met Ser Arg Thr Pro Ile Gln Glu Val Phe Pro Thr Gly
 130 135 140
 Ile Arg Ala Ile Asp Ala Leu Leu Thr Ile Gly Glu Gly Gln Arg Val
 145 150 155 160
 Gly Ile Phe Ser Glu Pro Gly Gly Gly Lys Ser Ser Leu Leu Ser Thr
 165 170 175
 Ile Ala Lys Gly Ser Gln Gln Thr Ile Asn Val Ile Ala Leu Ile Gly
 180 185 190
 Glu Arg Gly Arg Glu Val Arg Asp Tyr Val Asn Gln His Lys Glu Gly
 195 200 205
 Leu Ala Ala Gln Arg Thr Val Ile Ile Ala Ser Thr Ala Tyr Glu Thr
 210 215 220
 Ala Ala Ser Lys Val Ile Ala Gly Arg Ala Ala Ile Thr Ile Ala Glu
 225 230 235 240
 Tyr Phe Arg Asp Gln Gly Ala Arg Val Leu Phe Thr Met Asp Ser Leu
 245 250 255
 Ser Arg Trp Ile Glu Ser Leu Gln Glu Val Ala Ile Ala Arg Gly Glu
 260 265 270
 Thr Leu Ser Thr His His Tyr Ala Ala Ser Val Phe His His Val Ala
 275 280 285
 Glu Phe Leu Glu Arg Ala Gly Asn Asn Asp Lys Gly Ser Ile Thr Ser
 290 295 300
 Phe Tyr Ala Ile Leu His Tyr Ala Asn His Pro Asp Ile Phe Thr Asp
 305 310 315 320
 Tyr Val Lys Ser Leu Leu Asp Gly His Phe Phe Leu Ser Pro Gln Glu
 325 330 335
 Lys Ser Phe Ser Ser Pro Pro Ile Asn Val Leu Thr Ser Leu Ser Arg
 340 345 350
 Ser Ser Arg Gln Leu Ala Leu Pro His His Tyr Ala Ala Ala Gln Glu
 355 360 365
 Leu Leu Ser Leu Leu Lys Ala Tyr His Glu Ala Ile Asp Ile Ile Gln
 370 375 380
 Leu Gly Ala Tyr Val Ser Gly Gln Asp Ala His Leu Asp Arg Ala Ile
 385 390 395 400
 Arg Leu Leu Pro Ser Val Lys Gln Phe Leu Ser Gln Pro Tyr Ser His
 405 410 415
 Tyr Ser Ala Ile His Glu Thr Ile Glu Gln Leu Cys Gln Leu Leu Lys
 420 425 430
 His Glu

(2) INFORMATIONS POUR LA SEQ ID NO: 690:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(684418..684774)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 690:

```

Phe Phe Phe Gly Leu Val Val Phe Val Cys Arg His Lys His Leu Ser
1      5      10      15
Lys Thr Phe Ser Gly Pro Asp Ala Val Tyr Ile Glu Lys Phe Ala Leu
      20      25      30
Phe Val Asn Val Leu Asn Val Gly His Ile His Gly Tyr Met Thr Asp
      35      40      45
Ile Gly Ile Val Cys Ala Leu Arg Lys Phe Ser Arg Cys Ala Pro
      50      55      60
Val Phe Val Val Ser Arg Cys Ser Ile Val Glu Ser Ala Phe Phe Thr
65      70      75      80
Val Ser Asn Arg Val Arg Phe Leu Lys Ser Ser Ile Val Ser Ser Leu
      85      90      95
Asp Arg Ser Trp Ser Phe Leu Phe Met Phe Gln Gln Leu Ala Gln Leu
      100      105      110
Phe Asn Ser Phe Met Asn Ser
      115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 691:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 449 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 684857..686203

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 691:

```

Val Asp Leu Ser Phe Leu Leu Asp Gln Leu Leu Pro Ile Gln Gln Glu
1      5      10      15
His Leu Leu Glu Tyr Trp Pro Ser Leu Ser Pro Gln Gln Arg Leu Arg
      20      25      30
Leu Gly Thr Gln Ile Ala Gln Ile Asp Ile Pro Phe Phe Leu Arg Gln
      35      40      45
Gln Ala Leu Leu Gln Asn Pro Gln Ala Ser His Gln Glu Tyr Thr Pro
      50      55      60
Leu Ser Pro Val His Tyr Ala Gly Asp Asn Pro Ala Tyr Ala Gln Leu
65      70      75      80
Gly Phe Gln Leu Leu Gln Arg Gly Lys Val Gly Cys Val Val Leu Ala
      85      90      95
Gly Gly Gln Gly Ser Arg Leu Lys Phe Asp Gly Pro Lys Gly Leu Tyr
      100      105      110
Pro Val Ser Ser Val Lys Lys Lys Pro Leu Tyr Gln Leu Val Ala Glu
      115      120      125
Lys Val Ala Ala Ala Ser Lys Trp Val Gly Arg Pro Leu Pro Leu Ala
      130      135      140
Ile Met Thr Ser Pro Leu Asn His Lys Gln Thr Leu Ser Tyr Phe Ala
145      150      155      160
Thr Asn Asp Tyr Phe Asn Leu Ser Pro Ser Gln Val Asp Phe Phe Cys
      165      170      175
Gln Pro Leu Trp Pro Leu Leu Ser Leu Ser Gly Asp Leu Phe Leu Glu
      180      185      190

```

Ser Glu Asp Arg Leu Ser Leu Gly Pro Thr Gly Asn Gly Cys Leu Ser
 195 200 205
 Thr Leu Leu Gln Ser Ser Gly Ile Trp Asp Lys Trp His Gln Ala Gly
 210 215 220
 Ile Glu Met Val Ser Val Ile Pro Ile Asp Asn Pro Leu Ala Leu Pro
 225 230 235 240
 Phe Asp Arg Glu Leu Val Gly Phe His Ala Ala Glu His Asn Asp Val
 245 250 255
 Thr Ile Lys Thr Thr Leu Arg Gln Ser Ala Gln Glu Asp Val Gly Val
 260 265 270
 Leu Ile Glu Leu Ala Lys Gln Lys Ile Ala Val Val Glu Tyr Ser Thr
 275 280 285
 Leu Thr Thr Lys Glu Arg Cys Ala Lys Thr Thr Glu Gly Asp Leu Thr
 290 295 300
 Tyr Lys Leu Ala Asn Ile Gly Leu Tyr Cys Leu Ser Met Asp Phe Leu
 305 310 315 320
 Ala Gln Thr Ala Tyr Gln Pro Leu Pro Leu Tyr Lys Ala Asn Lys His
 325 330 335
 Ala Lys Gln Leu His Pro Ser Thr Thr Glu Lys Asn Ala Trp Lys Phe
 340 345 350
 Glu Glu Phe Ile Phe Asp Leu Phe Gln Tyr Ser Glu His Ser Gln Ala
 355 360 365
 Ile Val Tyr Pro Arg His Glu Cys Phe Ala Pro Leu Lys Asn Tyr Glu
 370 375 380
 Gly Asn His Ser Pro Ala Thr Val Arg Glu Ala Met Arg Lys Arg Glu
 385 390 395 400
 His Ala Leu Phe Thr Ala Val Thr Glu Arg Lys Leu Ser Pro Asn Thr
 405 410 415
 Ile Phe Glu Leu Glu Ala Asp Phe Tyr Tyr Pro Ser Ser His Thr Ser
 420 425 430
 Leu Glu Trp Glu Thr Lys Ile Phe Phe Gln Glu Thr Ile Ile Glu Ala
 435 440 445
 Ser

(2) INFORMATIONS POUR LA SEQ ID NO: 692:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 336 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 686197..687204

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 692:

Gly Leu Met Lys Glu Thr Ile Ala Tyr Leu Gly Met Gly Met Trp Gly
 1 5 10 15
 Phe Ser Leu Ala Asn Leu Leu Ala Asn Asn Gly His Arg Val Val Gly
 20 25 30
 Trp Ala Arg Asn Pro Ala Leu Ile Glu Gln Leu Ser Val Gln Arg Arg
 35 40 45
 His Pro Ala Ala Pro His Ile Ser Ile Pro Gln Asn Leu Ser Phe Thr
 50 55 60
 Tyr His Met Glu Glu Ala Leu Asp Gly Ala Thr Met Ile Val Glu Gly

(2) INFORMATION POUR LA SEQ ID NO: 693:

(A) LONGUEUR: 340 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 687341..688360

Met 1	Ser	Ser	Lys 5	Leu	Val	Asn	Tyr	Leu	Arg 10	Leu	Thr	Phe	Leu	Ser 15	Phe
Leu	Gly	Ile	Ala 20	Ser	Thr	Ser	Leu	Asp 25	Ala	Met	Pro	Ala	Gly 30	Asn	Pro
Ala	Phe	Pro	Val 35	Ile	Pro	Gly	Ile 40	Asn	Ile	Glu	Gln	Lys 45	Asn	Ala	Cys
Ser	Phe 50	Asp	Leu	Cys	Asn	Ser 55	Tyr	Asp	Val	Leu	Ser 60	Ala	Leu	Ser	Gly
Asn 65	Leu	Lys	Leu	Cys	Phe 70	Phe	Gly	Asp	Tyr	Ile 75	Phe	Ser	Glu	Glu	Ala 80

Gln Val Lys Asp Val Pro Val Val Thr Ser Val Thr Thr Ala Gly Ile
 85 90 95
 Gly Pro Ser Pro Asn Ile Thr Ser Thr Thr Lys Thr Arg Asn Phe Asp
 100 105 110
 Leu Val Asn Cys Asn Leu Asn Ala Asn Cys Val Ala Ala Phe Ser
 115 120 125
 Leu Pro Asp Arg Ser Leu Ser Ala Ile Pro Leu Phe Asp Val Ser Phe
 130 135 140
 Glu Val Lys Val Gly Gly Leu Lys Gln Tyr Tyr Arg Leu Pro Met Asn
 145 150 155 160
 Ala Tyr Arg Asp Phe Thr Ser Glu Pro Leu Asn Ser Glu Ser Glu Val
 165 170 175
 Thr Asp Gly Met Ile Glu Val Gln Ser Asn Tyr Gly Phe Val Trp Asp
 180 185 190
 Val Ser Leu Lys Lys Val Ile Trp Lys Asp Gly Val Ser Phe Val Gly
 195 200 205
 Val Gly Ala Asp Tyr Arg His Ala Ser Cys Pro Ile Asp Tyr Ile Ile
 210 215 220
 Ala Asn Ser Gln Ala Asn Pro Glu Val Phe Ile Ala Asp Ser Asp Gly
 225 230 235 240
 Lys Leu Asn Phe Lys Glu Trp Ser Val Cys Val Gly Leu Thr Thr Tyr
 245 250 255
 Val Asn Asp Tyr Val Leu Pro Tyr Leu Ala Phe Ser Ile Gly Ser Val
 260 265 270
 Ser Arg Gln Ala Pro Asp Asp Ser Phe Lys Lys Leu Glu Asp Arg Phe
 275 280 285
 Thr Asn Leu Lys Phe Lys Val Arg Lys Ile Thr Ser Ser His Arg Gly
 290 295 300
 Asn Ile Cys Ile Gly Ala Thr Asn Tyr Ile Ala Asp Asn Phe Phe Tyr
 305 310 315 320
 Asn Val Glu Gly Arg Trp Gly Ser Gln Arg Ala Val Asn Val Ser Gly
 325 330 335
 Gly Phe Gln Phe
 340

(2) INFORMATIONS POUR LA SEQ ID NO: 694:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 80 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(688193..688432)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 694:

Leu Asp Met Arg Gly Asn Leu Leu Leu Ile Ser Leu Glu Gly Glu Val
 1 5 10 15
 Lys Arg Arg Gly Phe Gly Gly Leu Glu Leu Glu Ser Ser Gly Asp Val
 20 25 30
 His Ser Ala Leu Ala Ser Pro Ser Ser Phe Tyr Val Val Glu Glu Val
 35 40 45
 Ile Gly Asp Ile Val Cys Arg Ser Asp Ala Asp Val Ser Thr Met Arg
 50 55 60
 Ala Gly Asn Phe Thr Asn Phe Lys Phe Glu Val Ser Glu Ala Ile Phe

(2) INFORMATION POUR LA SEQ ID NO: 696:

(A) LONGUEUR: 110 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(689631..689960)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 696:

(2) INFORMATION POUR LA SEQ ID NO: 697:

(A) LONGUEUR: 214 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(689846..690487)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 697:

Lys 1	Ser	Glu	Val	Glu 5	Pro	Ser	Ser	Leu	Asn 10	Tyr	Phe	Asn	Ala	Met 15	Val
Glu	Ala	Lys	Lys 20	Thr	Phe	Val	Glu	Thr 25	Ser	Pro	Ile	Gln	Met 30	Val	Tyr
Ser	Ser	Leu	Met	Leu	Asp	Lys	Tyr	Leu	Pro	Asn	Gln	Gln	Tyr	Ile	Leu

	35		40		45														
Glu	Thr	Leu	Gly	Ser	Gln	Met	Thr	Phe	Ser	Asn	Lys	Ala	Ala	Arg	Tyr				
	50					55					60								
Leu	Asn	Asp	Ile	Ile	Ala	His	Ala	Val	Ser	Phe	Gln	Thr	Ala	Asn	Val				
65					70					75					80				
Tyr	Tyr	Ser	Leu	Gly	Met	Tyr	Leu	Arg	Gln	Met	Asn	Gln	Gln	Glu	Phe				
				85					90					95					
Pro	Glu	Val	Ile	Ser	Arg	Ala	Asn	Asp	Thr	Val	Lys	Lys	Glu	Ile	Asp				
			100					105					110						
Arg	Ser	Arg	Ala	Asp	Leu	Phe	His	Cys	Lys	Lys	Ala	Ile	Glu	Lys	Ile				
		115					120					125							
Lys	Glu	Leu	Val	Thr	Ser	Ile	Asn	Ala	Asp	Thr	Glu	Leu	Thr	Ser	Ser				
	130					135					140								
Gln	Arg	Ala	Glu	Leu	Leu	Glu	Thr	Leu	Ala	Ser	Tyr	Ala	Phe	Glu	Phe				
145					150					155					160				
Glu	Asn	Leu	Tyr	His	Asn	Leu	Ser	Asn	Val	Tyr	Val	Met	Val	Ser	Lys				
				165				170						175					
Val	Gln	Ile	Ser	Gly	Val	Thr	Cys	Leu	Met	Lys	Trp	Met	Arg	Leu	Leu				
			180				185					190							
Leu	Leu	Arg	Leu	Asp	Arg	Arg	Asn	Ser	Ile	Leu	Gly	Phe	Ser	Ser	Leu				
		195					200					205							
Gln	His	Leu	Lys	Val	Leu														
	210																		

(2) INFORMATIONS POUR LA SEQ ID NO: 698:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 85 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(690463..690717)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 698:

Ala	Phe	Gly	Asp	Tyr	Asn	Gly	Val	Tyr	Leu	Phe	Asp	Asn	Lys	Gly	Leu
1			5					10					15		
Ala	Thr	Asn	Leu	Phe	Asn	Pro	Thr	Phe	Phe	Phe	Asp	Val	Val	Ser	Leu
		20					25					30			
Met	Thr	Ala	Asp	Pro	Thr	Lys	Thr	Met	Ser	Arg	Gln	Asp	Tyr	Asn	Lys
		35				40					45				
Val	Ile	Thr	Ala	Ser	Glu	Ser	Ser	Ile	Gln	Lys	Ile	Asn	Gln	Ala	Ile
	50				55					60					
Thr	Ala	Trp	Glu	Leu	Ala	Ile	Ala	Glu	Cys	Gly	Thr	Lys	Lys	Ala	Lys
65			70					75						80	
Ser	Asn	His	Pro	Val											
			85												

(2) INFORMATIONS POUR LA SEQ ID NO: 699:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(690672..691871)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 699:

```

Pro Glu Ser Arg Ser Met Leu Leu Gln Cys Ile Cys Arg Ser Val Phe
1      5      10      15
Phe Phe Gln Gln Leu Asp Glu Lys Ser Lys Gly Leu Lys Arg Ala Leu
20      25      30
Gly Leu Leu Glu Glu Val Asp Leu Glu Lys Phe Ile Pro Ser Leu Glu
35      40      45
Lys Ser Pro Thr Pro Ile Thr Thr Gly Thr Thr Ser Lys Ile Ser Ala
50      55      60
Asp Gly Ile Glu Ile Val Gly Glu Leu Ser Ser Glu Thr Ile Leu Ala
65      70      75      80
Asp Pro Asn Lys Ala Ala Ala Gln Val Phe Gly Glu Gly Leu Ala Asp
85      90      95
Ser Phe Asp Asp Trp Leu Arg Leu Ser Glu Asn Gly Gly Ile Gln Asp
100     105     110
Pro Thr Ala Ile Glu Glu Glu Ile Val Thr Lys Tyr Gln Thr Glu Leu
115     120     125
Asn Thr Leu Arg Asn Lys Leu Lys Gln Gln Ser Leu Thr Asp Asp Glu
130     135     140
Tyr Thr Lys Leu Tyr Ala Ile Pro Gln Asn Phe Val Lys Glu Ile Glu
145     150     155     160
Ser Leu Lys Asn Glu Asn Asn Val Arg Leu Ile Pro Lys Ser Lys Val
165     170     175
Thr Asn Phe Trp Gln Asn Ile Met Leu Thr Tyr Asn Ser Val Thr Ser
180     185     190
Leu Ser Glu Pro Val Ala Asp Ala Met Asn Thr Thr Met Thr Glu Tyr
195     200     205
Ser Leu Tyr Ile Glu Arg Ala Thr Glu Ala Ala Lys Leu Ile Arg Glu
210     215     220
Ile Thr Asn Thr Ile Lys Asp Ile Phe Asn Pro Val Trp Asp Val Arg
225     230     235     240
Glu Gln Thr Gly Ile Phe Arg Leu Lys Gly Ala Glu Tyr Asn Ala Leu
245     250     255
Glu Gly Asn Met Ile Gln Ser Leu Leu Ser Phe Ala Gly Leu Phe Arg
260     265     270
Gln Leu Met Ser Arg Thr Ala Thr Val Asp Glu Ile Gly Ala Leu Tyr
275     280     285
Pro Lys Asn Asp Lys Asn Glu Asp Val Ile His Thr Ala Ile Asp Asp
290     295     300
Tyr Val Asn Ser Leu Ala Asp Leu Lys Ala Asn Glu Gln Val Lys Leu
305     310     315     320
Asn Gly Leu Leu Ser Leu Val Tyr Ala Tyr Tyr Ala Ser Thr Leu Gly
325     330     335
Phe Ala Lys Lys Asp Val Phe Asn Asn Ala Gln Ala Ser Phe Thr Asp
340     345     350
Tyr Thr Asn Phe Leu Asn Gln Glu Ile Gln Tyr Trp Arg Pro Arg Glu
355     360     365
Thr Ser Ser Phe Asn Ile Ser Asn Gln Ala Leu Arg Thr Phe Lys Asn
370     375     380
Lys Pro Ser Val Ile Ile Thr Ala Tyr Ile Phe Leu Ile Ile Lys Asp
385     390     395     400

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(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(692041..693837)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 700:

Met 1	Thr	Gly	Asp	Trp 5	Ile	Ser	Lys	Ile	Thr 10	His	Ser	Gly	Leu	Lys 15	Ser
Trp	Ile	Glu	Glu 20	Val	Ile	Ala	Leu	Val 25	Ser	Pro	Asp	Asp	Val 30	Arg	Leu
Cys	Asp	Gly 35	Ser	Glu	Ala	Glu	Tyr 40	Gln	Gln	Leu	Cys	Gln 45	Gln	Met	Gln
Asp	Ala	Gly 50	Val	Met	Thr	Pro 55	Leu	Asn	Pro	Glu	Leu 60	His	Pro	Asn	Cys
Phe 65	Leu	Val	Arg	Ser	Ser 70	Pro	Ser	Asp	Val	Ala 75	Arg	Ala	Glu	Gln	Phe 80
Thr	Phe	Ile	Cys 85	Thr	Lys	Thr	Gln	Glu 90	Glu	Ala	Gly	Pro	Thr 95	Asn	Asn
Trp	Arg	Asp 100	Pro	Gln	Glu	Met	Arg	Ala 105	Glu	Leu	His	Ala	Leu 110	Phe	Arg
Gly	Cys	Met 115	Arg	Gly	Arg	Thr	Leu 120	Tyr	Ile	Val	Pro	Phe 125	Cys	Met	Gly
Pro	Leu	Asn 130	Ser	Pro	Phe	Ser 135	Leu	Ile	Gly	Val	Glu 140	Ile	Thr	Asp	Ser
Pro 145	Tyr	Val	Val	Cys	Ser 150	Met	Lys	Ile	Met	Thr 155	Arg	Met	Gly	Ala	Ser 160
Val	Leu	Ala	Met 165	Leu	Gly	Ser	Asn	Gly 170	Thr	Phe	Tyr	Lys	Cys 175	Leu	His
Ser	Val	Gly 180	Lys	Pro	Leu	Ala	Pro	Gly 185	Glu	Lys	Asp	Val 190	Ala	Trp	Pro
Cys	Asp 195	Pro	Glu	His	Met	Arg 200	Ile	Val	His	Phe	Gln 205	Asp	Asp	Ser	Ser
Val	Met 210	Ser	Phe	Gly	Ser	Gly 215	Tyr	Gly	Gly	Asn 220	Ala	Leu	Leu	Gly	Lys
Lys 225	Cys	Xaa	Thr	Leu	Arg 230	Leu	Ala	Ser	Tyr	Leu 235	Gly	His	Gln	Gln	Gly 240
Trp	Leu	Ala	Glu 245	His	Met	Leu	Ile	Ile	Gly 250	Val	Thr	Asn	Pro	Glu 255	Gly
Arg	Lys	Lys 260	Tyr	Phe	Ala	Ala	Ala 265	Phe	Pro	Ser	Ala	Cys 270	Gly	Lys	Thr
Asn	Leu 275	Ala	Met	Leu	Met	Pro 280	Lys	Leu	Pro	Gly	Trp	Lys 285	Val	Glu	Cys
Ile	Gly 290	Asp	Asp	Ile	Ala	Trp 295	Ile	Arg	Pro	Gly	Asn 300	Asp	Gly	Arg	Leu
Tyr 305	Ala	Val	Asn	Pro	Glu 310	Phe	Gly	Phe	Phe	Gly 315	Val	Ala	Leu	Gly	Thr 320
Ser	Glu	Thr	Thr 325	Asn	Pro	His	Ala	Leu 330	Ala	Thr	Cys	His 335	Ala	Asp	Ser
Leu	Phe	Thr	Asn 340	Val	Ala	Leu	Thr	Ala 345	Asp	Gly	Asp	Val 350	Trp	Trp	Glu

Gly Lys Thr Thr Thr Pro Pro Gln Gly Met Ile Asp Trp Lys Gly Arg
 355 360 365
 Ala Trp Val Ser Gly Gly Glu Pro Ala Ala His Pro Asn Ala Arg Phe
 370 375 380
 Thr Ala Pro Leu Asp His Cys Pro Ser Leu Asp Pro Gln Trp Asn Asn
 385 390 395 400
 Pro Gln Gly Val Pro Leu Glu Ala Val Ile Phe Gly Gly Arg Arg Thr
 405 410 415
 Glu Thr Ile Pro Leu Val Tyr Glu Ala Leu Ser Trp Glu His Gly Val
 420 425 430
 Met Met Gly Ala Gly Met Ser Ser Thr Thr Thr Ala Ala Ile Val Gly
 435 440 445
 Glu Leu Gly Lys Leu Arg His Asp Pro Phe Ala Met Leu Pro Phe Cys
 450 455 460
 Gly Tyr Asn Met Ala Ala Tyr Phe Glu His Trp Leu Ser Phe Ala Thr
 465 470 475 480
 Lys Gly Leu Gln Leu Pro Arg Ile Phe Gly Val Asn Trp Phe Arg Lys
 485 490 495
 Asp Glu His Gly Gln Phe Ile Trp Pro Gly Phe Ser Glu Asn Leu Arg
 500 505 510
 Val Leu Glu Trp Ile Phe Arg Arg Thr Asp Gly Glu Asp Ala Ile Ala
 515 520 525
 His Arg Thr Pro Val Xaa Tyr Leu Pro Thr Ala Glu Gly Leu Asn Thr
 530 535 540
 Ser Gly Leu Asp Leu Ser Glu Asp Ala Leu Arg Ala Leu Leu Thr Val
 545 550 555 560
 Asp Ala Gln Gly Trp Lys Ala Glu Val Ser Asn Ile Arg Lys Tyr Cys
 565 570 575
 Ser Ile Phe Gly Ala Asp Met Pro Gln Arg Ile Leu Glu Glu Leu Ser
 580 585 590
 Arg Ile Glu Ser Glu Leu Lys
 595

(2) INFORMATIONS POUR LA SEQ ID NO: 701:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(693837..694853)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 701:

Val Phe Asn Phe Phe Ser Gly Asn Val Gly Ile Asp Leu Gly Thr Ala
 1 5 10 15
 Asn Thr Leu Val Tyr Val Arg Gly Arg Gly Ile Val Leu Ser Glu Pro
 20 25 30
 Ser Val Val Ala Val Asp Ala Gln Thr His Ala Val Leu Ala Val Gly
 35 40 45
 His Lys Ala Lys Ala Met Leu Gly Lys Thr Pro Arg Lys Ile Val Ala
 50 55 60
 Val Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Glu Ile Ala Glu
 65 70 75 80
 Gly Met Leu Lys Ala Leu Ile Lys Arg Val Thr Pro Ala Arg Ser Met

				85					90					95					
Phe	Arg	Pro	Lys	Ile	Leu	Ile	Ala	Val	Pro	Ser	Gly	Ile	Thr	Gly	Val				
			100						105					110					
Glu	Lys	Arg	Ala	Val	Glu	Asp	Ser	Ala	Leu	His	Ala	Gly	Ala	Gln	Glu				
			115					120					125						
Val	Ile	Leu	Ile	Glu	Glu	Pro	Met	Ala	Ala	Ala	Ile	Gly	Val	Asp	Leu				
			130					135					140						
Pro	Val	His	Glu	Pro	Ala	Ala	Ser	Met	Ile	Ile	Asp	Ile	Gly	Gly	Gly				
145					150					155					160				
Thr	Thr	Glu	Ile	Ala	Ile	Ile	Ser	Leu	Gly	Gly	Ile	Val	Glu	Ser	Arg				
				165					170					175					
Ser	Leu	Arg	Ile	Ala	Gly	Asp	Glu	Phe	Asp	Glu	Cys	Ile	Ile	Asn	Tyr				
			180					185						190					
Met	Arg	Arg	Thr	Tyr	Asn	Leu	Met	Ile	Gly	Pro	Arg	Thr	Ala	Glu	Glu				
			195					200					205						
Ile	Lys	Ile	Thr	Ile	Gly	Ser	Ala	Tyr	Pro	Leu	Gly	Asp	Gln	Glu	Leu				
			210				215					220							
Glu	Met	Glu	Val	Arg	Gly	Arg	Asp	Gln	Val	Ala	Gly	Leu	Pro	Ile	Thr				
225					230					235					240				
Lys	Arg	Ile	Asn	Ser	Val	Glu	Ile	Arg	Glu	Cys	Leu	Ala	Glu	Pro	Ile				
				245					250					255					
Gln	Gln	Ile	Ile	Glu	Cys	Val	Arg	Leu	Thr	Leu	Glu	Lys	Cys	Pro	Pro				
			260					265					270						
Glu	Leu	Ser	Ala	Asp	Leu	Val	Glu	Arg	Gly	Met	Val	Leu	Ala	Gly	Gly				
			275					280					285						
Gly	Ala	Leu	Ile	Lys	Gly	Leu	Asp	Lys	Ala	Leu	Ser	Lys	Asn	Thr	Gly				
			290				295					300							
Leu	Ser	Val	Ile	Thr	Ala	Pro	His	Pro	Leu	Leu	Ala	Val	Cys	Leu	Gly				
305					310					315					320				
Thr	Gly	Lys	Ala	Leu	Glu	His	Leu	Asp	Gln	Leu	Lys	Lys	Arg	Lys	Glu				
				325					330					335					
Ser	Leu	Val																	

(2) INFORMATIONS POUR LA SEQ ID NO: 702:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 774 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(694942..697263)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 702:

Tyr	Ser	Tyr	Pro	Gly	Ser	Ser	Val	Trp	Phe	Leu	Leu	Arg	Glu	Arg	Phe				
1				5					10					15					
Ala	Ser	Ile	Pro	Lys	Phe	Ile	Ala	Glu	Leu	Ser	Asn	Val	Glu	Ala	Leu				
			20					25					30						
Asn	Val	Phe	Ser	Thr	Leu	Pro	Tyr	Thr	Glu	Glu	Leu	Gln	Gly	Val	Cys				
		35					40					45							
Asp	Ile	Ser	Tyr	Leu	Asp	Gly	Glu	Leu	Glu	Ala	Arg	Leu	Phe	Phe	Leu				
		50				55				60									
Tyr	Asp	Gly	Gln	Lys	Val	Pro	Ala	Thr	Ser	Phe	Ser	Leu	Gln	Tyr	Gln				
65					70					75					80				

```

545          550          555          560
Gln Glu Leu Ser Arg Leu Val Lys Gln Glu Gly Phe Glu Arg Ile His
                    565          570          575
Ile His Val Leu Ala Thr Leu Thr Arg Leu Lys Gln Ile Cys Cys His
                    580          585          590
Pro Ala Ile Phe Ala Lys Asp Thr Pro Glu Pro Gly Asp Ser Ala Lys
                    595          600          605
Tyr Asp Met Leu Met Asp Leu Leu Ser Ser Leu Val Asp Ser Gly His
                    610          615          620
Lys Thr Val Val Phe Ser Gln Tyr Thr Lys Met Leu Gly Ile Ile Arg
625          630          635          640
Gln Asp Leu Glu Ala Lys Gly Ile Pro Phe Val Tyr Leu Asp Gly Ser
                    645          650          655
Thr Lys Asn Arg Leu Glu Ile Val Gln Gln Phe Asn Glu Asp Pro Gly
                    660          665          670
Leu Leu Val Phe Leu Val Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn
                    675          680          685
Leu Val Gly Ala Asp Thr Val Ile His Tyr Asp Met Trp Trp Asn Pro
690          695          700
Ala Val Glu Asn Gln Ala Thr Asp Arg Val His Arg Ile Gly Gln Ser
705          710          715          720
Arg Ser Val Ser Ser Tyr Lys Leu Val Thr Leu Asn Thr Ile Glu Glu
                    725          730          735
Lys Ile Leu Ser Leu Gln Asn Arg Lys Lys Gly Leu Val Lys Lys Val
                    740          745          750
Ile Asn Ser Asp Asp Glu Val Val Ser Lys Leu Thr Trp Glu Glu Val
                    755          760          765
Leu Glu Leu Leu Gln Ile
770

```

(2) INFORMATIONS POUR LA SEQ ID NO: 703:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 305 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(697170..698084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 703:

```

Gly Ile Thr Arg Asp Phe Cys Arg Cys Ser Asp Ser Arg Gly Gly Thr
1          5          10          15
Lys Arg Ser Gly Thr Pro Lys Arg Asn Leu Arg Glu Tyr Asn His Ala
20          25          30
Ala Asn Val Leu Ser Glu Asn Pro Phe Phe Leu Pro Leu Glu Tyr Ser
35          40          45
Glu Lys Asp Ser Ala Gly Leu Ala Val Leu Phe Val Pro Gln Lys Asn
50          55          60
Glu Gly Glu Val Phe Ser Pro Asn Gln Pro Ile Glu Phe Gln Leu Val
65          70          75          80
Leu Arg Leu Pro Gly Arg Ser Lys Pro Phe Tyr Ile Ser Asn Ile Lys
85          90          95
Thr Phe Leu Glu Gly Val Leu Tyr Gln Glu Pro Ile Val Phe Ser Gly
100          105          110

```



```

Arg Arg Phe Phe Phe Thr Leu Gln Ser Phe Ser Ala Ser Asp Arg Lys
      115      120      125
Leu Ile Asp Leu Leu Ile Arg Tyr Ala Arg Tyr Ala Thr Gly Ser Ser
      130      135      140
Glu Glu Lys Leu Leu Lys Ser Ala Phe Leu Thr Pro Ala Ser Leu Gly
145      150      155      160
Met Ile Leu Ser Lys Met Phe Glu His Gln Met Ala Glu Ser Gly Gly
      165      170      175
Ser Gln Leu Gly Glu Arg Glu Cys Phe Gln Gly Ile Phe Cys Gly Asn
      180      185      190
Leu Glu Glu Pro Leu Leu Trp Ser Val Ser Pro Ala Lys Met Lys Phe
      195      200      205
His Leu Asp Tyr Phe Asp Thr Pro Tyr Lys Ala Leu Met Lys Pro
      210      215      220
Leu Ile Val Val Asp Glu Glu Glu Leu Gln Pro Glu Gln Ala Val Leu
225      230      235      240
Leu Glu Ser Asn Tyr Pro Gly Ile Ile His Lys Asn Val Tyr His His
      245      250      255
Phe Leu Pro Gln Ile Lys Arg Ala His Leu Arg Thr Phe Ala Gly Leu
      260      265      270
Arg Asp Ile Ala Ile Pro Glu Ala Leu Phe Gly Ser Phe Cys Glu Asn
      275      280      285
Ala Leu Pro Val Phe Arg Asn Leu Leu Arg Asn Cys Pro Met Ser Arg
      290      295      300
Leu
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 704:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 138 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(697979..698392)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 704:

```

His Thr Xaa Arg Leu Glu Lys Ser Tyr Phe Ala Gln Gly Ala Val Val
1      5      10      15
Ser Ala Lys Ile Leu Ser Met Asn Gly Glu Thr Val Cys Ile Ser Ala
      20      25      30
Gln Ile Arg Gly Ser Tyr Asp Asn Val Tyr Glu Cys Glu Ile Glu Val
      35      40      45
Asp Arg Ala Glu Ser Asp Thr Val Asp Ser Asn Cys Asp Cys Ser Tyr
      50      55      60
Asn Tyr Asp Cys Gln His Val Val Ala Leu Leu Phe Tyr Leu Glu Gln
      65      70      75      80
Tyr Phe Asn Glu Met Val Val Thr Tyr Ser Lys Glu Ala Asp Leu Ser
      85      90      95
Ser Asn Glu Glu Val Ser Lys Glu Leu Gln Glu Thr Phe Val Val Ala
      100      105      110
Ala Ile Arg Glu Glu Glu Arg Arg Asp Arg Glu His Gln Lys Glu Ile
      115      120      125
Phe Gly Asn Thr Ile Met Leu Leu Met Phe

```

130

135

(2) INFORMATIONS POUR LA SEQ ID NO: 705:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 432 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 698822..700117

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 705:

Phe	Ser	Ile	Asn	Ile	Glu	Glu	Asn	Ala	Gly	Cys	Val	Val	Ser	Ala	Lys	1	5	10	15
Val	Gln	Ala	Asn	Pro	Leu	Val	Thr	Gln	Lys	Cys	His	Lys	Glu	Ala	Leu	20	25	30	35
Lys	Thr	Val	Lys	Lys	Asn	Val	Val	Leu	Pro	Gly	Phe	Arg	Lys	Gly	Lys	40	45	50	55
Ala	Pro	Asp	Asn	Ile	Val	Glu	Ser	Arg	Tyr	Ser	Thr	Gln	Val	Glu	Gln	60	65	70	75
Glu	Leu	Arg	Arg	Leu	Phe	Leu	Arg	Ala	Ser	Phe	Glu	Ala	Leu	Ser	Gln	80	85	90	95
Met	Cys	Asp	Arg	Lys	Pro	Leu	Ser	Pro	Lys	Ala	Val	Arg	Ser	Ser	Ala	100	105	110	115
Ile	Asp	Thr	Cys	Asn	Pro	Val	Asn	Gly	Gly	Ser	Val	Ser	Phe	Leu	Tyr	120	125	130	135
Glu	Ala	Phe	Pro	Val	Ile	Pro	Ser	Leu	Pro	Trp	Glu	Gln	Leu	Ser	Leu	140	145	150	155
Pro	Asp	Pro	Glu	Pro	Val	Lys	Glu	Ile	Ser	Glu	Glu	Asp	Leu	Glu	Asn	160	165	170	175
Gly	Leu	Lys	Asn	Val	Ala	Tyr	Phe	Phe	Ala	Thr	Lys	Thr	Pro	Val	Thr	180	185	190	195
Arg	Pro	Ser	Gln	Glu	Gly	Asp	Phe	Ile	Ser	Leu	Ser	Leu	Tyr	Val	Ser	200	205	210	215
Lys	Arg	Gly	Asp	Glu	Asn	Ser	Thr	Pro	Val	Ala	Ile	Phe	Glu	Asn	Lys	220	225	230	235
Tyr	Phe	Lys	Ile	Ser	Glu	Glu	Asp	Met	Thr	Asp	Ser	Phe	Lys	Ala	Arg	240	245	250	255
Phe	Leu	Asn	Val	Ser	Thr	Gly	His	Arg	Val	Glu	Glu	Ile	Gly	Ser		260	265	270	275
Glu	Asp	Ile	Gln	Ser	Phe	Leu	Asn	Gly	Asp	Leu	Leu	Thr	Phe	Thr	Val	280	285	290	295
Asn	Ala	Val	Ile	Glu	Ile	Ser	Ser	Pro	Glu	Met	Asp	Asp	Glu	Lys	Ala	300	305	310	315
Arg	Glu	Leu	Gln	Ala	Glu	Ser	Leu	Glu	Asp	Leu	Lys	Lys	Lys	Leu	Arg	320	325	330	335
Ile	Gln	Leu	Glu	Asn	Gln	Ala	Lys	Glu	Ala	Gln	His	Gln	Lys	Arg	Phe	340	345	350	355
Ser	Asp	Ala	Glu	Asp	Ala	Leu	Ala	Gln	Leu	Ile	Asp	Phe	Asp	Leu	Pro	360	365	370	375
Glu	Ser	Leu	Leu	Arg	Glu	Arg	Glu	Glu	Leu	Leu	Ser	Arg	Glu	Lys	Leu	380	385	390	395
Leu	Asn	Ala	Arg	Leu	Val	Lys	Tyr	Cys	Ser	Asp	Ser	Glu	Leu	Glu	Glu	400	405	410	415

```

Gln Lys Gln Ala Leu Leu Glu Glu Ala Lys Ala Asp Ala Arg Lys Ala
      340                      345                      350
Val Lys Leu Leu Phe Leu Thr Gln Lys Val Phe Ser Glu Lys Gly Leu
      355                      360                      365
Ser Ile Ser Arg Glu Glu Leu Gln Tyr Met Met Asp Val Cys Ser Arg
      370                      375                      380
Glu Arg Phe Gly Gly Tyr Pro Pro Lys Asp Ile Ser Asn Glu Met Ile
      385                      390                      395                      400
Gln Glu Leu Val Leu Val Ala Arg Asp Arg Leu Thr Tyr Arg Lys Ala
      405                      410                      415
Ile Glu Ala Ile Ser Ser Glu Lys Lys Asp Leu Glu Val Val Pro Ser
      420                      425                      430

```

(2) INFORMATIONS POUR LA SEQ ID NO: 706:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 700287..700895

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 706:

```

Met Thr Leu Val Pro Tyr Val Val Glu Asp Thr Gly Arg Gly Glu Arg
1      5      10      15
Ala Met Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Met Ile
      20      25      30
Gly Gln Glu Ile Thr Glu Pro Leu Ala Asn Thr Val Ile Ala Gln Leu
      35      40      45
Leu Phe Leu Met Ser Glu Asp Pro Thr Lys Asp Ile Gln Ile Phe Ile
      50      55      60
Asn Ser Pro Gly Gly Tyr Ile Thr Ala Gly Leu Ala Ile Tyr Asp Thr
      65      70      75      80
Ile Arg Phe Leu Gly Cys Asp Val Asn Thr Tyr Cys Ile Gly Gln Ala
      85      90      95
Ala Ser Met Gly Ala Leu Leu Leu Ser Ala Gly Thr Lys Gly Lys Arg
      100     105     110
Tyr Ala Leu Pro His Ser Arg Met Met Ile His Gln Pro Ser Gly Gly
      115     120     125
Ile Ile Gly Thr Ser Ala Asp Ile Gln Leu Gln Ala Ala Glu Ile Leu
      130     135     140
Thr Leu Lys Lys His Leu Ser Asn Ile Leu Ala Glu Cys Thr Gly Gln
      145     150     155     160
Ser Val Glu Lys Ile Ile Glu Asp Ser Glu Arg Asp Phe Phe Met Gly
      165     170     175
Ala Glu Glu Ala Ile Ala Tyr Gly Leu Ile Asp Lys Val Ile Ser Ser
      180     185     190
Ala Lys Glu Thr Lys Asp Lys Ser Ile Ala Ser
      195     200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 707:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 418 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 700912..702165

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 707:

Gln	Lys	Lys	Asn	Leu	Ala	Val	Cys	Ser	Phe	Cys	Gly	Arg	Ser	Glu	Lys	1	5	10	15
Asp	Val	Glu	Lys	Leu	Ile	Ala	Gly	Pro	Ser	Val	Tyr	Ile	Cys	Asp	Tyr	20	25	30	
Cys	Ile	Lys	Leu	Cys	Ser	Gly	Ile	Leu	Asp	Lys	Thr	Pro	Ala	Pro	Ala	35	40	45	
Thr	Gln	Glu	Ile	Ala	Thr	Ser	Ser	Thr	Ser	Ser	Pro	Thr	Ser	Leu	Arg	50	55	60	
Val	Leu	Thr	Pro	Lys	Glu	Ile	Lys	Arg	His	Ile	Asp	Ser	Tyr	Val	Ile	65	70	75	80
Gly	Gln	Glu	Arg	Ala	Lys	Lys	Thr	Ile	Ser	Val	Ala	Val	Tyr	Asn	His	85	90	95	
Tyr	Lys	Arg	Ile	Arg	Ala	Leu	Met	Gln	Asp	Lys	Gln	Val	Ser	Tyr	Gly	100	105	110	
Lys	Ser	Asn	Val	Leu	Leu	Leu	Gly	Pro	Thr	Gly	Xaa	Gly	Lys	Thr	Leu	115	120	125	
Ile	Ala	Lys	Thr	Leu	Ala	Lys	Ile	Leu	Asp	Val	Pro	Phe	Thr	Ile	Ala	130	135	140	
Asp	Ala	Thr	Thr	Leu	Thr	Glu	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Val	Glu	145	150	155	160
Asn	Ile	Val	Leu	Arg	Leu	Leu	Gln	Ala	Ala	Asp	Tyr	Asp	Val	Ala	Arg	165	170	175	
Ala	Glu	Arg	Gly	Ile	Ile	Tyr	Ile	Asp	Glu	Ile	Asp	Lys	Ile	Gly	Arg	180	185	190	
Thr	Thr	Ala	Asn	Val	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	195	200	205	
Gln	Gln	Ala	Leu	Leu	Lys	Ile	Ile	Glu	Gly	Thr	Val	Ala	Asn	Ile	Pro	210	215	220	
Pro	Lys	Gly	Gly	Arg	Lys	His	Pro	Asn	Gln	Glu	Tyr	Ile	Arg	Val	Asn	225	230	235	240
Thr	Glu	Asn	Ile	Leu	Phe	Ile	Val	Gly	Gly	Ala	Phe	Val	Asn	Leu	Asp	245	250	255	
Lys	Ile	Ile	Ala	Lys	Arg	Leu	Gly	Arg	Thr	Thr	Ile	Gly	Phe	Ser	Glu	260	265	270	
Glu	Thr	Asp	Leu	Ala	Val	Thr	Asn	Arg	Asp	His	Leu	Leu	Ala	Lys	Val	275	280	285	
Glu	Thr	Glu	Asp	Leu	Ile	Thr	Phe	Gly	Met	Ile	Pro	Glu	Phe	Ile	Gly	290	295	300	
Arg	Phe	Asn	Cys	Ile	Val	Asn	Cys	Glu	Glu	Leu	Thr	Leu	Asp	Glu	Leu	305	310	315	320
Val	Glu	Ile	Leu	Thr	Glu	Pro	Ala	Asn	Ala	Ile	Xaa	Lys	Gln	Tyr	Arg	325	330	335	
Glu	Leu	Phe	Glu	Glu	Asn	Val	Lys	Leu	Ile	Phe	Glu	Lys	Glu	Ala		340	345	350	
Leu	Tyr	Ala	Ile	Ala	Gln	Lys	Ala	Lys	Gln	Ala	Lys	Thr	Gly	Ala	Arg	355	360	365	
Ala	Leu	Gly	Met	Ile	Leu	Glu	Asn	Leu	Leu	Arg	Asp	Leu	Met	Phe	Glu	370	375	380	

Ile Pro Ser Asp Pro Thr Val Glu Ala Ile Arg Ile Glu Glu Asp Thr
 385 390 395 400
 Ile Thr Gln Asn Lys Pro Pro Val Ile Ile Gln Lys Ser Pro Glu Ala
 405 410 415
 Ile Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 708:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 410 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 702183..703412

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 708:

Met Thr Gln Ser Thr Leu Glu Val Ala Lys Lys Ile Val Arg Lys Leu
 1 5 10 15
 Arg Asn Ala Gly Tyr Gln Ala Tyr Phe Val Gly Gly Ser Val Arg Asp
 20 25 30
 Met Leu Leu Gly Arg Pro Ile Glu Glu Val Asp Ile Ala Thr Asn Ala
 35 40 45
 Ser Pro Thr Ile Val Thr Thr Ile Phe Pro Asp Thr Leu Ser Ile Gly
 50 55 60
 Ala Ala Phe Gly Ile Ile Ala Val Lys Glu Asn Gly Gln Leu Phe Glu
 65 70 75 80
 Val Ala Thr Phe Arg Ser Asp Glu Asp Tyr Glu Asp Gly Arg His Pro
 85 90 95
 Asn Arg Val Val Phe Ala Ser Met Lys Asp Asp Ala Ile Arg Arg Asp
 100 105 110
 Phe Thr Ile Asn Gly Met Tyr Tyr Asp Pro Phe Leu Glu Lys Leu Phe
 115 120 125
 Asp Leu Val Glu Gly Arg Ala Asp Leu Glu Arg Xaa Ile Ile Arg Ala
 130 135 140
 Ile Gly Asn Pro Lys Gln Arg Phe Leu Glu Asp Lys Leu Arg Ile Leu
 145 150 155 160
 Arg Ala Ile Arg Phe Ala Ala Thr Leu Gly Phe Ala Leu Asp Pro Gln
 165 170 175
 Thr Glu Gln Ala Ile Ile Lys Glu Leu Pro Ser Leu Pro Asn Ser Val
 180 185 190
 Ala Pro Glu Arg Ile Trp Gln Glu Leu Lys Lys Met Leu Arg Thr Ala
 195 200 205
 Pro Tyr Glu Ser Leu Gln Leu Leu Thr Lys Leu Lys Val Leu Pro Ile
 210 215 220
 Leu Phe Pro Glu Leu Lys Val Ser Ser Ser Gly Phe Leu Arg Ser Ala
 225 230 235 240
 Ile Ala Phe Ala Gln Lys Ile His Asp Ser Gln Ile Pro Glu Ile Ala
 245 250 255
 Leu Leu Leu Pro Leu Phe Arg Glu Val Asp Lys Glu Lys Ala Leu Glu
 260 265 270
 Ala Phe Ser Arg Leu Arg Val Ser Asn Lys Glu Leu Lys Leu Leu Glu
 275 280 285
 Asp Trp Tyr Ala Ala Leu Pro Gln Phe Leu Ser Lys Gln Asn Asp Lys

Pro Val Asp Arg Pro Leu Lys Val Ala Leu Ile Gly His Pro Asn Val
 225 230 235 240
 Gly Lys Ser Ser Ile Ile Asn Ala Leu Leu Lys Glu Glu Arg Cys Ile
 245 250 255
 Thr Asp Asn Ser Pro Gly Thr Thr Arg Asp Asn Ile Asp Val Ala Tyr
 260 265 270
 Thr His Asn Asn Lys Glu Tyr Val Phe Ile Asp Thr Ala Gly Leu Arg
 275 280 285
 Lys Thr Lys Ser Ile Lys Asn Ser Val Glu Trp Met Ser Ser Ser Arg
 290 295 300
 Thr Glu Lys Ala Ile Ser Arg Thr Asp Ile Cys Leu Leu Val Ile Asp
 305 310 315 320
 Ala Thr Gln Gln Leu Ser Tyr Gln Asp Lys Arg Ile Leu Ser Met Ile
 325 330 335
 Ala Arg Tyr Lys Lys Pro His Val Ile Leu Val Asn Lys Trp Asp Leu
 340 345 350
 Met Phe Gly Val Arg Met Glu His Tyr Val Gln Asp Leu Arg Lys Met
 355 360 365
 Asp Pro Tyr Ile Gly Gln Ala His Ile Leu Cys Ile Ser Ala Lys Gln
 370 375 380
 Arg Arg Asn Leu Leu Gln Ile Phe Ser Ala Ile Asp Asp Ile Tyr Thr
 385 390 395 400
 Ile Ala Thr Thr Lys Leu Ser Thr Ser Leu Val Asn Lys Val Leu Ala
 405 410 415
 Ser Ala Met Gln Arg His His Pro Gln Val Ile Asn Gly Lys Arg Leu
 420 425 430
 Arg Ile Tyr Tyr Ala Ile His Lys Thr Thr Thr Pro Phe Thr Phe Leu
 435 440 445
 Leu Phe Ile Asn Ser Asn Ser Leu Leu Thr Lys Pro Tyr Glu Leu Tyr
 450 455 460
 Leu Lys Asn Thr Leu Lys Ala Ala Phe Asn Leu Tyr Arg Val Pro Phe
 465 470 475 480
 Asp Leu Glu Tyr Lys Ala Lys Pro Ala Arg Lys Ser Asn
 485 490

(2) INFORMATIONS POUR LA SEQ ID NO: 710:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 705011..705604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 710:

Lys Asn Lys Asn Leu Leu Leu Glu Ile Ile Lys Thr Lys Ile Ser Tyr
 1 5 10 15
 Phe Leu Glu Ile Leu Ile Pro Met His Tyr Glu Pro Tyr Asp Glu Phe
 20 25 30
 Glu Pro Asp Asn Glu Leu Asp His Leu Ile Cys Glu Ser Asp Lys Thr
 35 40 45
 Lys Pro Leu Asp Ala Tyr His Asp Thr Gly Val Tyr Ile Glu Glu Asp
 50 55 60
 Asp Arg Glu Asn Gly Asp Leu Leu Ile Val Leu Gly Lys Ser Ile Leu

65					70					75				80	
Asn	Gly	Ala	Ile	Arg	Gln	Phe	Tyr	Ile	Ser	Asp	His	Asn	Tyr	Ala	Tyr
				85					90					95	
Thr	Arg	Gly	Tyr	Tyr	Gln	Gly	Cys	Trp	Glu	Gly	Trp	Phe	Asn	Ile	Pro
			100					105					110		
Pro	Lys	Lys	Ile	Thr	Thr	Ala	Glu	Tyr	Asp	Cys	Asp	Gln	Leu	Leu	Gln
		115					120					125			
Pro	Asp	Leu	Leu	Leu	Thr	Thr	Asn	Val	Glu	Lys	Leu	Ile	His	Ala	Pro
	130					135					140				
Glu	Asp	Phe	Pro	Ala	Gln	Asn	Ala	Asn	Leu	Asp	Asn	Ile	Ile	Ile	Cys
145					150					155					160
Met	Thr	Ala	Leu	Asn	Gly	Glu	His	Arg	Val	Gln	Phe	Leu	Ile	Gly	Asp
			165					170						175	
Asn	His	Arg	Ser	Phe	Trp	Ile	Arg	His	His	Asp	Gly	Glu	Ser	Trp	Ser
			180				185						190		
Lys	Trp	Ser	Thr	Phe	Ile										
			195												

(2) INFORMATIONS POUR LA SEQ ID NO: 711:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 152 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(705704..706159)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 711:

Cys	Arg	Cys	Gly	Thr	Asp	Tyr	Ile	Gly	Asp	Leu	Leu	Ile	Glu	Ala	Phe
1				5					10				15		
Asp	Val	Lys	Phe	Ser	Ala	Met	Leu	Ala	Glu	Phe	Thr	Glu	Ile	Ile	Gly
		20						25				30			
Ser	Ala	Ala	Asn	Ala	Gln	Gly	Ile	Cys	Asn	Asp	Ile	Leu	Arg	Ser	Val
		35				40						45			
Ile	Ile	Ser	His	Ile	Asp	Glu	Trp	Lys	Val	His	Leu	Val	Asp	Met	
	50				55				60						
Asp	Leu	Leu	Arg	Ser	Glu	Val	Gly	Leu	Arg	Ser	Val	Gly	Gln	Lys	Asp
65					70				75					80	
Pro	Leu	Ile	Glu	Phe	Lys	Asn	Glu	Ser	Phe	Leu	Leu	Phe	Glu	Gly	Leu
			85					90					95		
Ile	Arg	Asp	Ile	Arg	Ile	Ala	Ile	Val	Lys	His	Leu	Phe	Ala	Leu	Glu
		100						105					110		
Leu	Ser	Leu	Thr	Arg	Ser	Asp	Arg	Pro	Asp	Asn	Ala	Ile	Pro	Thr	Val
		115				120						125			
Ala	Thr	Ala	Phe	His	Asn	His	Asp	Asn	Phe	Arg	Pro	Met	Glu	Leu	Thr
	130				135						140				
Ile	Val	Gly	Glu	Glu	Glu	Glu	Ser								
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 712:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(706138..706521)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 712:

```

Phe Ala Ile Ser Gly Pro Pro Glu Gly Glu Ala Met Ser Asp Pro Met
1      5      10      15
Phe Asp Arg Leu Ile Glu Thr Ala Gln Lys Arg Val Glu Gly Arg Asn
20      25      30
Tyr Thr Ile Arg Lys His Thr Leu Glu Tyr Asp Asp Val Met Asn Lys
35      40      45
Gln Arg Gln Thr Ile Tyr Ala Phe Arg Asn Asp Val Leu His Ala Glu
50      55      60
Asp Leu Phe Val Val Ala Lys Glu Gln Ile Glu His Val Ala Leu Ala
65      70      75      80
Leu Ala Phe Leu Ile Leu Lys Asp Ala His Ala Asp His Cys Ser Leu
85      90      95
Pro Lys Ile Glu Glu Trp Leu Ser Tyr Ser Phe Pro Val Lys Leu Asp
100      105      110
Asp Gln Glu Ile Arg Arg Leu Gly Asp Val Asp Ala Val Gln Thr Thr
115      120      125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 713:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 536 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(706496..708103)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 713:

```

Ser Ala Gly Ser Pro Pro Glu Lys Arg Lys Ala Ile Tyr Gln Cys Asp
1      5      10      15
Val Val Tyr Gly Thr Ala Ser Gly Phe Gly Phe Asp Tyr Leu Arg Asp
20      25      30
Asn Ser Ile Ala Thr Arg Lys Glu Glu Gln Val Gly Arg Gly Phe Tyr
35      40      45
Phe Ala Ile Ile Asp Glu Ile Asp Ser Val Leu Ile Asp Glu Ala Arg
50      55      60
Thr Pro Leu Ile Ile Ser Gly Pro Gly Glu Lys His Asn Pro Val Tyr
65      70      75      80
Phe Glu Leu Lys Asp Arg Val Ala Glu Leu Val Tyr Phe Gln Arg Glu
85      90      95
Met Cys Asn His Ile Ala Ile Glu Ala Arg Lys Val Leu Asp Pro Phe
100      105      110
Leu Gly Thr Asp Val Leu Pro Lys Asp Lys Lys Val Met Glu Ala Ile
115      120      125
Ser Glu Ala Cys Arg Ala Leu Trp Leu Val Ser Lys Gly Met Pro Leu

```


130	135	140
Asn Arg Val Leu Arg Arg Val Arg Glu His Pro Asp Leu Arg Ala Met		
145	150	155
Ile Asp Lys Trp Asp Val Phe Tyr His Ala Glu Gln Asn Lys Glu Glu		
	165	170
Cys Leu Glu Lys Leu Ser Ser Leu Tyr Ile Val Val Asp Glu His Asn		
	180	185
Asn Asp Phe Glu Leu Thr Asp Lys Gly Met Leu Gln Trp Ile Glu Lys		
	195	200
Ile Gly Gly Ala Ala Glu Asp Phe Val Met Met Asp Met Gly His Glu		
	210	215
Tyr Ala Leu Ile Glu Glu Asp Ala Thr Leu Ser Pro Ala Asp Lys Leu		
225	230	235
Asn Arg Lys Ile Ala Val Ser Glu Lys Asp Thr Gln Arg Lys Ala Arg		
	245	250
Ala His Gly Leu Arg Gln Leu Leu Arg Ala His Leu Leu Met Glu Lys		
	260	265
Asp Ile Asp Tyr Ile Val Arg Asp Asp Gln Ile Val Ile Ile Asp Glu		
	275	280
His Thr Gly Arg Pro Gln Pro Gly Arg Arg Phe Ser Glu Gly Leu His		
	290	295
Gln Ala Ile Glu Ala Lys Glu His Val Thr Ile Arg Lys Glu Ser Gln		
305	310	315
Thr Phe Ala Thr Val Thr Leu Gln Asn Phe Phe Arg Leu Tyr Glu Lys		
	325	330
Leu Ala Gly Met Thr Gly Thr Ala Ile Thr Glu Ser Arg Glu Phe Lys		
	340	345
Glu Ile Tyr Ser Leu Tyr Val Leu Gln Val Pro Thr Phe Lys Pro Cys		
	355	360
Leu Arg Ile Asp His Asn Asp Ala Phe Tyr Met Thr Glu Arg Glu Lys		
	370	375
Tyr Gln Ala Ile Val Ala Glu Ile Ile Ser Ala His Arg Ser Gly Lys		
385	390	395
Pro Ile Leu Ile Gly Thr Glu Ser Val Glu Val Ser Glu Lys Leu Ser		
	405	410
Arg Ile Leu Arg Gln Asn Arg Ile Asn His Thr Val Leu Asn Ala Lys		
	420	425
Asn His Ala Gln Glu Ala Glu Ile Ala Gly Ala Gly Lys Val Gly		
	435	440
Ala Val Thr Val Ala Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys		
	450	455
Leu Asp Glu Glu Ala Val Ala Ala Gly Gly Leu Tyr Val Ile Gly Thr		
465	470	475
Ser Arg His Gln Ser Arg Arg Ile Asp Arg Gln Leu Arg Gly Arg Cys		
	485	490
Ala Arg Leu Gly Asp Pro Gly Ala Ala Lys Phe Phe Leu Ser Phe Glu		
	500	505
Asp Arg Leu Met Arg Leu Phe Ala Ser Pro Lys Leu Asn Thr Leu Ile		
	515	520
Arg His Phe Arg Ser Ser Arg Arg		525
530	535	

(2) INFORMATIONS POUR LA SEQ ID NO: 714:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 107 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(708078..708398)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 714:

```

Glu Arg Met Pro Ala Phe Gly Arg Asn Ser Gly Gly Gly Ile Trp Val
1      5      10      15
Ser Ser Ala Val Gly Tyr Gly Ser Leu Arg Cys Ala Asp Ser Gly Xaa
      20      25      30
Ile Ala Met His Lys Gly Phe Ile Thr Glu Met Gln Thr Gly Glu Gly
      35      40      45
Lys Thr Leu Thr Ala Val Met Pro Leu Tyr Leu Asn Ala Leu Ser Gly
      50      55      60
Lys Pro Val His Leu Val Thr Val Asn Asp Tyr Leu Ala Gln Arg Asp
65      70      75      80
Cys Glu Trp Val Gly Ser Val Leu Arg Trp Leu Gly Leu Thr Thr Gly
      85      90      95
Val Leu Val Cys Arg Glu Pro Thr Arg Glu Ala
      100      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 715:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 120 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(708248..708607)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 715:

```

Met Asp Phe Leu Lys Arg Phe Phe Gly Ser Ser Gln Glu Arg Ile Leu
1      5      10      15
Lys Arg Phe Gln Lys Leu Val Glu Glu Val Asn Ala Cys Asp Glu Lys
      20      25      30
Phe Ser Ser Leu Ser Asp Asp Glu Leu Arg Glu Lys Thr Pro Gln Leu
      35      40      45
Lys Gln Arg Tyr Gln Asp Gly Glu Ser Leu Asp Lys Leu Leu Pro Glu
      50      55      60
Ala Tyr Gly Val Val Lys Asn Val Cys Arg Arg Leu Ala Gly Thr Pro
65      70      75      80
Val Glu Val Ser Gly Tyr His Gln Gln Trp Asp Met Val Pro Tyr Asp
      85      90      95
Val Gln Ile Leu Gly Xaa Ser Leu Cys Ile Lys Ala Leu Ser Pro Arg
      100      105      110
Cys Lys Pro Gly Lys Glu Arg His
      115      120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 716:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 469 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(708872..710278)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 716:

Glu	Asn	Val	Ser	Leu	His	Lys	Asn	Lys	Asp	Leu	Lys	Arg	Phe	Phe	Trp
1				5					10				15		
Tyr	Cys	Lys	Arg	Glu	Lys	Thr	Gln	Lys	Leu	Cys	Ile	Met	Trp	Leu	Ile
			20					25					30		
Val	Ala	Trp	Thr	Leu	Leu	Ala	Cys	Leu	Ala	Met	Ala	Leu	Val	Phe	Lys
		35					40					45			
Ala	Tyr	Arg	His	Val	Ile	Ser	Phe	Arg	Ser	Tyr	Val	Asn	Gln	Val	Met
50						55					60				
Arg	Asp	Val	Arg	Leu	Ser	Val	Asp	Leu	Lys	Glu	Trp	Ala	Val	Ala	Glu
65					70					75					80
Met	Arg	Leu	Ala	Pro	Ile	Leu	Lys	Lys	Arg	Gln	Tyr	Arg	Arg	Lys	Tyr
				85					90					95	
Leu	Phe	Glu	Tyr	Ile	Arg	Ile	Leu	Arg	Glu	Leu	Glu	Arg	Phe	Glu	Glu
			100					105					110		
Ala	Glu	Lys	Leu	Leu	Gly	Glu	Ala	Lys	Lys	Leu	Lys	Leu	Ala	Gly	Ala
		115					120					125			
His	Phe	Phe	Leu	Glu	Val	Ala	His	Lys	Ala	Phe	Arg	His	Gly	Ala	Tyr
130						135					140				
Lys	Glu	Ala	Ala	His	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Glu	Leu	Met	Gly
145					150					155					160
Glu	Arg	Glu	Val	Ala	Arg	Tyr	Thr	Ile	Ser	Leu	Val	Tyr	Leu	Gly	Glu
				165					170					175	
Val	Asp	Ala	Ala	Cys	Arg	Ile	Ile	Glu	Pro	Trp	Ile	Gly	Pro	Leu	Ala
			180					185					190		
His	Gln	Glu	Val	Phe	Ile	Ser	Val	Gly	His	Ile	Tyr	Phe	Ala	Thr	Lys
195							200					205			
Arg	Tyr	Ala	Asp	Ala	Ile	Asp	Phe	Tyr	Arg	Arg	Ala	Arg	Ser	Leu	Gly
210						215					220				
Ser	Cys	Pro	Ile	Asp	Val	Leu	Tyr	Asn	Leu	Ala	His	Ser	Leu	Arg	Ile
225					230					235					240
Cys	Gly	Gln	Tyr	Val	Asp	Ala	Gly	Met	Leu	Phe	Arg	Glu	Leu	Leu	Gly
				245					250					255	
Asp	Pro	Val	Tyr	Lys	Asp	Glu	Ala	Met	Phe	Asn	Ile	Gly	Leu	Cys	Glu
			260					265					270		
Gln	Lys	Leu	Gly	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Ile	Tyr	Gln	Asn	Ser
		275					280					285			
Glu	Leu	Trp	Val	Arg	Gly	Asp	Ala	Leu	Met	Met	Arg	Tyr	Ala	Ala	Leu
290						295					300				
Ala	Ala	Ala	Asp	Gln	Gln	Asp	Tyr	Gln	Leu	Ala	Glu	His	Cys	Trp	Thr
305					310					315					320
Leu	Ala	Phe	Arg	Cys	Gln	Ser	Tyr	Ala	Asp	Asp	Trp	Asn	Cys	Cys	Val
				325					330					335	
His	Tyr	Gly	Leu	Ala	Leu	Cys	His	Leu	Lys	Lys	Tyr	Ala	Glu	Ala	Glu
			340					345					350		
Lys	Val	Tyr	Leu	Arg	Val	Ile	Gln	Lys	Thr	Pro	Asp	Cys	Leu	Val	Ala
		355					360					365			
Cys	Lys	Ala	Leu	Ala	Trp	Leu	Ala	Gly	Val	Gly	His	Ala	Thr	Met	Ile
370						375					380				

Ser Ala Arg Glu Gly Ile Ala Tyr Ala Lys Arg Ala Leu Gln Ile Lys
 385 390 395 400
 Arg Ser Pro Glu Val Leu Glu Leu Leu Ser Ala Cys Glu Ala Arg Glu
 405 410 415
 Gly Asn Phe Asp Val Ala Tyr Asp Ile Gln Ala Ile Leu Ala Glu Arg
 420 425 430
 Asp Thr Thr Ala Lys Glu Arg Glu Arg Arg Ser Gln Ile Leu Lys Asn
 435 440 445
 Leu Arg Gln Lys Leu Pro Ile Asp Gln Gln His Ile Val Glu Val Ser
 450 455 460
 Leu Leu Leu Ala Ala
 465

(2) INFORMATIONS POUR LA SEQ ID NO: 717:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 301 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(710262..711164)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 717:

Met Ala Ala Arg Glu Met Leu Tyr Val Asn Arg Glu Thr Gly Lys Val
 1 5 10 15
 Glu Gln Glu Arg Ile Ile Cys Ser Ser Leu Val Lys Phe Phe Ile Glu
 20 25 30
 Thr Arg Ile Gly Arg Ala Leu Tyr Ser Val Leu Cys Lys Asn Ser Leu
 35 40 45
 Phe Ser Arg Ile Val Gly Trp Cys Gln Arg Leu Arg Val Thr Arg Tyr
 50 55 60
 Phe Ile Lys Pro Phe Val Thr Lys Tyr Arg Ile Cys Ile Glu Glu Ser
 65 70 75 80
 Ala Ser Pro Leu His Asp Tyr Ala Ser Phe Asn Asp Phe Phe Val Arg
 85 90 95
 Lys Leu Lys Pro Asp Ala Arg Pro Ile Cys Gln Gly Glu Asp Ile Cys
 100 105 110
 Val Thr Pro Ala Asp Gly Ala Tyr Leu Val Phe Pro Ser Met Ala Asp
 115 120 125
 Leu Ser Leu Phe Thr Ile Lys Asn Lys Pro Phe Ser Leu Glu Ser Phe
 130 135 140
 Leu Gly Asp Pro Gln Leu Ala His Gln Tyr Ala Gln Gly Ser Met Ala
 145 150 155 160
 Ile Ala Arg Leu Ala Pro Phe Asp Tyr His Arg Phe His Phe Pro Ile
 165 170 175
 Ala Gly Ile Ala Glu Ala Pro Arg Arg Ile Asn Gly His Leu Phe Ser
 180 185 190
 Ile His Pro Leu Met Leu Lys Arg Asn Phe Glu Val Phe Thr Glu Asn
 195 200 205
 Lys Arg Glu Ile Thr Ile Ile Thr Ser Lys Glu Phe Gly Glu Val Ala
 210 215 220
 Tyr Val Glu Val Gly Ala Leu Asn Val Gly Ser Ile His Gln Thr Phe
 225 230 235 240
 Ser Pro Gly Ser Tyr Val Lys Lys Gly Ala Glu Lys Gly Phe Phe Ala

(2) INFORMATION POUR LA SEQ ID NO: 718:

(A) LONGUEUR: 444 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 711432..712763

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 718:

Met 1	Leu	Arg	Asn	Asp 5	Thr	Ile	Thr	Ala	Ile 10	Ala	Thr	Pro	Pro	Gly 15	Glu
Gly	Ser	Ile	Ala 20	Ile	Val	Arg	Val	Ser	Gly 25	Pro	Asp	Ala 30	Ile	Ser	Ile
Ser	Asp	Arg 35	Ile	Phe	Ser	Gly	Asn 40	Ile	Ala	Gly	Tyr 45	Ala	Ser	His	Thr
Ala	His 50	Leu	Gly	Thr	Val	Ser 55	His	Asn	Ala	Val	Cys 60	Ile	Asp	Gln	Ala
Leu 65	Val	Leu	Val	Met 70	Arg	Ala	Pro	Arg	Ser	Phe 75	Thr	Gly	Glu	Asp	Ile 80
Val	Glu	Phe	Gln	Cys 85	His	Gly	Gly	Tyr	Phe 90	Ala	Cys	Ser	Gln	Ile	Val 95
Asn	Ala	Leu 100	Leu	Ala	Glu	Gly	Ala	Arg 105	Ala	Ala	Leu	Pro	Gly 110	Glu	Phe
Ser	Gln	Arg 115	Ala	Phe	Leu	Asn	Gly 120	Lys	Ile	Asp	Leu 125	Ile	Gln	Ala	Glu
Ala	Ile 130	Gln	Gln	Leu	Ile	Ala	Ala 135	Asp	Asn	Ile	Asp 140	Ala	Phe	Arg	Ile
Ala 145	Gln	Asn	Gln	Phe 150	Gln	Gly	His	Thr	Ser	Gln	Ala 155	Ile	Ser	Ser	Ile 160
Ser	Ser	Leu	Ile	Ile 165	Glu	Ala	Leu	Ala	Tyr 170	Ile	Glu	Val	Leu	Ala	Asp 175
Phe	Pro	Glu	Glu	Asp 180	Ile	Glu	Thr	Glu 185	Asp	Ser	Leu	Pro	Lys 190	His	Arg
Ile	Met 195	Glu	Ala	Leu	Ser	Ile	Thr 200	Asp	Glu	Leu	Leu 205	Ser	Ser	Phe	Asp
Glu	Gly 210	Gln	Arg	Leu	Ala	Gln 215	Gly	Thr	Ser	Ile	Val 220	Leu	Ala	Gly	Leu
Pro 225	Asn	Ala	Gly	Lys 230	Ser	Ser	Ile	Leu	Asn	Ala 235	Leu	Thr	Gln	Lys	Asn 240
Arg	Ala	Ile	Val	Thr 245	Asp	Ile	Pro	Gly	Thr 250	Thr	Arg	Asp	Ile	Leu	Glu 255
Glu	Asn	Trp 260	Val	Leu	Gln	Gly	Lys 265	Asn	Leu	Arg	Leu	Ile	Asp 270	Ser	Ala
Gly	Leu 275	Arg	Glu	Thr	Glu	Asn 280	Leu	Val	Glu	Lys	Glu 285	Gly	Ile	Ala	Arg

Ala Arg Glu Ala Met Ser Gln Ala Glu Gly Ile Leu Trp Val Val Asp
 290 295 300
 Ala Ser Gln Pro Leu Pro Glu Phe Pro Thr Ile Leu Tyr Gln Lys Pro
 305 310 315 320
 Thr Ile Leu Leu Trp Asn Lys Cys Asp Ile Val Ser Pro Pro Gln Ile
 325 330 335
 Glu Val Pro Phe Gln Gln Ile Ser Val Ser Ala Lys Thr Gly Glu Gly
 340 345 350
 Leu Leu Glu Leu Lys Gln Ala Leu Gln Lys Trp Leu Asn Thr Thr Gln
 355 360 365
 Leu Gly Lys Ser Ser Lys Ile Phe Leu Val Ser Ala Arg His His Ser
 370 375 380
 Leu Leu His Ser Val Tyr Thr Cys Leu Thr Ala Ala Leu Asn Gly Phe
 385 390 395 400
 Thr Glu His Leu Pro Asn Glu Cys Ile Ala Leu Asp Leu Arg Gln Ala
 405 410 415
 Leu His Ser Ile Gly Asn Leu Ser Gly Ser Glu Val Thr Glu Asn Val
 420 425 430
 Leu Gly Glu Ile Phe Ser Lys Phe Cys Ile Gly Lys
 435 440

(2) INFORMATIONS POUR LA SEQ ID NO: 719:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 224 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 712767..713438

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 719:

Pro Leu Met Lys Ser Leu Asn Val Gln Ala Lys Arg Ala Phe Ile Ile
 1 5 10 15
 Ser Thr Leu Asn Arg Leu Phe Pro Asn Pro Ala Pro Ser Leu Thr Gly
 20 25 30
 Trp Gln Thr Pro Phe Gln Leu Leu Ile Ala Ile Leu Leu Ser Gly Asn
 35 40 45
 Ser Thr Asp Lys Ala Val Asn Ser Val Thr Pro Ser Leu Phe Ala Lys
 50 55 60
 Ala Pro Asp Ala Gln Ser Met Ser Met Leu Ala Pro Ser Glu Ile Tyr
 65 70 75 80
 Ser Leu Ile Ala Pro Cys Gly Leu Gly Glu Arg Lys Ala Ala Tyr Ile
 85 90 95
 His Ala Leu Ser His Ile Leu Val Asp Arg Tyr His Gln Glu Thr Pro
 100 105 110
 His Thr Leu Pro Glu Leu Thr Ala Leu Pro Gly Val Gly Arg Lys Thr
 115 120 125
 Ala Ser Val Phe Leu Ser Ile Tyr Tyr Gly Glu Asn Thr Phe Pro Val
 130 135 140
 Asp Thr His Ile Leu Arg Leu Ala His Arg Trp Gln Leu Ser Asn Glu
 145 150 155 160
 Thr Glu Ser Phe Ser Cys Arg Lys Arg Phe Ser Thr Val Ile Trp Thr
 165 170 175
 Lys Ala Leu Ser Glu Ile Ala Phe Thr Thr His Leu Leu Cys Lys Ser

(2) INFORMATION POUR LA SEQ ID NO: 720:

(A) LONGUEUR: 194 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(713651..714232)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 720:

(2) INFORMATION POUR LA SEQ ID NO: 721:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(714120..714632)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 721:

```

Asn Asn Thr Asp Tyr Val Lys Asn Arg Gln Lys Asp Leu Asn Pro Tyr
1      5      10      15
Met Leu Leu Asp Ser Arg Phe Pro Thr Asp Tyr Tyr Leu Arg Ile Leu
      20      25      30
Glu Leu Val Ile Arg Asp Ala Ser Cys Lys Leu Val Tyr Asn Arg Arg
      35      40      45
Leu His Met Leu Glu Ala Ile Pro Leu Asp Gln Lys Leu Ser Thr Asp
      50      55      60
Gln Glu Gly Glu Ser Ser Ile Leu Arg Glu Val Ile Ser Glu Leu Leu
65      70      75      80
Ala His Ser Gly Glu Ser Tyr Ala Ile Ser Ala Gln Leu Leu Ala Val
      85      90      95
Ile Asp Ile Tyr Leu Lys Gln Glu Gln Pro Ser Asn Ser Trp Phe Ala
      100      105      110
Arg Ile Phe Arg Lys Arg Glu Arg Ala Arg Lys Arg Gln Thr Ile Asn
      115      120      125
Lys Leu Leu Leu Leu Lys Ser Ile Leu Phe Phe Glu Arg Gln Arg Pro
      130      135      140
Val Lys Lys Val Glu Ser Val Ala Asp Ser Ile Leu Gln Arg Ser Lys
145      150      155      160
Gly Lys Phe Phe Val Leu Gly Arg Phe Tyr Thr
      165      170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 722:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 253 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(714834..715592)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 722:

```

Ala Ser Ile Trp Lys Arg Arg Val Ala Arg Arg Asn Glu Asn Tyr Asp
1      5      10      15
Val Lys Lys Ala Glu Glu Gln Gln Gly Ile Val Gln Tyr Leu Gln Asp
      20      25      30
Ser Lys Met Pro Ala Leu Thr Arg Ala Tyr Arg His Leu Arg Ala Phe
      35      40      45
Asn Ser Ala Cys Leu Arg Thr Ile Arg Glu Phe Phe Ala Thr Ile Phe
      50      55      60
Arg Ala Leu Arg Asp Ala Tyr Tyr Arg His Cys Thr Arg Ser Gly Ile
65      70      75      80
Asn Phe Cys Gly Ala Asp Lys Asp Ser Leu Glu Val Leu Val Ala Val
      85      90      95
Gly Leu Leu Leu Arg Met Ala Thr Leu Arg Ser Phe Glu His Val Gly
      100      105      110
Gly Asn Tyr Glu Asp Arg Leu Val Asn Asn Asp Ala Pro Val Thr Gly
      115      120      125
Ala Gly Arg Thr Leu Val Tyr Asp Ala Val Asp Asp Ile Glu Ser Ile

```


130		135		140
Leu Asn Thr Arg Thr Asn Trp Pro Gln His Val Met Ile Gly Phe Ser				
145		150		155
Arg Gly Leu Val Gln Leu Cys Ala Thr Pro Tyr Asn Ala Thr Ser Gln				160
		165		170
Glu Cys Phe Lys Ser Ile Val Arg Leu Glu Lys Glu Asp Pro Ser Ser				175
		180		185
Asp Tyr Ser Gln Ala Leu Leu Leu Ala Gly Ile Ile Asp Arg Leu Ala				190
		195		200
Glu Lys Ala Pro Met Ala Ala Lys Tyr Val Leu Asp Ala Leu Arg Val				205
		210		215
Arg Thr Ser Glu Leu Ile Gly Glu Leu Ile Ile Leu Asp Leu Leu Pro				220
225		230		235
Pro Val Trp Lys Val Gly Arg Gly Xaa Tyr Ser Leu Leu				240
		245		250

(2) INFORMATIONS POUR LA SEQ ID NO: 723:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 99 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(715558..715854)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 723:

Ala Leu Tyr Gly Gly Asn Ser Gly Pro Glu Gly Phe Ser Ser Ala Ser				
1		5		10
Arg Gly Asp Glu Ile Asp Asp Val Pro Asp Ser Glu Glu Gly Glu Leu				15
		20		25
Glu Glu Arg Val Ser Asp His Ala Glu Ser Ile Ile Thr Glu Ser Ser				30
		35		40
Glu Thr Leu Phe Arg Thr Thr Ser Ser Ser Gly Val Ser Glu Asp Leu				45
		50		55
Gln Gln His Val Ser Leu Glu Glu Ser Pro Arg Gln Arg Gly Phe Leu				60
65		70		75
Gly Arg Ile Arg Asp Ala Val Xaa Phe Tyr Leu Glu Ala Ser Cys Cys				80
		85		90
Thr Lys Glu				95

(2) INFORMATIONS POUR LA SEQ ID NO: 724:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 339 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(715921..716937)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 724:

```

Asn Leu Ile Lys Ile Val Gly Ile Lys Ser Tyr Cys Phe Gly Gly Gly
1      5      10      15
Phe Met Ser Ile Arg Pro Thr Asn Gly Ser Gly Asn Gly Tyr Pro Ser
20      25      30
Ile Asn Pro Ser Asn Asp Asn Gln Asp Gly Leu Val Gln Ser Thr Ser
35      40      45
Gly Pro Asn Tyr Gly Gly His Thr Val Ser Ser Arg Gly Gly Phe Gln
50      55      60
Gly Ile Cys Val Arg Ile Ala Asp Leu Phe Arg Asn Cys Phe Ser Arg
65      70      75      80
Asn Arg Gly Thr Thr Thr Pro Ser Arg Pro Val Ile Thr Gln Ala Asp
85      90      95
Ile Tyr His Pro Thr Ile Phe Gly Gln Gly Ala Gln Pro Ile Val Ser
100      105      110
Thr Gly Asp Lys Lys Leu Asp Ser Ala Ile Ile Gln Ala Asp Leu Arg
115      120      125
Ala Gln Asn Lys Gln Thr Leu Ala Thr His Ile Gln Ser Lys Leu Gly
130      135      140
Ser Met Glu Gly Gln Ser Pro Gln Asp Tyr Lys Ala Gly Ala Tyr Ser
145      150      155      160
Ala Leu Arg Leu Met Leu Phe Thr Pro Gly Glu Thr Thr Val Ser Ser
165      170      175
Glu Arg Glu Arg Gln Ala Cys Val Thr Gly Arg Asp Leu Trp Glu Gln
180      185      190
Ala Ala Gly Asp Leu Ala Thr Asn Gly Asn Thr Asp Gly Leu Met Leu
195      200      205
Met Ala Asn Leu Ser Val Gly Gly Lys His Val Pro Ala Gly His Leu
210      215      220
Arg Glu Tyr Met Asn Thr Val Lys Gly Thr Phe Thr Asp Glu Asn Glu
225      230      235      240
Ala Thr Asp Pro Thr Val Asp Ala Ile Leu Asp Leu Ala Ala Lys Ile
245      250      255
Asp Ala Thr Glu Phe Ser Ser Pro Gly Ser Gly Pro Val Ile Leu Asn
260      265      270
Tyr Ile Gly Asn Cys Gly Gln Val Val Leu Glu Asn Glu Lys Met Asn
275      280      285
Gln Leu Val Leu Glu Asp Gln Asn Gly Gln Asp Pro Gln Arg Val Gln
290      295      300
Asp Asn Ser Lys Glu Leu Gln Lys Leu Leu Glu Asn Ala Arg Lys Thr
305      310      315      320
Asp Pro Glu Leu Tyr Phe Gln Thr Leu Thr Val Ile Thr Ser Ser Val
325      330      335
Phe Leu Asp

```

(2) INFORMATIONS POUR LA SEQ ID NO: 725:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 403 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(717149..718357)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 725:

Met	Asp	Lys	Leu	Ser	Ile	Arg	Asp	Leu	Ser	Leu	Glu	Gly	Lys	Lys	Val
1				5					10					15	
Leu	Val	Arg	Val	Asp	Phe	Asn	Val	Pro	Ile	Lys	Asp	Gly	Lys	Ile	Leu
			20					25					30		
Asp	Asp	Val	Arg	Ile	Arg	Ser	Ala	Met	Pro	Thr	Ile	His	Tyr	Leu	Leu
		35					40					45			
Lys	Gln	Asp	Ala	Ala	Val	Ile	Leu	Val	Ser	His	Leu	Gly	Leu	Pro	Lys
	50					55					60				
Gly	Gly	Val	Phe	Glu	Glu	Ala	Tyr	Ser	Leu	Ala	Pro	Ile	Val	Pro	Val
65					70					75					80
Leu	Glu	Gly	Tyr	Leu	Gly	His	His	Val	Pro	Leu	Ser	Pro	Asp	Cys	Ile
				85					90					95	
Gly	Glu	Val	Ala	Arg	Gln	Ala	Val	Ala	Gln	Leu	Ser	Pro	Gly	Arg	Val
			100					105					110		
Leu	Leu	Leu	Glu	Asn	Val	Arg	Phe	His	Lys	Gly	Glu	Glu	His	Pro	Asp
		115					120					125			
Glu	Asp	Pro	Ser	Phe	Ala	Ile	Glu	Leu	Ala	Ala	Tyr	Ala	Asp	Phe	Tyr
	130					135					140				
Val	Asn	Asp	Ala	Phe	Gly	Thr	Ser	His	Arg	Lys	His	Ala	Ser	Val	Tyr
145					150					155					160
Arg	Val	Pro	Gln	Leu	Phe	Pro	Asp	Arg	Ala	Ala	Ala	Gly	Phe	Leu	Met
				165					170					175	
Glu	Lys	Glu	Leu	Glu	Phe	Leu	Gly	Gln	His	Leu	Leu	Val	Glu	Pro	Lys
			180					185					190		
Arg	Pro	Phe	Thr	Ala	Ile	Leu	Gly	Gly	Ala	Lys	Met	Ser	Ser	Lys	Ile
		195					200					205			
Gly	Val	Ile	Glu	Ala	Leu	Leu	Ser	Cys	Val	Asp	His	Leu	Val	Leu	Ala
	210					215					220				
Gly	Gly	Met	Gly	Tyr	Thr	Phe	Leu	Arg	Ala	Met	Asn	Arg	Gln	Val	Gly
225					230					235					240
Asn	Ser	Leu	Val	Glu	Glu	Ser	Gly	Ile	Pro	Leu	Ala	Lys	Lys	Val	Leu
				245					250					255	
Glu	Lys	Ala	Gln	Ala	Leu	Gly	Val	Lys	Ile	His	Leu	Pro	Val	Asp	Ala
			260					265					270		
Lys	Val	Ala	Lys	Gln	Cys	Asp	Ser	Gly	Glu	Asp	Trp	Arg	Glu	Leu	Ser
		275					280					285			
Ile	Gln	Glu	Gly	Ile	Pro	Glu	Gly	Leu	Ala	Gly	Phe	Asp	Ile	Gly	Ala
	290					295					300				
Gln	Thr	Ile	Glu	Leu	Phe	Ser	Lys	Val	Ile	Gln	Glu	Ser	Ala	Thr	Ile
305					310					315					320
Phe	Trp	Asn	Gly	Pro	Val	Gly	Val	Tyr	Glu	Val	Pro	Pro	Phe	Asp	Gln
				325					330					335	
Gly	Ser	Lys	Ala	Ile	Ala	Gln	Cys	Leu	Ala	Ser	His	Ser	Ser	Ala	Val
			340					345					350		
Thr	Val	Val	Gly	Gly	Gly	Asp	Ala	Ala	Ala	Val	Val	Ala	Leu	Ala	Gly
		355					360					365			
Cys	Thr	Ser	Gln	Ile	Ser	His	Val	Ser	Thr	Gly	Gly	Gly	Ala	Ser	Leu
	370					375					380				
Glu	Phe	Leu	Glu	Lys	Gly	Ser	Leu	Pro	Gly	Thr	Glu	Ile	Leu	Ser	Pro
385					390					395					400
Ala	Gln	Ser													

(2) INFORMATIONS POUR LA SEQ ID NO: 726:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 121 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 718500..718862

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 726:

```

Gln Asn Ser Ala Arg Ser Asn Lys Lys Asn Thr Ile Glu Ser Ala Ala
1      5      10      15
Pro Ala Gly Thr Val Ile Asn His Glu Ser Thr Ile Ser Leu Met Ile
20      25      30
Arg Lys Leu Met Ala Arg Lys Pro Leu Ala Asn Pro Ile Pro Asn Thr
35      40      45
Asp Pro Thr Thr Thr Cys Val Val Asp Ile Gly Asn Pro Lys Glu Glu
50      55      60
Ala Ala Ala Ile Val Ile Ala Glu Leu Ile Pro Thr Glu Lys Pro Arg
65      70      75      80
Asp Gly Val Asn Ser Val Ile Phe Phe Pro Ile Val Ser Ile Thr Arg
85      90      95
Gln Pro His Val Ala Asn Pro Gln Thr Lys Pro Ser Pro Pro Lys Asp
100     105     110
Ile Asn Thr Lys Arg Thr Phe Glu Glu
115     120

```

(2) INFORMATIONS POUR LA SEQ ID NO: 727:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 433 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(718499..719797)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 727:

```

Asp Ala Arg Arg Glu Ile Gly Met Trp Leu Leu Leu Val Cys Val Val
1      5      10      15
Val Gly Gly Phe Tyr Thr Ala Trp Asn Ile Gly Ala Asn Asp Val Ala
20      25      30
Asn Ala Val Gly Pro Ser Val Gly Ala Gly Ala Leu Thr Leu Lys Gln
35      40      45
Ala Val Leu Ile Ala Ala Val Phe Glu Phe Leu Gly Ala Val Leu Leu
50      55      60
Gly Asp Arg Val Ile Gly Thr Ile Glu Ser Gly Leu Val Ala Pro Ser
65      70      75      80
Gly His Val Leu Ser Ser Gln Asp Tyr Val Phe Gly Met Ala Ala Ala
85      90      95
Leu Leu Ala Thr Gly Val Trp Leu Gln Ile Ala Ser Phe Cys Gly Trp
100     105     110
Pro Val Ser Thr Thr His Ala Ile Val Gly Ala Val Leu Gly Phe Gly

```

	115		120		125														
Ile	Ile	Leu	Lys	Glu	Asp	Ala	Val	Ile	Tyr	Trp	Asn	Ser	Cys	Gly	Arg				
	130					135					140								
Val	Phe	Val	Ser	Trp	Leu	Ala	Ser	Pro	Ile	Ile	Gly	Gly	Tyr	Phe	Ala				
145					150					155									160
Phe	Leu	Ile	Phe	Ser	Phe	Ile	Arg	Lys	Ala	Ile	Leu	Tyr	Lys	Lys	Asp				
			165					170						175					
Pro	Val	Ser	Ala	Met	Val	Arg	Ile	Ala	Pro	Phe	Leu	Ser	Ala	Ile	Ile				
			180					185					190						
Ile	Phe	Ala	Leu	Gly	Leu	Val	Leu	Ile	Leu	Ser	Gly	Ala	Val	Ala	Pro				
	195						200					205							
Val	Ile	Ser	Phe	Ser	Pro	Ala	Leu	Arg	Ile	Val	Cys	Gly	Leu	Ser	Leu				
210						215					220								
Phe	Ala	Phe	Phe	Phe	Thr	Ile	Trp	Gly	Ile	Arg	Phe	Phe	Lys	Leu	Ala				
225					230					235									240
Ile	Leu	Pro	Gln	Glu	Val	Leu	Pro	Gly	Thr	Leu	Leu	Asp	Arg	Leu	Leu				
			245					250						255					
Ser	Lys	Ser	Thr	Asp	Tyr	Gly	Arg	Lys	Tyr	Leu	Ile	Val	Glu	Arg	Ile				
			260					265					270						
Phe	Ala	Tyr	Leu	Gln	Met	Ile	Ile	Ala	Cys	Phe	Met	Ser	Phe	Ala	His				
	275					280						285							
Gly	Ser	Asn	Asp	Val	Ala	Asn	Ala	Ile	Ala	Pro	Val	Ala	Gly	Ile	Tyr				
290						295					300								
Arg	Thr	Leu	Tyr	Pro	Gln	Ser	Tyr	Ser	Ser	Lys	Val	Leu	Leu	Val	Phe				
305					310					315									320
Met	Ser	Leu	Gly	Gly	Leu	Gly	Leu	Val	Cys	Gly	Leu	Ala	Thr	Trp	Gly				
			325						330					335					
Trp	Arg	Val	Ile	Asp	Thr	Ile	Gly	Lys	Lys	Ile	Thr	Glu	Leu	Thr	Pro				
		340						345					350						
Ser	Arg	Gly	Phe	Ser	Val	Gly	Met	Ser	Ser	Ala	Ile	Thr	Ile	Ala	Ala				
	355						360						365						
Ala	Ser	Ser	Leu	Gly	Phe	Pro	Ile	Ser	Thr	Thr	His	Val	Val	Val	Gly				
	370					375					380								
Ser	Val	Leu	Gly	Ile	Gly	Phe	Ala	Arg	Gly	Leu	Arg	Ala	Ile	Asn	Leu				
385					390					395					400				
Arg	Ile	Ile	Lys	Asp	Ile	Val	Leu	Ser	Trp	Phe	Ile	Thr	Val	Pro	Ala				
			405						410					415					
Gly	Ala	Ala	Leu	Ser	Ile	Val	Phe	Phe	Leu	Leu	Leu	Arg	Ala	Leu	Phe				
			420					425					430						
Cys																			

(2) INFORMATIONS POUR LA SEQ ID NO: 728:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 164 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(719782..720273)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 728:

Trp	Tyr	Glu	Lys	Arg	Cys	Lys	Lys	Thr	Leu	Gly	Phe	Gly	Ser	Ile	Ser
1					5				10					15	

```

Ser Cys Ile Pro Arg Ser Ala Val Gly Asp His Phe Asp Thr Arg Phe
      20      25      30
Leu Ser Arg Xaa Ala Glu Asp Ile Ala Ile Leu Leu Thr Val Lys Glu
      35      40      45
Leu Gln Phe Tyr Pro Glu Phe Glu Glu Leu Phe Phe Glu Phe Leu Gln
      50      55      60
Lys Thr Val Gln Ser Phe Glu Ala Val Ala Lys Thr Ile Arg Glu Met
      65      70      75      80
Asp Arg Leu Leu Glu Ser Ser Phe Gly Gly Asn Arg Ala Asp Lys Thr
      85      90      95
Arg Val Leu Val Ser Glu Val Ser Asn Leu Glu His Glu Cys Asp Leu
      100      105      110
Leu Gln Arg Glu Leu Met Lys Val Phe Phe Ser Asp Asp Phe Ala Ile
      115      120      125
Gly Thr Lys Gly Phe Val Leu Trp Met Gln Ile Ile Lys Gly Ile Ser
      130      135      140
Gly Ile Ser Asn Asn Ser Glu Lys Leu Ala Tyr Arg Val Ser Met Thr
      145      150      155      160
Leu Glu Glu Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 729:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 103 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(720144..720452)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 729:

```

Met Gln Val Leu Ala Ser Leu Phe Gly Gln Ser Pro Phe Ala Pro Leu
1      5      10      15
Gln Ala His Leu Glu Leu Val Ser Ser Thr Ile Asn Val Leu Phe Pro
      20      25      30
Leu Phe Ser Ala Leu Lys Glu Gly Asp Tyr Glu Arg Val Gly Val Leu
      35      40      45
Ala Gln Leu Val Ser Ser Lys Glu Arg Gln Ala Asp Gly Met Lys Asn
      50      55      60
Asp Val Arg Arg His Leu Ala Ser Gly Val Phe Leu Pro Val Phe Arg
      65      70      75      80
Ala Ala Leu Leu Glu Ile Ile Ser Ile Gln Asp Ser Leu Ala Asp Xaa
      85      90      95
Leu Arg Ile Ser Gln Phe Cys
      100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 730:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 321 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 730:

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 721559..722356

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 731:

```

Gly Ala Gly Tyr Met Asn Asn Pro Leu Leu Leu Gln Ala Ser Arg Leu
1      5      10      15
Thr Lys His Tyr Tyr Lys Arg Ser Phe Trp Phe Gln Lys Lys Lys Val
20      25      30
Ala Thr Thr Pro Leu Asn Gln Val Ser Phe Ser Leu Pro Arg His Lys
35      40      45
Ile Ile Gly Leu Ile Gly Glu Ser Gly Ser Gly Lys Thr Thr Leu Ala
50      55      60
Leu Gly Leu Ala Gly Leu Ile Pro Leu Thr Ser Gly His Leu Ile Leu
65      70      75      80
Asn Asp Lys Ala Ile Pro Leu His Asn Lys Lys Gly Arg Gln Tyr Leu
85      90      95
Ser Ser Gln Val Arg Met Val Phe Gln Asn Pro Arg Ser Ser Leu Asn
100      105      110
Pro Arg Lys Thr Ile Phe Asp Thr Leu Ser His Ser Leu Leu Tyr His
115      120      125
Arg Leu Val Ser Lys Glu Glu Leu Gly Ala Thr Val Glu Lys Ala Leu
130      135      140
Ser Leu Val Gly Leu Ser Thr Asp Tyr Leu Tyr Ser Tyr Pro His Gln
145      150      155      160
Leu Ser Gly Gly Gln Leu Gln Arg Ile Ser Ile Ala Arg Ala Leu Leu
165      170      175
Gly Ala Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp
180      185      190
Leu Ser Met Gln Ala Gln Ile Leu Asn Met Leu Thr Ser Leu Gln Gln
195      200      205
Gln Ala Arg Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val
210      215      220
Arg Ser Phe Cys Ser Glu Leu Ile Ile Met Tyr Lys Gly Gln Ile Val
225      230      235      240
Glu Thr Gly Ala Thr Glu Glu Ile Phe Cys Asn Pro Gln His Ser Tyr
245      250      255
Thr Arg Met Leu Leu His Ser Gln Leu Pro
260      265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 732:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 284 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(722397..723248)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 732:

```

Glu Asn Ile Val Ser Arg Leu Pro Ser Glu Asp Thr Leu Leu Glu Val
1      5      10      15
Asn Ile Glu Asp Ile Arg Val Ser Pro Phe Gln Pro Arg Arg Thr Phe

```


Arg	Asn	Arg	Ile	Phe	Thr	Met	Tyr	Asn	Val	Lys	Lys	Asp	Phe	Pro	Ile
1				5					10					15	
Phe	Lys	Asn	Gln	Gly	Asp	Pro	Tyr	Val	Tyr	Leu	Asp	Ser	Ala	Ala	Thr
			20					25					30		
Thr	His	Lys	Pro	Gln	Cys	Val	Ile	Asp	Ser	Ile	Val	Asp	Tyr	Tyr	Ser
		35				40					45				
Ser	Ser	Tyr	Ala	Thr	Val	Asn	Arg	Ala	Leu	Tyr	Thr	Ala	Ser	His	Asp
	50					55				60					
Ile	Thr	Phe	Ala	His	Trp	Gln	Val	Arg	Ser	Lys	Val	Gly	Ser	Trp	Ile
65				70						75				80	

Gly Ala Gln Tyr Asp Gln Glu Ile Ile Phe Thr Arg Gly Thr Thr Ser
 85 90 95
 Ser Leu Asn Leu Leu Ala Ile Ala Ala Asn Asp Ser Trp Leu Ala Gly
 100 105 110
 Gly Thr Val Val Ile Ser Glu Ala Glu His His Ala Asn Leu Val Ser
 115 120 125
 Trp Glu Leu Ala Cys Gln Arg Ser Gly Ala Thr Ile Lys Lys Val Arg
 130 135 140
 Val Asp Asp Glu Gly Met Val Asp Cys Asn His Leu Glu Gln Leu Leu
 145 150 155 160
 Lys Gln Gly Val Gln Leu Val Ser Leu Ala His Val Ser Asn Val Ser
 165 170 175
 Gly Ala Val Leu Pro Leu Pro Glu Ile Ala His Leu Val His Arg Tyr
 180 185 190
 Glu Ala Leu Phe Ala Val Asp Gly Ala Gln Gly Val Gly Lys Gly Pro
 195 200 205
 Leu Asn Leu Ser Glu Trp Gly Val Asp Phe Tyr Ala Phe Ser Gly His
 210 215 220
 Lys Leu Tyr Ala Pro Thr Gly Ile Gly Val Leu Tyr Gly Lys Lys Glu
 225 230 235 240
 Leu Leu Glu Ser Leu Pro Pro Val Glu Gly Gly Gly Asp Met Val Ile
 245 250 255
 Val Tyr Asp Phe Glu Glu Leu Ser Tyr Gln Glu Pro Pro Leu Arg Phe
 260 265 270
 Glu Ala Gly Thr Pro His Ile Ala Gly Val Leu Gly Leu Gly Ala Ala
 275 280 285
 Ile Asp Tyr Leu Gln Ala Leu Pro Phe Ser Ile Thr Asp Arg Leu Thr
 290 295 300
 Glu Leu Thr His Phe Leu Tyr Glu Gln Leu Leu Thr Val Pro Gly Ile
 305 310 315 320
 Gln Ile Ile Gly Pro Lys Gln Gly Ala Ala Arg Gly Ser Leu Cys Ser
 325 330 335
 Ile Ser Ile Pro Gly Val Gln Ala Ser Asp Leu Gly Phe Leu Leu Asp
 340 345 350
 Gly Arg Gly Ile Ser Val Arg Ser Gly His Gln Cys Ser Gln Pro Ala
 355 360 365
 Met Val Arg Trp Asp Leu Gly His Val Leu Arg Ala Ser Leu Gly Ile
 370 375 380
 Tyr Asn Asp Gln Gln Asp Ile Leu Leu Phe Val Glu Ala Leu Lys Asp
 385 390 395 400
 Ile Leu Arg Ala Tyr Arg Ser
 405

(2) INFORMATIONS POUR LA SEQ ID NO: 734:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 396 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(724576..725763)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 734:

Thr Met Trp Gly Thr His Gln Gln Arg Gln Ile His Pro Asp Ala Arg

1				5					10					15			
Leu	Ala	Asp	Val	Thr	Arg	Ser	Val	Trp	Arg	Gln	Tyr	Gln	Arg	Asp	His		
			20					25					30				
Val	Phe	Arg	Glu	Ala	Cys	Ser	Trp	Leu	Lys	Glu	Met	Thr	Gln	Glu	Asp		
		35					40					45					
Ser	Trp	Ile	Tyr	Cys	Val	Gly	Gly	Cys	Glu	Ile	Gly	Ala	Ile	Ser	Pro		
	50					55					60						
Glu	Glu	Arg	Ser	Ala	Thr	Cys	Val	Phe	Val	Asn	Gly	Cys	Phe	Ala	Pro		
65					70					75					80		
Ser	Leu	Ser	Val	Leu	Pro	Ala	Glu	Ile	Ile	Val	Ala	Pro	Leu	Arg	Glu		
				85					90					95			
Ala	Arg	Ala	Phe	Phe	Gln	Lys	His	Asp	Glu	Glu	Asp	Val	Val	Glu	Glu		
			100					105					110				
Leu	His	Ser	Leu	Leu	Arg	Gly	Glu	Gly	Thr	Val	Ile	Tyr	Ile	Pro			
		115					120					125					
Glu	Gly	Arg	Glu	Leu	Gln	Thr	Pro	Leu	Phe	Val	Gln	His	His	Tyr	Val		
	130					135					140						
Cys	Ser	Glu	Glu	Glu	Asn	Lys	Lys	Thr	Val	Ser	Val	Pro	Tyr	Ile	Val		
145					150					155					160		
Phe	Val	Leu	Gly	Lys	Gly	Ala	Ala	Ile	Ser	Ile	Glu	Met	Gly	Met	Ser		
			165						170					175			
Ala	Leu	Pro	Asp	Asn	Val	Tyr	Leu	Phe	Gly	Lys	Thr	Leu	Cys	Phe	Leu		
			180					185					190				
Gly	Glu	Glu	Ala	Glu	Leu	Val	Leu	Thr	Met	Lys	Pro	Leu	Pro	Lys	Gly		
		195					200					205					
Thr	Glu	Arg	Ile	Ile	Trp	Ala	His	His	Val	Glu	Val	Glu	Arg	Arg	Gly		
	210					215						220					
Ala	Cys	Ala	Leu	Ile	Gln	Asp	Met	Arg	Ser	Met	Gly	Lys	Gly	Trp	Phe		
225					230					235					240		
Arg	Asn	Ser	Phe	Phe	Leu	Lys	Gly	Glu	Ala	Ala	His	Gly	Glu	Ser	Leu		
			245						250					255			
Val	Lys	Val	Leu	Gly	Gly	Asp	Phe	Leu	Gly	Val	His	Asn	Thr	Met	His		
		260						265					270				
His	Asp	Asp	Arg	Glu	Thr	Thr	Ser	Arg	Gln	Asn	Ile	Arg	Ser	Ile	Leu		
		275					280					285					
Glu	Glu	Gly	Ser	Phe	Ser	Phe	Glu	Gly	Gly	Ile	Tyr	Ile	Ser	Pro	Arg		
	290					295					300						
Gly	Thr	Leu	Ser	Asn	Ala	Tyr	Gln	Lys	His	Asp	Thr	Leu	Leu	Leu	Ser		
305					310					315					320		
Asn	Arg	Ala	Ser	Ala	Ser	Thr	Phe	Pro	Arg	Leu	Glu	Ile	Leu	Thr	Asp		
			325						330					335			
Asp	Val	Lys	Ala	Ser	His	Gly	Ala	Thr	Val	Gly	Ser	Leu	Asn	Ala	His		
			340					345					350				
Leu	Leu	Thr	Tyr	Leu	Arg	Ser	Arg	Gly	Phe	Ser	Leu	Ile	Glu	Ala	Lys		
		355					360					365					
Gln	Ala	Leu	Gln	Lys	Ser	Phe	Leu	Thr	Leu	Asp	Ile	Glu	Lys	Pro	Tyr		
	370					375					380						
Phe	Pro	Lys	Leu	Gln	Lys	Gln	Asp	Leu	Tyr	His	Val						
385					390					395							

(2) INFORMATIONS POUR LA SEQ ID NO: 735:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(725767..726516)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 735:

```

Met Tyr Met Tyr Val Val Lys Lys Lys Arg Ser Leu Glu Gly Leu Ser
1      5      10      15
Leu Ser Ile His Pro Gly Glu Leu His Ile Ile Met Gly Pro Asn Gly
20      25      30
Ala Gly Lys Ser Thr Leu Ala Lys Val Leu Ser Gly Asp Glu Ser Val
35      40      45
Glu Val Ser Ser Gly Thr Met Thr Leu Ala Gly Gln Asp Leu Leu Glu
50      55      60
Leu Ser Pro Glu Glu Arg Ala His Ala Gly Met Phe Ile Ser Phe Gln
65      70      75      80
His Pro Pro Glu Ile Pro Gly Val Asn Asn Arg Ile Phe Leu Lys Glu
85      90      95
Ala Cys Asn Ala Cys Arg Lys Ala Arg Asn Gln Val Val Leu Asp Asp
100      105      110
Ala Ala Phe Glu Glu Leu Leu Thr His Leu Glu Glu Val Tyr Gly Phe
115      120      125
Pro Gly Phe His Phe Phe Ser Asn Arg Asn Val Asn Glu Gly Phe Ser
130      135      140
Gly Gly Glu Lys Lys Lys Asn Glu Leu Trp Gln Met Leu Ala Leu Glu
145      150      155      160
Pro Lys Met Val Val Leu Asp Glu Pro Asp Ser Gly Leu Asp Val Asp
165      170      175
Ala Leu Lys Gly Ile Cys Ser Val Leu Gln Arg Tyr Arg Gln Gln His
180      185      190
Pro Glu Thr Ala Phe Cys Ile Val Thr His Asn Pro Arg Leu Gly Asp
195      200      205
Leu Leu Gln Pro Asp His Val His Ile Leu Leu Asn Gly Arg Val Val
210      215      220
Phe Ser Gly Asp Met His Leu Met Glu Glu Leu Glu Arg Lys Ser Tyr
225      230      235      240
Gln Glu Leu Leu Asp Val Val Thr Gln Glu
245      250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 736:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 94 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(726538..726819)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 736:

```

Leu His Ala Gly Asp Ser Met Leu Val Gly Glu Arg Cys Gly Ala Tyr
1      5      10      15
Thr Asp Pro Gln Ile Val Val Asn Asn Gly Glu Ser Cys Val Glu His
20      25      30
Glu Ala Ala Thr Ser Lys Leu Arg Glu Asp Gln Leu Phe Tyr Leu Arg

```

(2) INFORMATION POUR LA SEQ ID NO: 737:

(A) LONGUEUR: 247 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(726753..727493)

Phe 1	Ser	Glu	Ala	Leu 5	Phe	Arg	Ile	Val	Val 10	Pro	Ala	Arg	Asp	Asn 15	Phe
Phe	Ala	Ala	Leu 20	Asn	Ser	Ala	Val	Phe 25	Ser	Asp	Gly	Ser	Phe 30	Val	Tyr
Ile	Pro	Lys 35	Gly	Val	Cys	Cys	Pro 40	Met	Glu	Ile	Ser	Thr 45	Tyr	Phe	Arg
Ile	Asn 50	Asp	Lys	Glu	Ser	Gly 55	Gln	Phe	Glu	Arg	Thr 60	Leu	Ile	Ile	Ala
Glu 65	Asp	Asp	Ser	Tyr	Val 70	Ser	Tyr	Leu	Glu	Gly 75	Cys	Thr	Ala	Pro	Ser 80
Phe	Ser	Ser	His 85	Gln	Leu	His	Ala	Ala 90	Val	Val	Glu	Leu	Val 95	Ala	His
Asn	Arg	Ser	Val 100	Ile	Arg	Tyr	Ser	Thr 105	Val	Gln	Asn	Trp	Tyr 110	Pro	Gly
Asp	Arg	Lys 115	Thr	Gly	Lys	Gly	Gly 120	Ile	Tyr	Asn	Phe	Val 125	Thr	Lys	Arg
Gly 130	Leu	Cys	Ala	Gly	Glu	His 135	Ser	Lys	Ile	Ser	Trp 140	Ser	Gln	Val	Glu
Val 145	Gly	Ala	Ala	Ile	Thr 150	Trp	Lys	Tyr	Pro	Ser 155	Cys	Ile	Leu	Lys	Gly 160
Glu	Asn	Ser	Val 165	Gly	Glu	Phe	Tyr	Ser	Ile 170	Ala	Leu	Thr	Asn 175	Gly	Lys
Met	Gln	Ala 180	Asp	Thr	Gly	Thr	Lys 185	Met	Leu	His	Ile	Gly 190	Lys	Gly	Ser
Ser	Ser	Thr 195	Ile	Val	Ser	Lys	Gly 200	Ile	Ser	Ala	Glu	Glu 205	Ser	His	Asn
Thr 210	Phe	Arg	Ser	Leu	Val	Ser 215	Ile	Ser	Ser	Gln	Ala 220	Val	Gly	Ser	Cys
Asn 225	Tyr	Thr	Gln	Ala 230	Thr	Leu	Cys	Leu	Leu	Glu 235	Ser	Ala	Ala	Gly	Leu 240
Ile	Arg	Ile	His 245	Lys	Leu	Leu									

(2) INFORMATION POUR LA SEQ ID NO: 738:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 172 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(727469..727984)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 738:

```

Met Asp Ala Pro Val Asp Lys Phe Leu Gln Gln Gln Glu Tyr Pro Tyr
1      5      10      15
Gly Phe Val Thr Pro Ile Gln Ser Glu Gly Leu Ala Pro Gly Ile Ser
      20      25      30
Glu Glu His Ile Glu Gln Leu Val His Leu Arg Gly Glu Pro Lys Phe
      35      40      45
Leu Leu Asp Phe Arg Leu Lys Ala Phe Arg Leu Trp Gln Lys Met Glu
      50      55      60
Glu Pro Thr Trp Ala Arg Leu Arg Tyr Pro Pro Ile Ala Tyr Asp Asp
65      70      75      80
Ile Val Tyr Phe Ser Ala Pro Lys Thr Lys Lys Pro Leu Gly Lys Leu
      85      90      95
Glu Asp Ala Asp Pro Glu Ile Leu Glu Thr Phe Lys Lys Leu Gly Ile
      100      105      110
Pro Ile Asp Glu Gln Lys Arg Leu Leu Asn Val Gln Asp Val Ala Met
      115      120      125
Asp Leu Val Phe Asp Ser Val Ser Ile Gly Thr Thr Phe Lys Lys Thr
      130      135      140
Leu Glu Asp Ala Gly Val Ile Phe Cys Ser Phe Arg Glu Ala Ile His
145      150      155      160
Asn Tyr Pro Asp Leu Val Lys Arg Tyr Leu Gly Ser
      165      170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 739:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(728329..728778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 739:

```

Val Ile Tyr Phe Leu Glu Ile Arg Phe Trp Val Val Ala Arg Glu Gly
1      5      10      15
Phe Gly Val Phe Leu Arg Leu Val Leu Val Phe Trp Val Gly His Tyr
      20      25      30
Asn Leu Gly Leu Cys Tyr Leu Thr Leu Asp Lys Thr Arg Leu Ala Leu
      35      40      45
Lys Ala Phe Gln Glu Ser Leu Leu Asn Ala Glu Asp Ala Asp Ala
      50      55      60
His Phe Tyr Ile Gly Leu Ala His Met Asp Leu Lys Gln Asn Glu Gln

```

65					70					75				80	
Ala	Tyr	Asp	Ala	Phe	Tyr	Arg	Ala	Leu	Gly	Ile	Asn	Leu	Asp	His	Glu
				85					90					95	
Arg	Ser	His	Tyr	Leu	Leu	Gly	Tyr	Leu	His	His	Met	Gln	Gly	Glu	Ser
			100					105					110		
Glu	Lys	Ala	Glu	Thr	Glu	Leu	Ser	Phe	Leu	Val	Ala	Lys	Glu	Ser	Val
		115					120					125			
Phe	Ala	Pro	Leu	Leu	Gln	Lys	Thr	Val	Ser	Ser	Ser	Val	Phe	Leu	Ser
		130				135					140				
Lys	Lys	Glu	Thr	Leu	Phe										
145					150										

(2) INFORMATIONS POUR LA SEQ ID NO: 740:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 196 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(728759..729346)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 740:

Gln	Gly	Thr	Thr	Met	Glu	Glu	Ala	Glu	Lys	His	Leu	Ala	Lys	Glu	Phe
1				5				10					15		
Leu	Cys	Ser	Gly	Ile	Asn	Leu	Phe	Leu	Ser	Gly	Glu	Tyr	Glu	Gln	Ala
			20					25					30		
Glu	Glu	Arg	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Asp	Ser	Glu	Ala	Gly	Leu
		35					40					45			
Ala	Tyr	Cys	Tyr	Leu	Gly	Ile	Ile	Ala	Leu	Glu	Thr	Gly	Arg	Thr	Ala
	50				55						60				
Glu	Ala	Leu	Val	Trp	Cys	Lys	Gln	Gly	Leu	Glu	Ala	Glu	Pro	Gly	Asp
65					70					75				80	
Ser	Tyr	Leu	Arg	Tyr	Cys	Tyr	Gly	Val	Ala	Leu	Asp	Lys	Ala	Asp	Arg
			85					90					95		
Leu	Glu	Glu	Ala	Ile	Gly	His	Tyr	Gln	Val	Tyr	Ala	Glu	Leu	His	Pro
			100					105					110		
Glu	Asp	Ile	Glu	Cys	Leu	Phe	Ser	Leu	Gly	Ser	Ala	Tyr	His	Arg	Leu
		115					120					125			
Leu	Arg	Tyr	Glu	Glu	Ala	Ile	Ala	Cys	Phe	Asp	Arg	Ile	Ala	Gln	Leu
	130					135					140				
Asp	Pro	Trp	Asn	Pro	Gln	Gly	Leu	Tyr	Asn	Lys	Ala	Val	Ile	Leu	Ser
145					150					155				160	
Asp	Met	Glu	Asp	Glu	Glu	Gly	Ala	Ile	Asp	Leu	Leu	Glu	Ser	Thr	Val
			165						170					175	
Lys	Arg	Asn	Pro	Leu	Tyr	Trp	Lys	Ala	Trp	Val	Lys	Leu	Gly	Tyr	Leu
		180						185					190		
Leu	Ser	Arg	Asn												
		195													

(2) INFORMATIONS POUR LA SEQ ID NO: 741:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 995 acides aminés

(B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(729442..732426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 741:

```

Thr Leu Ala Glu Asn Val Leu Gln Tyr Asn Val Gly Ile Ser Tyr Arg
1      5      10      15
Ala Ile Arg Asp Ile Pro Thr Arg Val Trp His Thr Asp Glu Gln Gly
20      25      30
Asn Lys Arg Leu Val Pro Val Arg Lys Asp Tyr Ile Lys Lys Phe Ala
35      40      45
Asp Phe Leu Ala Gln Glu Leu His Met Asp Arg Asp Phe Val Glu Asp
50      55      60
Thr Ile His Ala Lys Ala Ser Val Leu Gly Ser Val Pro Tyr Ile Leu
65      70      75      80
Gln Thr Asn Val Ser Glu Arg Thr Phe Leu Arg Leu Lys Met Leu Glu
85      90      95
Lys Asp Trp Pro Gly Leu His Val Glu Ser Ser Val Arg Arg His Tyr
100      105      110
Pro Glu Gly Arg Thr Val Ala Asp Leu Leu Gly Tyr Val Gly Pro Ile
115      120      125
Ser Ala Glu Glu His Arg Lys Ile Thr Arg Glu Leu Gly Asn Leu Arg
130      135      140
Glu Cys Ile Arg Ala Tyr Glu Glu Gly Glu Asp Pro Lys Phe Pro Ala
145      150      155      160
Gly Ile Ser Ser Val Asp Gln Val Arg Lys Leu Leu His Glu Leu Glu
165      170      175
Met His Ala Tyr Gly Leu Asn Ser Leu Ile Gly Lys Leu Val Val Glu
180      185      190
Ala Phe Cys Asp Arg Lys Leu Arg Gly Leu Ile Gly Lys Arg Ser Met
195      200      205
Leu Val Asp Arg Arg Gly Asn Phe Ile Gln Glu Met Glu Gly Ser Ser
210      215      220
Val Gly Ser Pro Gly Arg Thr Ile Gln Leu Thr Ile Ser Thr Glu Leu
225      230      235      240
Gln Ala Phe Ala His Glu Leu Leu Ala Glu His Glu Arg Gly Glu Cys
245      250      255
Phe Thr Ile Ile Asp Ser Gly Val Ser Asn Asn Ile Leu Pro Pro Phe
260      265      270
Phe Pro Trp Ile Lys Gly Gly Ala Ile Val Ala Met Asp Pro Lys Asn
275      280      285
Gly Gln Ile Leu Ala Met Ala Ser Ser Pro Arg Tyr Asp Asn Asn Asp
290      295      300
Phe Ile Asn Met Lys Asp Ser Pro Asn Gln Glu Glu Cys Arg Ser Ser
305      310      315      320
Val Leu Arg Trp Leu Glu Asn Leu Glu Tyr Ile Gly Glu Val Phe Asp
325      330      335
Arg Arg Val Pro Leu Arg Arg Glu Arg Leu Asp Pro Leu Ser Gly Lys
340      345      350
Tyr Phe Asp Glu Glu Leu Ser Phe Ser Tyr Arg Ala Phe Leu Asp Phe
355      360      365
Ile Leu Pro Asp Thr Ser Lys Val Lys Gln Met Leu Cys Glu Lys Gly
370      375      380
Ser Ile Gly Leu Ser Ile Tyr Leu Gln Gly Thr Ile Glu Gln Leu Leu

```


385											390											400
Glu	Met	Phe	Glu	Cys	Glu	Glu	Lys	Glu	Cys	Gly	Leu	Val	Phe	Asp	Val							
				405					410					415								
Leu	Phe	Pro	Lys	Glu	Asp	Gly	His	Glu	Ile	Ile	Gly	Glu	Val	Thr	Ser							
				420					425					430								
Leu	Lys	Arg	Gln	Lys	Gln	Phe	Lys	Ala	Ile	Leu	Ala	Glu	Arg	Glu	Glu							
				435					440					445								
Glu	Val	Gln	Ala	Phe	Arg	Glu	Arg	Leu	Gly	Ser	Ile	Phe	Ala	Asp	Leu							
				450					455					460								
Ser	Ala	Asn	Tyr	Asp	Lys	Ile	Leu	Phe	Leu	Asp	Leu	Leu	Arg	Thr	Ala							
465					470					475					480							
Val	Asp	Pro	Glu	Lys	Val	Ser	Ile	Ser	Leu	Leu	Ala	Glu	Ile	Gly	His							
				485					490					495								
Met	Ser	Val	Leu	Asp	Phe	Val	Asp	Tyr	Gln	Gly	His	Phe	Ile	Ala	Leu							
				500					505					510								
Arg	Lys	Ser	Phe	Ala	Lys	Leu	Met	Glu	Asn	Ala	Phe	Ile	Asp	His	Asp							
				515					520					525								
Phe	Thr	Ala	Trp	Arg	Glu	Glu	His	Phe	Thr	Gln	Phe	Ile	Lys	Gln	Lys							
				530					535					540								
Arg	Asp	Glu	Glu	Leu	Glu	Arg	Lys	Gln	Arg	Tyr	Pro	Thr	Pro	Tyr	Val							
545					550					555					560							
Asp	Tyr	Leu	Val	Glu	Glu	Arg	Ser	Arg	Gln	Tyr	Ala	Leu	Phe	Cys	Arg							
				565					570					575								
Glu	His	Met	Asp	Ser	Phe	Ile	Thr	Phe	Leu	Leu	Ser	Glu	Ile	Glu	Pro							
				580					585					590								
Pro	Leu	Gly	Asn	Pro	Tyr	Tyr	Gln	Glu	Ile	Ala	Cys	Trp	Arg	Gln	Glu							
				595					600					605								
Leu	Arg	Ser	Gly	Ala	Tyr	Pro	Ala	Leu	Glu	Trp	Arg	Glu	His	Tyr	Asp							
				610					615					620								
Phe	Leu	His	Lys	His	Leu	Ser	Gln	Thr	Ser	Tyr	Asp	Leu	Cys	Glu	Leu							
625					630					635					640							
Phe	Ala	Ala	Phe	Arg	Glu	Phe	Ser	Glu	Leu	Lys	Arg	Pro	Leu	Tyr	Gly							
				645					650					655								
Gln	Tyr	Pro	Leu	Thr	Leu	Thr	Arg	Asn	Ile	Glu	Gln	Ile	Glu	Gln	Asp							
				660					665					670								
Leu	Ile	Ala	Ser	Phe	Tyr	Pro	Leu	Tyr	Gly	Tyr	Gly	His	Leu	Ser	Ala							
				675					680					685								
His	Ala	Phe	Gly	Gln	Ala	Ala	Thr	Leu	Gly	Ser	Ile	Phe	Lys	Leu	Val							
				690					695					700								
Ser	Ala	Tyr	Ser	Val	Leu	Val	Gln	His	Leu	Ser	Asp	Gln	Glu	Asp	Leu							
705					710					715					720							
Ser	Lys	Leu	Leu	Val	Ile	Val	Asp	Lys	Gln	Ser	Leu	Gly	Leu	Arg	Ser							
				725					730					735								
Gly	Lys	Pro	His	Val	Gly	Phe	Phe	Lys	Asp	Gly	Ser	Pro	Ile	Ala	Ser							
				740					745					750								
Phe	Phe	Lys	Gly	Gly	Ile	Leu	Pro	Gly	Asn	Asp	Tyr	Ser	Gly	Arg	Gly							
				755					760					765								
Tyr	Ile	Asp	Leu	Ile	Ala	Ala	Leu	Glu	Met	Ser	Ser	Asn	Pro	Tyr	Phe							
				770					775					780								
Ser	Leu	Leu	Val	Ser	Glu	Tyr	Leu	Ser	Asp	Pro	Glu	Asp</										

Tyr Gln Pro Ser Leu Ile Gln Gly Glu Trp Tyr Gln Gly Ser Phe Ser
 865 870 875 880
 Pro Glu Gln Ala Lys Lys Lys Arg Glu Ile Phe Leu Pro Asp Ser Ile
 885 890 895
 Val Asp Leu Phe Lys Arg Gly Met His Asn Val Ile Trp Gly Gln Tyr
 900 905 910
 Gly Thr Thr Arg Phe Met Arg Gln Arg Phe Ala Pro Glu Arg Leu Ala
 915 920 925
 Arg Ile Ile Gly Lys Thr Ser Thr Ala Glu Val Ile Ala Arg Val Gly
 930 935 940
 Leu Asp Arg Glu Arg Gly Arg Met Lys Leu Lys Asp Val Trp Phe Ala
 945 950 955 960
 Ala Val Gly Tyr Glu Asp Glu Ala Leu Ser His Pro Asp Ile Val Val
 965 970 975
 Val Val Tyr Leu Arg Leu Gly Glu Phe Gly Arg Asp Leu Arg Leu Trp
 980 985 990
 Gln Cys Val
 995

(2) INFORMATIONS POUR LA SEQ ID NO: 742:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 394 acides aminés.

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 733246..734427

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 742:

Met Lys Lys Leu Leu Lys Ser Val Leu Val Phe Ala Ala Leu Ser Ser
 1 5 10 15
 Ala Ser Ser Leu Gln Ala Leu Pro Val Gly Asn Pro Ala Glu Pro Ser
 20 25 30
 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys
 35 40 45
 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr
 50 55 60
 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Gln Thr Asp Val Asn Lys
 65 70 75 80
 Glu Phe Gln Met Gly Ala Lys Pro Thr Thr Ala Thr Gly Asn Ala Ala
 85 90 95
 Ala Pro Ser Thr Cys Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His
 100 105 110
 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Tyr Met Ala Leu Asn
 115 120 125
 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Thr Ser Gly
 130 135 140
 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly
 145 150 155 160
 Asp Asn Glu Asn His Ala Thr Val Ser Asp Ser Lys Leu Val Pro Asn
 165 170 175
 Met Ser Leu Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Thr Phe
 180 185 190
 Ala Trp Ser Ala Gly Ala Arg Ala Ala Leu Trp Glu Tyr Gly Cys Ala

	195		200		205														
Thr	Leu	Gly	Xaa	Ser	Phe	Gln	Tyr	Ala	Gln	Ser	Lys	Pro	Lys	Val	Glu				
	210					215					220								
Glu	Leu	Asn	Val	Leu	Cys	Asn	Ala	Ala	Glu	Phe	Thr	Ile	Asn	Lys	Pro				
225					230					235					240				
Lys	Gly	Tyr	Val	Gly	Gln	Glu	Phe	Pro	Leu	Asp	Leu	Lys	Ala	Gly	Thr				
				245					250					255					
Asp	Gly	Val	Thr	Gly	Thr	Lys	Asp	Ala	Ser	Ile	Asp	Tyr	His	Glu	Trp				
			260					265					270						
Gln	Ala	Ser	Leu	Ala	Leu	Ser	Tyr	Arg	Leu	Asn	Met	Phe	Thr	Pro	Tyr				
	275						280					285							
Ile	Gly	Val	Lys	Trp	Ser	Arg	Ala	Ser	Phe	Asp	Ala	Asp	Thr	Ile	Arg				
290						295					300								
Ile	Ala	Gln	Pro	Lys	Ser	Ala	Thr	Thr	Val	Phe	Asp	Val	Thr	Thr	Leu				
305					310					315					320				
Asn	Pro	Thr	Ile	Ala	Gly	Ala	Gly	Asp	Val	Lys	Ala	Ser	Ala	Glu	Gly				
				325					330					335					
Gln	Leu	Gly	Asp	Thr	Met	Gln	Ile	Val	Ser	Leu	Gln	Leu	Asn	Lys	Met				
			340					345					350						
Lys	Ser	Arg	Lys	Ser	Cys	Gly	Ile	Ala	Val	Gly	Thr	Thr	Ile	Val	Asp				
	355					360					365								
Ala	Asp	Lys	Tyr	Ala	Val	Thr	Val	Glu	Thr	Arg	Leu	Ile	Asp	Glu	Arg				
370					375					380									
Ala	Ala	His	Val	Asn	Ala	Gln	Phe	Arg	Phe										
385					390														

(2) INFORMATIONS POUR LA SEQ ID NO: 743:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 734814..735659

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 743:

Leu	Glu	Leu	Pro	Cys	Lys	Leu	Thr	Leu	Lys	Glu	Leu	Leu	Glu	Ser	Gly				
1				5					10					15					
Ala	His	Phe	Gly	His	Gln	Thr	Ser	Arg	Trp	Asn	Pro	Lys	Met	Lys	Pro				
			20					25					30						
Phe	Ile	Phe	Glu	Glu	Lys	Asn	Gly	Leu	Tyr	Ile	Ile	Asp	Leu	Ala	Lys				
		35					40					45							
Thr	Leu	Gly	Gln	Leu	Lys	Lys	Ala	Val	Ser	Cys	Ile	Gln	Lys	Thr	Ile				
	50					55					60								
Asp	Gln	Glu	Arg	Ser	Ile	Leu	Phe	Val	Gly	Thr	Lys	Lys	Gln	Ala	Lys				
65					70				75					80					
Gln	Ile	Ile	Arg	Glu	Ala	Ala	Ile	Glu	Cys	Gly	Glu	Phe	Phe	Ala	Ser				
			85					90					95						
Glu	Arg	Trp	Leu	Gly	Gly	Met	Leu	Thr	Asn	Met	Ala	Thr	Ile	Arg	Asn				
			100				105					110							
Ser	Val	Lys	Thr	Leu	Asn	Arg	Ile	Glu	Leu	Asp	Leu	Glu	Ala	Ser	Asn				
		115					120					125							
Ser	Gly	Leu	Thr	Lys	Lys	Glu	Leu	Ala	Leu	Leu	Ala	Lys	Arg	His	Arg				
	130					135					140								

Lys Leu Leu Asn Asn Leu Glu Gly Val Arg His Met Asn Ser Leu Pro
 145 150 155 160
 Gly Leu Leu Ile Val Ile Asp Pro Gly Tyr Glu Arg Ile Ala Val Ala
 165 170 175
 Glu Ala Gly Lys Leu Gly Ile Pro Val Met Ala Leu Val Asp Thr Asn
 180 185 190
 Cys Asp Pro Thr Pro Ile Asn His Val Ile Pro Cys Asn Asp Asp Ser
 195 200 205
 Ile Lys Ser Ile Arg Leu Ile Val Asn Thr Leu Lys Asp Ala Val Ile
 210 215 220
 Asp Ala Lys Lys Arg Leu Gly Val Glu Ile Leu Ser Pro Val Arg Pro
 225 230 235 240
 Ala Glu Arg Pro Ala Glu Glu Ala Val Glu Glu Leu Pro Leu Pro Thr
 245 250 255
 Gly Glu Ala Gln Asp Glu Ala Ser Ser Lys Glu Gly Val Leu Leu Trp
 260 265 270
 Ala Asp Ile Asp Asn Cys Glu Ala Leu Lys
 275 280

(2) INFORMATIONS POUR LA SEQ ID NO: 744:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 282 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 735659..736504

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 744:

Met Ser Asp Phe Ser Met Glu Thr Leu Lys Asn Leu Arg Gln Gln Thr
 1 5 10 15
 Gly Val Gly Leu Thr Lys Cys Lys Glu Ala Leu Glu His Ala Lys Gly
 20 25 30
 Asn Leu Glu Asp Ala Val Val Tyr Leu Arg Lys Leu Gly Leu Ala Ser
 35 40 45
 Ala Gly Lys Lys Glu His Arg Glu Thr Lys Glu Gly Val Ile Ala Ala
 50 55 60
 Arg Val Asp Glu Arg Gly Ala Ala Leu Val Glu Val Asn Val Glu Thr
 65 70 75 80
 Asp Phe Val Ala Asn Asn Ser Val Phe Arg Ala Phe Val Thr Ser Leu
 85 90 95
 Leu Ser Asp Leu Leu Asp His Lys Leu Ser Asp Val Glu Ala Leu Ala
 100 105 110
 Arg Val Met Ser Ser Gln Glu Pro Ser Leu Ser Val Glu Glu Leu Lys
 115 120 125
 Ala Val Thr Met Gln Thr Val Gly Glu Asn Ile Arg Ile Ser Arg Ala
 130 135 140
 Phe Tyr Thr Pro Val Asn Ser Gly Gln Ser Val Gly Ile Tyr Ser His
 145 150 155 160
 Gly Asn Gly Lys Ala Val Ala Ile Val Phe Leu Ser Gly Ser Glu Asn
 165 170 175
 Gln Glu Ala Leu Ala Lys Asp Ile Ala Met His Ile Val Ala Ser Gln
 180 185 190
 Pro Gln Phe Leu Ser Lys Glu Ser Val Pro Gln Glu Ile Leu Glu Arg

(2) INFORMATION POUR LA SEQ ID NO: 745:

(A) LONGUEUR: 245 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 736520..737254

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 745:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 746:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 178 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 737254..737787

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 746:

```

Met Thr Leu Ala Ser Ala Glu Lys Glu Met Ala Gly Val Leu Thr Phe
1          5          10          15
Phe Gln Lys Glu Thr Arg Gly Phe Arg Thr Gly Lys Ala His Pro Ala
20          25          30
Leu Val Glu Thr Val Thr Val Glu Val Tyr Gly Thr Thr Met Arg Leu
35          40          45
Ser Asp Ile Ala Ser Ile Ser Val Ser Asp Met Arg Gln Leu Leu Ile
50          55          60
Ser Pro Tyr Asp Ala Gly Thr Val Ser Ala Ile Ser Lys Gly Ile Leu
65          70          75          80
Ala Ala Asn Leu Asn Leu Gln Pro Ile Val Glu Gly Ala Thr Val Arg
85          90          95
Ile Asn Val Pro Ala Tyr Gly Arg Ile Pro Thr Arg Ser Asn Lys Gln
100          105          110
Leu Lys Arg Lys Ser Glu Glu Ala Lys Val Ala Ile Arg Asn Ile Arg
115          120          125
Arg Thr Phe Asn Asp Arg Leu Xaa Lys Asp Asp Asn Leu Thr Glu Asp
130          135          140
Ala Val Lys Ser Leu Glu Lys Lys Ile Gln Glu Leu Thr Asp Lys Phe
145          150          155          160
Cys Lys Gln Ile Glu Glu Leu Ala Lys Gln Lys Glu Ala Glu Leu Ala
165          170          175

Thr Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 747:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 246 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 737942..738679

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 747:

```

Gln Gly Phe Glu Ser Pro Trp Gly His Tyr Lys Lys Lys Cys Gly Ser
1          5          10          15
Leu Ala Gln Arg Leu Glu His Leu Thr Phe Asn Glu Arg Val Glu Gly

```

(2) INFORMATIONS POUR LA SEQ ID NO: 748:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 301 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 738838..739740

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 748:

Pro	Asn	Ser	Phe	Arg	Leu	Ser	Lys	Val	Arg	Lys	Phe	Phe	Val	Leu	Pro
1				5					10					15	
Leu	Lys	Asp	Leu	Pro	Ile	Trp	Gln	Arg	Glu	Cys	Leu	Leu	Glu	His	Tyr
			20					25					30		
Leu	Phe	Pro	Tyr	His	Leu	Gly	Ser	Cys	Leu	Glu	Gly	Glu	Ala	Leu	Ile
		35				40						45			
Val	Asn	Gln	Ala	Gly	Thr	Leu	Leu	Ala	Gly	Ile	Asn	Leu	Arg	Asp	His
	50					55					60				
Val	Val	Ile	His	Gly	Val	Asp	Phe	Val	Trp	Gln	Pro	Glu	Val	Leu	Leu
65					70					75					80
Gln	Lys	Leu	Ile	Asp	Leu	Asp	Ile	Arg	Leu	Gln	Gln	Ser	Leu	Ser	Phe
				85					90					95	
Ala	Phe	Ser	Ser	Asp	Phe	Gly	Phe	Leu	Thr	Ala	Asp	Pro	Leu	Arg	Cys
			100					105					110		

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 301 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 738838..739740

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 748:

Pro	Asn	Ser	Phe	Arg	Leu	Ser	Lys	Val	Arg	Lys	Phe	Phe	Val	Leu	Pro
1				5					10					15	
Leu	Lys	Asp	Leu	Pro	Ile	Trp	Gln	Arg	Glu	Cys	Leu	Leu	Glu	His	Tyr
			20					25					30		
Leu	Phe	Pro	Tyr	His	Leu	Gly	Ser	Cys	Leu	Glu	Gly	Glu	Ala	Leu	Ile
		35					40					45			
Val	Asn	Gln	Ala	Gly	Thr	Leu	Leu	Ala	Gly	Ile	Asn	Leu	Arg	Asp	His
	50					55					60				
Val	Val	Ile	His	Gly	Val	Asp	Phe	Val	Trp	Gln	Pro	Glu	Val	Leu	Leu
65					70					75					80
Gln	Lys	Leu	Ile	Asp	Leu	Asp	Ile	Arg	Leu	Gln	Gln	Ser	Leu	Ser	Phe
				85					90					95	
Ala	Phe	Ser	Ser	Asp	Phe	Gly	Phe	Leu	Thr	Ala	Asp	Pro	Leu	Arg	Cys
			100					105					110		

Gly Thr Ala Leu Ile Ala Arg Ala Phe Val His Val Pro Ala Leu Lys
 115 120 125
 Tyr Gly Asp Ala Leu Ser Glu Leu Leu Val Pro Tyr Gln Arg Glu Phe
 130 135 140
 Ala Ser Ser Ser Leu Leu Pro Leu Ser Gln Glu Ser Leu Gly Asp Ile
 145 150 155 160
 Leu Cys Leu Ser Asn Ile Cys Ser Leu Gly Leu Ser Glu Glu Gln Ile
 165 170 175
 Leu Ser Ser Leu Arg Leu Val Val Ser Lys Ile Leu Ser Ala Glu Lys
 180 185 190
 Glu Ala Arg Asn Gln Leu Val Lys Glu Asn Xaa Thr Glu Xaa Lys Asn
 195 200 205
 Arg Ile Leu Arg Ser Val Gly Met Leu Thr His Ser Cys Cys Leu Asp
 210 215 220
 Leu Gln Glu Ala Leu Asp Ala Thr Ser Trp Ile Gln Leu Gly Met Ser
 225 230 235 240
 Met Gln Trp Ile Glu Asp Ser Glu Asn His Pro Leu Trp Asn Pro Leu
 245 250 255
 Phe Trp Asp Leu Arg Arg Gly His Leu Ala Leu Tyr Asn Gln Asp Thr
 260 265 270
 Ala Asn Arg Ser Ile Glu Lys Glu Val Ile Ala Gln Ile Arg Ala Lys
 275 280 285
 Ala Thr Lys Pro Gln Ala Glu Arg Leu Ile Ile Arg Ile
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 749:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 666 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(740060..742057)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 749:

Arg Val Arg Ile Leu Lys Lys Ser Asp Asn Thr Val Asn Phe Glu Asp
 1 5 10 15
 Ile Ser Ile Leu Glu Leu Leu Gln Phe Val Ser Lys Ile Ser Gly Thr
 20 25 30
 Asn Phe Val Phe Asp Ser Asn Asp Leu Gln Phe Asn Val Thr Ile Val
 35 40 45
 Ser His Asp Pro Thr Ser Val Asp Asp Leu Ala Thr Ile Leu Leu Gln
 50 55 60
 Val Leu Lys Met His Asp Leu Lys Val Val Glu Gln Gly Asn Asn Val
 65 70 75 80
 Leu Ile Tyr Arg Asn Pro Lys Leu Ser Lys Leu Ser Thr Val Val Thr
 85 90 95
 Asp Gly Ser Ala Lys Asp Thr Cys Glu Ala Val Val Val Thr Arg Val
 100 105 110
 Phe Arg Leu Tyr Ser Val Ser Pro Ser Ala Ala Val Gly Ile Ile Gln
 115 120 125
 Pro Leu Leu Ser His Asp Ala Ile Ile Ser Ala Ser Glu Ser Thr Arg
 130 135 140
 His Ile Ile Val Ser Asp Ile Ala Gly Asn Ile Glu Lys Val Arg Glu

145	150	155	160
Leu Leu Gln Ala	Leu Asp Ser Pro Gly Thr	Ala Ile Asp Met Ser	Glu
Tyr Asp Val Gln	Phe Ala Asn Pro Ala	Leu Val Ser Tyr Cys	Gln
Asp Val Leu Gly	Ala Met Ala Glu Glu Glu	Ala Phe Gln Ile	Phe Ile
Gln Pro Gly Thr	Asn Lys Ile Phe Val	Ile Ser Ser Pro Arg	Leu Thr
Ala Lys Thr Ile	Gln Leu Glu Ser Leu	Asp Ile Pro Glu Met	Ala
His Thr Leu Asp	Asp Val Thr Ser Pro	Ala Ala Leu Gly Ser	Ser
Gly Ala Ala Asn	Pro Lys Ser Leu Arg	Phe Phe Met Tyr Lys	Leu Lys
Tyr Gln Asn Gly	Ala Ala Ile Ala	Gln Ala Ile Gln Asp	Ile Gly Tyr
Asn Leu Tyr Val	Thr Thr Ala Met	Asp Glu Asp Phe	Ile Asn Thr Leu
Asn Ser Ile Gln	Trp Leu Pro Val	Asn Asn Ser Ile	Val Val Ile Gly
Asn Gln Ala Asn	Val Asp Lys Val Val	Ser Leu Leu Asn Gly	Leu Asp
Leu Pro Pro Lys	Gln Val Tyr Ile Glu	Val Leu Ile Leu Glu	Thr Ser
Leu Glu Lys Ser	Trp Asp Phe Gly	Val Gln Trp Ala Ala	Leu Gly Asp
Glu Gln Gly Lys	Val Ala Tyr Ala	Ser Gly Leu Leu Ser	Asn Thr Gly
Leu Thr Asp Pro	Leu Arg Asn Gln	Ser Leu Pro Val	Ala Leu Asn Pro
Gly Asn Ile Ser	Leu Pro Thr Pro	Gly Gln Leu Ala	Gly Ile Ser Asp
Met Met Tyr Gly	Ser Ser Ala Phe	Gly Leu Gly Ile	Ile Gly Asn Val
Leu Ser His Asn	Gly Lys Ser Tyr	Leu Thr Leu Gly	Gly Leu Leu Ser
Ala Leu Asp Gln	Asp Gly Asp Thr	Thr Val Val Leu	Asn Pro Arg Ile
Met Ala Gln Asp	Thr Gln Ala Ser	Phe Phe Val Gly	Gln Thr Ile
Pro Phe Gln Thr	Thr Ser Thr Val	Ile Gln Glu Thr	Gly Ser Val Thr
Gln Asn Ile Glu	Tyr Glu Asp Ile	Gly Val Asn Leu	Val Val Thr Ser
Thr Ile Ala Pro	Asn Asn Val Val	Thr Leu Gln Ile	Glu Gln Thr Ile
Ser Glu Leu His	Ser Ala Gln Gly	Val Leu Thr Pro	Val Thr Asp Lys
Thr Phe Ala Ala	Thr Arg Leu Gln	Val Pro Asp Gly	Cys Phe Leu Val
Met Ser Gly His	Ile Arg Asp Lys	Leu Thr Lys Ile	Val Ser Gly Val
Pro Leu Leu Ser	Leu Pro Leu Ile	Lys Gly Leu Phe	Ser Arg Ser
Ile Asp Gln Arg	Gln Lys Arg Asn	Ile Met Ile Phe	Ile Lys Pro Lys
Val Ile Ser Ser	Phe Glu Glu Gly	Thr Ala Leu Ser	Asn Thr Glu Gly

Tyr Arg Tyr Asn Trp Glu Ser Glu Arg Gly Ser Leu Glu Val Ala Pro
 625 630 635 640
 Arg His Ala Pro Glu Cys Gln His Ile Pro Lys Val Gln Ala Glu Ser
 645 650 655
 Asn Phe Lys Met Leu Glu Ile Glu Ala Glu
 660 665

(2) INFORMATIONS POUR LA SEQ ID NO: 750:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 275 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(742045..742869)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 750:

Gln Lys Ser Leu Ser Leu Asn Thr Tyr Gln Leu Lys Lys Ser Pro Val
 1 5 10 15
 Asn Ile Val Thr Ser Asn Ile Gly Ser Lys Ile Leu Arg Ile Ile Gln
 20 25 30
 Asn Asn Lys Lys Leu Gly Leu Leu Ser Ala Leu Val Val Leu Asp Ala
 35 40 45
 Ala Leu Leu Ser Val Asn Ser Arg Ser Gly Glu Gly Leu Ile Gly Gln
 50 55 60
 Ser Ala Ser Leu Pro Asn Tyr His Glu Ala Glu Gln Gln Ile Ala Ala
 65 70 75 80
 Cys Pro Lys Asn Ile Ala Lys Asn Leu Ala Lys Lys Ser Ser Pro Gly
 85 90 95
 Ala Lys Pro Thr Val Gly Ala Pro Ser Pro Ala Arg Pro Val Ser Val
 100 105 110
 Lys Ala Ala Pro Ala Lys Pro Gln Ala Pro Val Ala Gln Thr Arg His
 115 120 125
 Phe Lys Lys Ser His Gln Ile Phe Ser Pro Asn Phe Thr Gln Ser Ser
 130 135 140
 Gln Gln Val Asn Lys Leu Glu Glu Arg Arg Arg Pro Leu Glu Ser Arg
 145 150 155 160
 Tyr Leu Gln Gly Ala Ala Lys Gln Ala Ala Ala Lys Glu Lys Lys
 165 170 175
 Ala Leu Glu Gln Glu Val Ser Lys Gln Glu Glu Glu Ala Ser Lys Leu
 180 185 190
 Trp Glu Glu Lys Gln Ser Tyr Ala Arg Arg Ala Val Asn Ala Ile Asn
 195 200 205
 Phe Ser Val Arg Lys Gln Ile Glu Glu Gln Gln Lys Thr Ile Ser Asn
 210 215 220
 Pro Gly Asn Asp Gln Thr Leu Pro Gly Lys Lys Asp Pro His Thr Ser
 225 230 235 240
 Gly Glu Pro Val Ile Gln Thr Val Gln Asp Cys Ser Gln Asp Gln Glu
 245 250 255
 Ala Arg Glu Lys Ser Ser Arg Ala Ile Lys Gln Thr Phe Ser Asp Val
 260 265 270
 Ser Gly Ser
 275

Val	Phe	Met	Leu	Arg	Ser	Gly	Val	Ser	Phe	Ser	Ser	Ser	Lys	Thr	Asn
1			5						10					15	
Tyr	Leu	Leu	Thr	Arg	Glu	Leu	Ser	Arg	Lys	Val	Gly	Leu	Thr	Val	Tyr
			20					25					30		

Gln Gly Val Asp Glu His Ser Ser Arg Pro Val Val Ile Lys Thr Leu
 35 40 45
 Val Ser Pro Gly Ile His Asp Arg Arg Phe Leu Arg Ala Phe Glu Glu
 50 55 60
 Glu Ala Arg Ile Met Gln Leu Val Thr His Pro Ala Phe Val Arg Leu
 65 70 75 80
 Glu Asp Arg Gly Glu Cys Glu Gln Gly Arg Tyr Leu Val Ser Glu Tyr
 85 90 95
 Ile Leu Gly Ser Ser Leu Arg Asp Ser Ile Leu Ser Ser Gln Ile Ser
 100 105 110
 Leu Asp Lys Ala Ile Ser Ile Val Leu Gln Val Ala Gln Val Ile Thr
 115 120 125
 Thr Leu His Arg His Gly Val Leu His Leu Asp Ile Lys Pro Glu Asn
 130 135 140
 Ile Val Leu Ser Gln Ser Gly Glu Ile Lys Leu Ile Asp Tyr Gly Leu
 145 150 155 160
 Ser Ala Trp Gln Phe Asn His Trp Gly Ser Pro Ala Tyr Met Ser Pro
 165 170 175
 Glu Gln Ser Arg Gln Glu Pro Pro Ser Pro Ala Ser Asp Val Tyr Ser
 180 185 190
 Leu Ala Leu Leu Ala Tyr Glu Leu Ile Met Gly Gln Leu Ala Leu Gly
 195 200 205
 Lys Val Tyr Val Ser Leu Leu Pro Ser Lys Ile Ser Lys Ile Leu Ile
 210 215 220
 Gln Ala Leu Gln Pro Ser Pro Ala Ala Arg Phe Ser Ser Met Gln Glu
 225 230 235 240
 Phe Ala Glu Ala Leu Gln Asp Tyr Leu Leu His Asp Val His Glu Asp
 245 250 255
 Tyr Arg Lys Lys Asp His Val Val Ala Gln Ile Glu Gln Trp His Asn
 260 265 270
 Gln Arg Ala Trp Leu Ser Pro Glu Lys Leu Ser Ala Pro Glu Glu Ile
 275 280 285
 Cys Val His Ile Tyr Ser Gln Lys Glu Pro Cys Tyr Leu His Asn Ile
 290 295 300
 Tyr Tyr Asp Met Leu Thr Ser Gly Asn Val Ala Glu Phe Trp Phe Ser
 305 310 315 320
 Thr Leu Gln Glu Thr Val Val Leu Arg Leu Ala
 325 330

(2) INFORMATIONS POUR LA SEQ ID NO: 753:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 95 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(744430..744714)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 753:

Leu Lys Leu Gln Asp Cys Lys Arg Cys Asn Gln Lys Arg Arg Leu Lys
 1 5 10 15
 Asn Leu Val Lys Glu Val Arg Gln Leu Pro Leu Pro Ser Ala Thr Lys
 20 25 30
 Ile Val Ala Glu Val Ala Arg Tyr Ser Leu Ser Val Gly Glu Phe Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 754:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 125 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(744611..744985)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 754:

Asn	Tyr	Ser	Ala	Glu	Pro	Cys	Arg	Phe	Leu	Glu	Glu	Lys	Asp	Gln	Ala
1				5					10					15	
Phe	Asp	Met	Gln	Lys	Val	Asp	Leu	Gln	Thr	Pro	Ile	Thr	Leu	Ala	Val
			20					25					30		
Glu	Val	Gly	Phe	Cys	Gln	Ile	Ser	Glu	Glu	Asp	Trp	His	Gln	Val	Val
		35					40					45			
Pro	Gly	Ser	Phe	Ile	Leu	Leu	Asp	Ala	Cys	Leu	Tyr	Asp	Pro	Asp	Thr
	50					55					60				
Gly	Asp	Ala	Gly	Ala	Phe	Leu	Ser	Ile	Gln	Arg	Thr	Arg	Phe	Phe	Gly
65					70					75					80
Gly	Arg	Phe	Leu	Asp	Lys	Gln	Ser	Gly	Ser	Phe	Lys	Ile	Thr	Gly	Leu
			85						90					95	
Gln	Glu	Met	Gln	Pro	Glu	Glu	Ala	Pro	Glu	Glu	Pro	Ser	Glu	Gly	Gly
			100					105					110		
Pro	Ala	Thr	Pro	Phe	Ala	Phe	Gly	Asn	Lys	Asn	Arg	Cys			
		115					120					125			

(i) CARACTERISTIQUES DE LA SEQUENCE:
(A) LONGUEUR: 200 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(744958..745557)

Gly Ile Pro Met Ala Val Ala Ala Glu Pro Ser Ser Asn Trp Leu Lys
1 5 10 15
Ala Arg Asp Glu Leu Leu Ser Ser Leu Gln Glu Gln Lys Glu Gly Met
20 25 30

Phe Ser Phe Pro Val Phe Pro Lys Gln Glu Cys Glu Gln Lys Leu Lys
 35 40 45
 Asp Lys Phe His Met Glu Glu Val Glu Leu Ser Phe Glu Ser Arg Gly
 50 55 60
 Leu Leu Ser Val Ala Ala Val Gln Glu Tyr Gly Glu Arg Ile Leu
 65 70 75 80
 Leu Gln Pro Phe Leu Ala Asn Pro Phe Glu Ser Gly Glu Phe Tyr Ile
 85 90 95
 Val Ser Ser Glu Glu Asp Leu Gln Ala Leu Ile Gly Thr Ile Phe Asn
 100 105 110
 Asp Ser Ser Leu Ala Ser Tyr Phe Tyr Glu Lys Asp Arg Leu Leu Gly
 115 120 125
 Phe His Tyr Tyr Phe Val Ala Glu Ile Cys Lys Leu Leu Gln Glu Ser
 130 135 140
 Pro Trp Ile Pro Ser Met Ser Val Lys Val Thr Gly Asp Val Ala Phe
 145 150 155 160
 Ser Ala Arg Ala Leu Glu Gly Glu Tyr His Val Ile Gln Val Ser Cys
 165 170 175
 Cys Leu Asp Gly Ser Cys Ile Arg Phe Ser Ile Leu Val Pro Glu Thr
 180 185 190
 Thr Ala Gln Ser Leu Val Asp Ser
 195 200

(2) INFORMATIONS POUR LA SEQ ID NO: 756:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 284 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(745561..746412)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 756:

Phe Met Glu Leu Asn Lys Thr Ser Glu Ser Leu Phe Ser Ala Lys Ile
 1 5 10 15
 Asp His Asn His Pro Arg Thr Glu Ala His Glu Pro Arg Asp Gln Arg
 20 25 30
 Glu Val Arg Val Phe Ser Leu Glu Gly Arg Ser Ser Thr Arg Gln Glu
 35 40 45
 Lys Ala Asp Arg Met Pro Gly Arg Thr Ser Ser Arg Gln Glu Ser Ser
 50 55 60
 Lys Ser Ser Glu Glu Gly Ala Val His Glu Ser Thr Ala Gly Val Ser
 65 70 75 80
 Ser Lys Glu Glu Glu Glu Ser Lys Gly Asp Gly Phe Phe Thr Gly Gly
 85 90 95
 Asn Pro Thr Ser Gly Met Ala Leu Val Glu Thr Pro Met Ala Val Val
 100 105 110
 Ser Glu Ala Met Met Glu Thr Ser Thr Met Thr Val Ser Gln Val Asp
 115 120 125
 Leu Gln Trp Val Glu Gln Leu Val Thr Ser Thr Val Glu Ser Leu Leu
 130 135 140
 Val Ala Asp Ile Asp Gly Lys Gln Leu Val Glu Ile Val Leu Asp Asn
 145 150 155 160
 Ser Asn Thr Val Pro Ala Ala Phe Cys Gly Ala Asn Leu Thr Leu Val

				165					170					175			
Gln	Thr	Gly	Glu	Glu	Ile	Ser	Val	Ser	Phe	Ser	Asn	Phe	Val	Asp	Gln		
			180					185					190				
Ala	Gln	Leu	Thr	Glu	Ala	Thr	Gln	Leu	Val	Gln	Gln	Asn	Pro	Lys	Gln		
		195					200					205					
Leu	Val	Ser	Leu	Val	Glu	Ser	Leu	Lys	Ala	Arg	Gln	Leu	Asn	Leu	Thr		
	210					215					220						
Glu	Leu	Val	Val	Gly	Asn	Val	Ala	Val	Ser	Leu	Pro	Met	Ile	Glu	Lys		
225					230					235					240		
Ile	Glu	Thr	Pro	Leu	His	Met	Ile	Ala	Ala	Thr	Ile	Arg	His	His	Asp		
				245					250					255			
Gln	Glu	Gly	Asp	Gln	Glu	Gly	Glu	Gly	Arg	Gln	Asp	Gln	His	Gln	Gly		
			260				265						270				
Gln	His	Gln	Glu	Lys	Lys	Val	Glu	Glu	Ala	His	Ile						
		275					280										

(2) INFORMATIONS POUR LA SEQ ID NO: 757:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(746416..746772)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 757:

Glu	Ser	Leu	Tyr	Ala	Glu	Asn	Ser	Pro	Leu	Arg	Glu	Gln	Leu	Asp	Asp		
1				5					10					15			
Gly	Thr	Thr	Ser	Asp	Ala	Ile	Leu	Lys	Met	Lys	Ala	Tyr	Ile	Lys	Val		
			20					25					30				
Val	Ala	Ile	Gln	Leu	Ser	Glu	Glu	Glu	Glu	Lys	Val	Asn	Lys	Gln	Lys		
		35					40					45					
Glu	Asn	Val	Leu	Ala	Ala	Xaa	Lys	Glu	Leu	Glu	Arg	Ala	Glu	Val	Glu		
	50					55					60						
Leu	Thr	Lys	Arg	Arg	Lys	Glu	Glu	Glu	Lys	Thr	Arg	Leu	His	Lys	Glu		
65					70					75				80			
Glu	Trp	Met	Lys	Glu	Ala	Leu	Lys	Glu	Glu	Ala	Arg	Gln	Glu	Glu	Lys		
			85						90					95			
Glu	Gln	Asp	Glu	Met	Gly	Gln	Leu	Leu	His	Gln	Leu	Leu	Lys	Gln	Lys		
		100						105					110				
Gln	Arg	Glu	Ser	Gly	Glu	Asn											

(2) INFORMATIONS POUR LA SEQ ID NO: 758:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 442 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(746944..748269)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 758:

```

Met Glu Glu Ile Thr Thr Glu Phe Asn Thr Leu Met Thr Glu Leu Pro
1      5      10      15
Asp Val Gln Leu Thr Ala Val Val Gly Arg Ile Ile Glu Val Val Gly
20      25      30
Met Leu Ile Lys Ala Val Val Pro Asp Val Arg Val Gly Glu Val Cys
35      40      45
Leu Val Lys Arg His Gly Met Glu Pro Leu Val Thr Glu Val Val Gly
50      55      60
Phe Thr Gln Asn Phe Val Phe Leu Ser Pro Leu Gly Glu Leu Thr Gly
65      70      75      80
Val Ser Pro Ser Ser Glu Val Met Ala Thr Gly Leu Pro Leu His Ile
85      90      95
Arg Ala Gly Glu Gly Leu Leu Gly Arg Val Leu Asn Gly Leu Gly Asn
100     105     110
Pro Ile Asp Thr Glu Thr Lys Gly Pro Leu Glu Asn Val Asp Ala Ile
115     120     125
Tyr Pro Ile Phe Lys Ala Pro Pro Asp Pro Leu His Arg Ala Lys Leu
130     135     140
Arg Thr Ile Leu Ser Thr Gly Val Arg Cys Ile Asp Gly Met Leu Thr
145     150     155     160
Val Ala Lys Gly Gln Arg Ile Gly Ile Xaa Ala Gly Ala Gly Val Gly
165     170     175
Lys Ser Ser Leu Leu Gly Met Ile Ala Arg Asn Ala Glu Glu Ala Asp
180     185     190
Ile Asn Val Ile Ala Leu Ile Gly Glu Arg Gly Arg Glu Val Arg Glu
195     200     205
Phe Ile Glu Asn Asp Leu Gly Glu Glu Gly Met Lys Arg Ser Ile Ile
210     215     220
Val Val Ser Thr Ser Asp Gln Ser Ser Gln Leu Arg Leu Asn Ala Ala
225     230     235     240
Tyr Val Gly Thr Ala Ile Ala Glu Tyr Phe Arg Asp Gln Gly Lys Thr
245     250     255
Val Val Leu Met Met Asp Ser Val Thr Arg Phe Ala Arg Ala Leu Arg
260     265     270
Glu Val Gly Leu Ala Ala Gly Glu Pro Pro Ala Arg Ala Gly Tyr Thr
275     280     285
Pro Ser Val Phe Ser Thr Leu Pro Lys Leu Leu Glu Arg Ala Gly Ala
290     295     300
Ser Asp Lys Gly Thr Ile Thr Ala Phe Tyr Thr Val Leu Val Ala Gly
305     310     315     320
Asp Asp Met Asn Glu Pro Val Ala Asp Glu Val Lys Ser Ile Leu Asp
325     330     335
Gly His Ile Val Leu Ser Asn Ala Leu Ala Gln Ala Tyr His Tyr Pro
340     345     350
Ala Ile Asp Val Leu Ala Ser Ile Ser Arg Leu Leu Thr Ala Ile Val
355     360     365
Pro Glu Glu Gln Arg Arg Ile Ile Gly Arg Ala Arg Glu Val Leu Ala
370     375     380
Lys Tyr Lys Ala Asn Glu Met Leu Ile Arg Ile Gly Glu Tyr Arg Arg
385     390     395     400
Gly Ser Asp Arg Glu Val Asp Phe Ala Ile Asp His Ile Asp Lys Leu
405     410     415
Asn Arg Phe Leu Lys Gln Asp Ile His Glu Lys Thr Asn Tyr Glu Glu
420     425     430
Ala Ala Gln Gln Leu Arg Ala Ile Phe Arg

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435

440

(2) INFORMATIONS POUR LA SEQ ID NO: 759:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 231 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(748274..748966)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 759:

Ile	Arg	Glu	Arg	Val	Gly	Tyr	Ser	Met	Ile	Asp	Pro	Leu	Lys	Leu	Phe	1	5	10	15
Pro	Asn	Phe	Asp	Gly	Asp	Lys	Glu	Ser	Ala	Ala	Val	Asn	Lys	Pro	Ser	20	25	30	
Ala	Ser	Pro	Met	Pro	Ser	Glu	Leu	Ser	Lys	Asn	Val	Ala	Ser	Phe	Ser	35	40	45	
Leu	Gly	Gly	Gly	Gly	Ala	Ala	Leu	Asp	Ser	Thr	Val	Ser	Thr	Glu	Lys	50	55	60	
Leu	Ser	Leu	Met	Ala	Met	Met	Gln	Asp	Lys	Asn	Ser	Gln	Leu	Ile	Asp	65	70	75	80
Pro	Glu	Leu	Glu	Glu	Ala	Leu	Asn	Ser	Glu	Glu	Leu	Gln	Glu	Gln	Ile	85	90	95	
His	Leu	Leu	Lys	Ser	Arg	Leu	Trp	Asp	Ala	Gln	Thr	Gln	Met	Gln	Met	100	105	110	
Gln	Asp	Pro	Asp	Lys	Leu	Ala	Ser	Glu	His	Val	Asp	Ala	Leu	Gly	Val	115	120	125	
Ile	Val	Asp	Leu	Ile	Asn	Gly	Asp	Phe	Gln	Ala	Ile	Ala	Glu	His	Thr	130	135	140	
Gln	Gln	Thr	Val	Lys	Gln	Gly	Asn	Gly	Asp	Glu	Glu	Lys	Ser	Val	Thr	145	150	155	160
Arg	Lys	Ile	Val	Asp	Trp	Val	Ser	Ser	Gly	Glu	Glu	Ile	Leu	Asn	Arg	165	170	175	
Ala	Leu	Leu	Tyr	Phe	Ser	Asp	Arg	Asn	Gly	Glu	Arg	Glu	Thr	Leu	Ala	180	185	190	
Asp	Phe	Leu	Lys	Val	Gln	Tyr	Ala	Val	Gln	Arg	Ala	Thr	Gln	Arg	Ala	195	200	205	
Glu	Leu	Phe	Ala	Ser	Ile	Leu	Gly	Ala	Thr	Val	Ser	Ser	Val	Lys	Thr	210	215	220	
Ile	Met	Thr	Thr	Gln	Leu	Gly										225	230		

(2) INFORMATIONS POUR LA SEQ ID NO: 760:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 154 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(748965..749426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 760:

```

Asn Lys Arg Trp Val Met Ala Asp Leu Asp Val Phe Lys Glu Asp Phe
1          5          10          15
Ala Leu Leu Phe Glu Ala Gly Met Val Ala Ile Lys Gln Gly Asp Glu
20          25          30
Ala Ser Ala Lys Ala Leu Phe Gln Ala Leu Gln Val Leu Asp Pro Glu
35          40          45
His Thr Ala His Glu Leu Gly Ser Gly Leu Leu His Leu His Lys Met
50          55          60
Glu Leu Thr Lys Ala Glu Val Leu Phe Arg Ala Ile Val Glu Lys Asp
65          70          75          80
Pro Glu Asn Trp Ser Ala Lys Ala Phe Leu Ser Leu Thr Leu Met Met
85          90          95
Ile Val Leu Gln Gln Gly Ser Ser Phe Glu Val Arg Arg Ser Ser Leu
100         105         110
Glu Arg Cys Leu Gln Leu Ala Asp Gln Val Leu Glu Ser Cys Glu Val
115         120         125
Glu Ser Thr Arg Ala Leu Ala Lys Ser Val Leu Asp Trp His Asp Gly
130         135         140
Leu Val Ala Lys Ser Gly Gly Pro Leu Asn
145         150

```

(2) INFORMATIONS POUR LA SEQ ID NO: 761:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 90 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(749433..749702)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 761:

```

Thr Val Lys Glu Arg Val Ser Met Ala Ser Gly Ser Cys Ser Ala Phe
1          5          10          15
Asn Phe Asn Gln Met Leu Asp Gly Val Cys Lys Tyr Val Gln Gly Val
20          25          30
Gln Gln Tyr Leu Thr Glu Leu Glu Thr Ser Thr Gln Gly Thr Val Asp
35          40          45
Leu Gly Thr Met Phe Asn Leu Gln Phe Arg Met Gln Ile Leu Ser Gln
50          55          60
Tyr Met Glu Ser Val Ser Asn Ile Leu Thr Ala Val Asn Thr Glu Met
65          70          75          80
Ile Thr Met Ala Arg Ala Val Lys Gly Ser
85          90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 762:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 103 acides aminés
- (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(749721..750029)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 762:

```

Asn Ile Lys Leu Ser Thr Ile Asn Arg Gln Phe Glu Val Tyr Leu Ile
1          5          10          15
Leu Pro Gly Arg Asn Lys Ser Met Phe Asn Met Glu Asn Ser Ala Ala
          20          25          30
Lys Gly Glu Lys Ala Ala Arg Gln Leu Phe Asp Leu Glu Gln Asp Met
          35          40          45
His Asp Val Ala Lys Ala His Glu Val Asn Ala Asn Val Gln Ser Lys
          50          55          60
Val Gln Thr Leu Thr Ser Ser Leu Arg Glu Gly Ala Phe Lys Glu Ser
65          70          75          80
Phe Glu Lys Gln Gln Thr Leu Leu Ala Gly Ile Cys Ser Ser Ser Lys
          85          90          95
Gly Ala Arg Thr Tyr Gln Pro
          100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 763:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 767 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(750007..752307)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 763:

```

Met Leu Pro Arg Pro Val Ser Val Asp Gly Thr Val Ile Thr Ala Pro
1          5          10          15
Val Leu Leu Lys Asp Gly Val Ser Phe Val Met Gly Ser Cys Gln Val
          20          25          30
Ser Phe Phe Lys Gly Glu Glu Val Glu Gly Asp Ile Glu Leu Ser Phe
          35          40          45
Gln Thr Glu Gly Gly Asn Glu Gly Glu Pro Ala Ala Gln Gly Ser Ser
50          55          60
Ser Val Ser Ser Glu Gly Pro Lys Lys Glu Thr Gly Asn Pro Ser Leu
65          70          75          80
Pro Ser Glu Thr Lys Val Ser Gly Glu Val Ser Ser Ser Ala Ile Ala
          85          90          95
Lys Glu Gln Glu Leu Ala Val Phe Phe Leu Ala Ser Val Glu Lys Glu
          100          105          110
Pro Gly Thr Pro Lys Glu Val Ser Glu Pro Lys Val Ser Ser Gln Glu
          115          120          125
Gly Gln Thr Pro Ser Val Thr Gly Glu Lys Lys Asp Leu Glu Leu Pro
          130          135          140
Leu Ala Ser Gln Glu Gln Pro Lys Gln Thr Thr Pro Ser Gly Ser Gly
145          150          155          160

```

Glu Pro Thr Gln Ser Gln Asn Ala Ser Met Glu Glu Asn Arg Thr Ser
 165 170 175
 Pro Asp Gln Asn Gln Gln Pro Gln Leu Ser Ser Ala Ser Glu Ser Gly
 180 185 190
 Ser Gln Ser Pro Glu Asn Gln Glu Gln Gln Pro Ser Gln Thr Pro Pro
 195 200 205
 Pro Ser Pro Glu Thr Pro Glu Pro Ser Gly Glu Pro Asn Ser Ala Thr
 210 215 220
 Glu Glu Asn Ser Pro Ser Pro Met Glu Lys Ala Ser Val Thr Glu Glu
 225 230 235 240
 Gly Ser Ser Gly Thr Ser Glu Glu Glu Lys Glu Gly Glu Glu Asp Thr
 245 250 255
 Ala Glu Ser Ala Ala Asn Glu Glu Leu Lys Ala Glu Ala Ser Gln Glu
 260 265 270
 Glu Glu Lys Lys Glu Glu Asp Lys Xaa Glu Val Leu Ala Pro Phe Asn
 275 280 285
 Val Gln Asp Leu Phe Arg Phe Asp Gln Gly Ile Phe Pro Ala Glu Ile
 290 295 300
 Glu Asp Leu Ala Gln Lys Gln Val Ala Val Asp Leu Thr Gln Pro Ser
 305 310 315 320
 Arg Phe Leu Leu Lys Val Leu Ala Gly Ala Asn Ile Gly Ala Glu Phe
 325 330 335
 His Leu Asp Ser Gly Lys Thr Tyr Ile Val Gly Ser Asp Pro Gln Val
 340 345 350
 Ala Asp Ile Val Leu Ser Asp Met Ser Ile Ser Arg Gln His Ala Lys
 355 360 365
 Ile Ile Ile Gly Asn Asp Asn Ser Val Leu Ile Glu Asp Leu Gly Ser
 370 375 380
 Lys Asn Gly Val Ile Val Glu Gly Arg Lys Ile Glu His Gln Ser Thr
 385 390 395 400
 Leu Ser Ala Asn Gln Val Val Ala Leu Gly Thr Thr Leu Phe Leu Leu
 405 410 415
 Val Asp Tyr Thr Ala Pro Ser Asp Thr Val Met Ala Thr Ile Ser Ser
 420 425 430
 Glu Asp Tyr Gly Leu Phe Gly Arg Pro Gln Ser Pro Glu Glu Ile Ala
 435 440 445
 Ala Arg Ala Ala Glu Glu Glu Glu Glu Lys Arg Lys Arg Ala Thr Leu
 450 455 460
 Pro Thr Gly Ala Phe Ile Leu Thr Leu Phe Ile Gly Gly Leu Ala Leu
 465 470 475 480
 Leu Phe Gly Ile Gly Thr Thr Ser Leu Phe His Thr Lys Glu Val Val
 485 490 495
 Ser Ile Asp Gln Ile Asp Leu Ile His Asp Ile Glu His Val Ile Gln
 500 505 510
 Gln Phe Pro Thr Val Arg Phe Thr Phe Asn Lys Asn Asn Gly Gln Leu
 515 520 525
 Phe Leu Ile Gly His Val Arg Asn Ser Ile Asp Lys Ser Glu Leu Leu
 530 535 540
 Tyr Lys Val Asp Ala Leu Ser Phe Val Lys Ser Val Asp Asp Asn Val
 545 550 555 560
 Ile Asp Asp Glu Ala Val Trp Gln Glu Met Asn Ile Leu Leu Ser Lys
 565 570 575
 Asn Pro Glu Phe Lys Gly Ile Ser Met Gln Ser Pro Glu Pro Gly Ile
 580 585 590
 Phe Val Ile Ser Gly Tyr Leu Lys Thr Glu Glu Gln Ala Ala Cys Leu
 595 600 605
 Ala Asp Tyr Leu Asn Leu His Phe Asn Tyr Leu Ser Leu Leu Asp Asn
 610 615 620
 Lys Val Ile Ile Glu Ser Gln Val Met Lys Ala Leu Ala Gly His Leu

625					630					635				640
Val	Gln	Ser	Gly	Phe	Ala	Asn	Val	His	Val	Ser	Phe	Thr	Asn	Gly
				645					650					655
Ala	Val	Leu	Thr	Gly	Tyr	Ile	Asn	Asn	Lys	Asp	Ala	Asp	Lys	Phe
			660					665					670	Arg
Thr	Val	Val	Gln	Glu	Leu	Gln	Asp	Ile	Ala	Gly	Ile	Arg	Ala	Val
			675				680					685		Lys
Asn	Phe	Val	Val	Leu	Leu	Xaa	Ala	Glu	Glu	Gly	Val	Ile	Asp	Leu
			690			695					700			Asn
Met	Arg	Tyr	Pro	Gly	Arg	Tyr	Arg	Val	Thr	Gly	Phe	Ser	Lys	Cys
705					710					715				720
Asp	Ile	Ser	Ile	Asn	Val	Val	Val	Asn	Gly	Arg	Ile	Leu	Thr	Arg
				725					730					735
Asp	Ile	Leu	Asp	Gly	Met	Thr	Val	Thr	Ser	Ile	Gln	Pro	His	Cys
			740					745					750	Ile
Phe	Leu	Glu	Arg	Glu	Gly	Leu	Lys	Tyr	Lys	Ile	Glu	Tyr	Asn	Lys
		755					760					765		

(2) INFORMATIONS POUR LA SEQ ID NO: 764:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(752503..752913)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 764:

Ala	Arg	Glu	His	Met	Leu	Glu	Lys	Leu	Ile	Lys	Asn	Phe	Val	Ala	Tyr
1				5					10					15	
Met	Gly	Val	Ala	Ser	Glu	Leu	Glu	Phe	Asp	Ala	Asp	Gly	Ser	Tyr	Val
			20					25					30		
Leu	Pro	Ile	Ser	Ser	Leu	Val	Arg	Met	Arg	Val	Arg	Gln	Asn	Ala	Asp
			35				40					45			
Glu	Glu	Ile	Ile	Ile	Ser	Ala	Phe	Leu	Gly	Glu	Ile	Pro	Ala	Phe	Met
			50			55					60				
Asp	Ile	Glu	Lys	Ala	Tyr	Ala	Arg	Met	Met	Glu	Gly	Asn	Leu	Phe	Gly
65					70					75				80	
Gln	Glu	Thr	Gly	Gly	Ala	Ala	Leu	Gly	Leu	Asp	Ser	Asp	Gly	His	Ala
				85					90					95	
Val	Leu	Val	Arg	Arg	Val	Pro	Gly	Glu	Val	Ser	Gln	Glu	Asp	Phe	Ala
			100					105					110		
Ser	Phe	Ile	Gly	Gly	Val	Leu	Asn	Tyr	Ala	Glu	Ala	Trp	Leu	Glu	Asp
			115				120					125			
Leu	Gly	Leu	Ser	Lys	Thr	Glu	Gln	Xaa							
			130				135								

(2) INFORMATIONS POUR LA SEQ ID NO: 765:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 324 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(753616..754587)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 765:

```

Arg Val Leu Leu Gly Val Ile Gly Val Ser Tyr Arg Glu Thr Thr Leu
1      5      10      15
Gln Gln Arg Glu Gln Val Leu His Ile Leu Gln Gln Ala Gln Gly Ser
20      25      30
Phe Arg Pro Glu Val Phe Gln Glu Arg Asp Tyr Val Leu Leu Ala
35      40      45
Thr Cys His Arg Val Glu Leu Tyr Ser Val Ala Pro Ala Glu Leu Phe
50      55      60
Asp Ser Leu Ala Gln Glu Ile Lys Leu Leu Gly Val Ser Pro Tyr Phe
65      70      75      80
Tyr Arg Asn Gln Asp Cys Phe Ala His Leu Phe Cys Val Ala Gly Gly
85      90      95
Leu Asp Ser Leu Val Leu Gly Glu Thr Glu Ile Gln Gly Gln Val Lys
100      105      110
Arg Ala Tyr Leu Gln Ala Ala Arg Glu Gln Lys Leu Ser Phe Ala Leu
115      120      125
His Phe Leu Phe Gln Lys Ala Leu Lys Glu Gly Lys Val Phe Arg Ala
130      135      140
Lys Gly Gly Ala Pro Tyr Ala Ala Ile Thr Ile Pro Ile Leu Val Asp
145      150      155      160
Gln Glu Leu Arg Arg Arg Gln Ile Asp Lys Lys Ala Ser Leu Leu Phe
165      170      175
Ile Gly Tyr Ser Glu Ile Asn Arg Ser Val Ala Tyr His Leu Arg Arg
180      185      190
Gln Gly Phe Ser Cys Ile Thr Phe Cys Ser Arg Gln Gln Leu Pro Thr
195      200      205
Leu Ser Met Arg Gln Val Val Arg Glu Glu Leu Cys Phe Gln Asp Pro
210      215      220
Tyr Arg Val Val Phe Leu Gly Ser Leu Glu Leu Gln Tyr Ala Leu Pro
225      230      235      240
His Ser Leu Trp Glu Ser Ile Trp Asp Ile Pro Asp Arg Ile Val Phe
245      250      255
Asp Phe Ala Val Pro Arg Ala Leu Pro Ser His Thr Val Phe Pro His
260      265      270
Arg Tyr Met Asp Met Asp Gln Ile Ser Asp Trp Leu Arg Glu His Arg
275      280      285
Lys Glu Val Asn Ser Ala His Leu Asp Ser Leu Arg Glu Val Ala Tyr
290      295      300
Arg Tyr Trp Asn Ser Leu Asn Gln Arg Leu Glu Arg His Asp Cys Val
305      310      315      320
Gly Ala Asn Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 766:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 605 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 755000..756814

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 766:

Met	Arg	Lys	Lys	Thr	Ala	Tyr	Ser	Glu	Ser	Ser	Ile	Ile	Ser	Leu	Ala	1	5	10	15
Ser	Leu	Asp	His	Ile	Arg	Leu	Arg	Ala	Gly	Met	Tyr	Ile	Gly	Arg	Leu	20	25	30	
Gly	Asp	Gly	Ser	Gln	Ala	Glu	Asp	Gly	Ile	Tyr	Thr	Leu	Phe	Lys	Glu	35	40	45	
Val	Val	Asp	Asn	Ala	Ile	Asp	Glu	Phe	Val	Met	Gly	Tyr	Gly	His	Thr	50	55	60	
Ile	His	Ile	Thr	Gly	Asp	Ala	His	Glu	Leu	Ser	Ile	Arg	Asp	Glu	Gly	65	70	75	80
Arg	Gly	Ile	Pro	Leu	Gly	Lys	Val	Ile	Asp	Cys	Val	Ser	Lys	Ile	Asn	85	90	95	
Thr	Gly	Ala	Lys	Tyr	Thr	Gln	Asp	Val	Phe	His	Phe	Ser	Val	Gly	Leu	100	105	110	
Asn	Gly	Val	Gly	Leu	Lys	Ala	Val	Asn	Ala	Leu	Ser	Gln	His	Phe	Ser	115	120	125	
Val	Arg	Ser	Val	Arg	Asn	Lys	Lys	Phe	Leu	Lys	Ala	Ser	Phe	Ser	Lys	130	135	140	
Gly	Ile	Leu	Leu	His	Thr	Glu	Gln	Gly	Ala	Thr	Gln	Asp	Pro	Asp	Gly	145	150	155	160
Thr	Glu	Val	Val	Phe	Ser	Pro	Asp	His	Glu	Leu	Phe	Glu	Asn	Phe	Ser	165	170	175	
Phe	Gln	Val	Glu	Phe	Leu	Lys	Lys	Lys	Ile	Arg	Gln	Tyr	Thr	Tyr	Leu	180	185	190	
His	Pro	Gly	Leu	Thr	Ile	Ile	Tyr	Asn	Gly	Glu	Arg	Ile	Val	Ser	Thr	195	200	205	
Arg	Gly	Leu	Leu	Asp	Leu	Phe	Glu	Glu	Glu	Val	Gln	Thr	Pro	Leu	Leu	210	215	220	
Tyr	Ser	Pro	Ile	Thr	Phe	Gln	Tyr	Ser	Asp	Leu	Ala	Phe	Leu	Phe	Ser	225	230	235	240
His	Thr	Glu	Thr	Ser	Glu	Gln	Tyr	Phe	Ser	Phe	Val	Asn	Gly	Gln		245	250	255	
Glu	Thr	Thr	Asp	Gly	Gly	Thr	His	Leu	Val	Ala	Phe	Lys	Glu	Gly	Ile	260	265	270	
Val	Lys	Gly	Val	Asn	Glu	Phe	Phe	Gly	Lys	Asn	Phe	Ser	Ser	Gln	Asp	275	280	285	
Ile	Arg	Glu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ile	Lys	Ile	Ala	Ser	Pro	290	295	300	
Ile	Phe	Glu	Ser	Gln	Thr	Lys	Asn	Lys	Leu	Gly	Asn	Thr	Asn	Ile	Arg	305	310	315	320
Ala	Glu	Leu	Ala	Lys	Arg	Val	Lys	Glu	Ala	Val	Leu	Ser	Ser	Leu	Lys	325	330	335	
Lys	Asn	Pro	Ser	Ser	Ala	Glu	Arg	Ile	Gln	Glu	Lys	Ile	Lys	Leu	Asn	340	345	350	
Glu	Lys	Thr	Arg	Lys	Asn	Ala	Gln	Phe	Leu	Lys	Gln	Glu	Leu	Lys	Asp	355	360	365	
Lys	Gln	Lys	Lys	Leu	His	Tyr	Lys	Ile	Pro	Lys	Leu	Arg	Asp	Cys	Lys	370	375	380	
Phe	His	Leu	Thr	Asp	Asn	Ser	Leu	Tyr	Gly	Lys	Asn	Ser	Ser	Ile	Phe	385	390	395	400
Ile	Thr	Glu	Gly	Glu	Ser	Ala	Ser	Ala	Ser	Ile	Leu	Ala	Ser	Arg	Asn	405	410	415	

Pro Leu Thr Gln Ala Val Phe Ser Leu Arg Gly Lys Pro Met Asn Val
 420 430
 Phe Ser Ser Lys Glu Glu Thr Ile Tyr Lys Asn Asp Glu Leu Phe Tyr
 435 440 445
 Leu Ala Thr Ala Leu Gly Leu His Lys Asp Ser Leu Gln Asn Leu Arg
 450 455 460
 Tyr Asn Gln Val Ile Leu Ala Thr Asp Ala Asp Val Asp Gly Met His
 465 470 475 480
 Ile Arg Asn Leu Met Ile Thr Phe Phe Leu Lys Thr Phe Leu Pro Leu
 485 490 495
 Val Ala Ser Asn His Leu Phe Ile Leu Glu Thr Pro Leu Phe Lys Val
 500 505 510
 Arg His Lys Asp Ala Thr Phe Tyr Cys Tyr Ser Glu Glu Lys Leu
 515 520 525
 Ser Thr Ile Glu His Ile Gly Lys Lys Glu Ser Ser Leu Glu Ile Thr
 530 535 540
 Arg Phe Lys Gly Leu Gly Glu Ile Ser Pro Lys Glu Phe Lys Ser Phe
 545 550 555 560
 Ile Gly Ala Asp Met Arg Leu Thr Pro Val Ser Leu Pro Asp Thr Glu
 565 570 575
 Thr Leu Asp Thr Leu Leu Gln Phe Tyr Met Gly Lys Asn Thr Lys Glu
 580 585 590
 Arg Lys Leu Phe Ile Ile Glu Asn Leu Val Thr Asn Leu
 595 600 605

(2) INFORMATIONS POUR LA SEQ ID NO: 767:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 502 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 756796..758301

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 767:

Glu Ser Cys Tyr Gln Pro Leu Ala Ile Asn Glu Leu Met Ser Asp Leu
 1 5 10 15
 Ser Asp Leu Phe Lys Thr His Phe Thr Gln Tyr Ala Ser Tyr Val Ile
 20 25 30
 Leu Glu Arg Ala Ile Pro His Val Leu Asp Gly Leu Lys Pro Val Gln
 35 40 45
 Arg Arg Leu Leu Trp Thr Leu Phe Arg Met Asp Asp Gly Lys Met His
 50 55 60
 Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala Leu His Pro His Gly
 65 70 75 80
 Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu Ala Asn Lys Gly Phe
 85 90 95
 Leu Ile Glu Thr Gln Gly Asn Phe Gly Asn Pro Leu Thr Gly Asp Pro
 100 105 110
 His Ala Ala Ala Arg Tyr Ile Glu Ala Arg Leu Ser Pro Leu Ala Lys
 115 120 125
 Glu Val Leu Phe Asn Thr Asp Leu Met Thr Phe His Asp Ser Tyr Asp
 130 135 140
 Gly Arg Glu Gln Glu Pro Asp Ile Leu Ala Ala Lys Ile Pro Leu Leu


```

145          150          155          160
Leu Leu His Gly Val Asp Gly Ile Ala Val Gly Met Thr Thr Lys Ile
          165          170          175
Phe Pro His Asn Phe Cys Asp Leu Leu Glu Ala Gln Ile Ala Ile Leu
          180          185          190
Asn Asp Gln Pro Phe Ser Leu Leu Pro Asp Phe Pro Ser Gly Gly Thr
          195          200          205
Met Asp Ala Ser Asp Tyr Gln Asp Gly Leu Gly Ser Ile Val Leu Arg
          210          215          220
Ala Thr Ile Asp Ile Ile Asn Asp Lys Thr Leu Leu Ile Lys Glu Ile
225          230          235          240
Cys Pro Ser Thr Thr Thr Glu Thr Leu Ile Arg Ser Ile Glu Asn Ala
          245          250          255
Ala Lys Arg Gly Ile Ile Lys Ile Asp Ser Ile Gln Asp Phe Ser Thr
          260          265          270
Asp Leu Pro His Ile Glu Ile Lys Leu Pro Lys Gly Ile His Ala Lys
          275          280          285
Asp Leu Leu Arg Pro Leu Tyr Thr His Thr Glu Cys Gln Val Ile Leu
290          295          300
Thr Ser Arg Pro Thr Ala Ile Tyr Gln Gly Lys Pro Trp Glu Thr Thr
305          310          315          320
Ile Ser Glu Ile Leu Arg Leu Gln Thr Glu Thr Leu Gln Asn Tyr Leu
          325          330          335
Lys Lys Glu Leu Leu Ile Leu Glu Asp Ser Leu Ser Arg Glu Leu Tyr
          340          345          350
His Lys Thr Leu Glu Tyr Leu Phe Ile Lys His Lys Leu Tyr Asp Thr
          355          360          365
Val Arg Ser Met Leu Ser Lys Arg Lys Thr Ser Pro Ser Ser Ser Ala
370          375          380
Ile His Asn Ala Val Leu Glu Ala Leu Thr Pro Phe Leu Asp Thr Leu
385          390          395          400
Pro Ala Pro Asp Lys Gln Ala Thr Ala Gln Leu Ala Ala Leu Thr Ile
          405          410          415
Lys Lys Ile Leu Cys Phe Asp Glu Asn Ser Tyr Glu Lys Glu Leu Ala
          420          425          430
Cys Leu Glu Lys Lys Arg Ser Ser Val Gln Lys Asp Leu Ser Gln Leu
          435          440          445
Lys Lys Tyr Thr Val Leu Tyr Ile Lys Lys Leu Leu Glu Thr Tyr Arg
450          455          460
Gln Leu Gly His Arg Lys Thr Lys Ile Ala Lys Phe Asp Asp Leu Pro
465          470          475          480
Thr Glu Arg Val Ser Ala His Lys Lys Ala Lys Glu Pro Ala Ala Leu
          485          490          495
Asp Gln Glu Glu Asn Phe
          500

```

(2) INFORMATIONS POUR LA SEQ ID NO: 768:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 82 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(758446..758691)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 768:

```

Asp Leu Leu Arg Met Lys Glu Phe Leu Ala Tyr Ile Val Lys Asn Leu
1          5          10          15
Val Asp Lys Pro Glu Glu Val His Leu Lys Glu Val Gln Gly Thr Asn
          20          25          30
Thr Ile Ile Tyr Glu Leu Thr Val Ala Lys Gly Asp Ile Gly Lys Ile
          35          40          45
Ile Gly Lys Glu Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val
          50          55          60
Ser Val Ala Ser Arg Asp Asn Val Lys Val Ser Leu Glu Ile Met Glu
65          70          75          80
Glu Arg

```

(2) INFORMATIONS POUR LA SEQ ID NO: 769:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(759338..759775)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 769:

```

Ile Pro Ala Pro Thr Ala Val Phe Ser Phe Val Ile Asp Glu Gln Leu
1          5          10          15
Thr Gly Arg Leu Asp Lys Gly Leu Val Ser Tyr Asn Gly Ala Tyr Ser
          20          25          30
Arg Ala Phe Tyr Gln Gln Gln Ile Glu Leu Gly Arg Val Arg Val Asn
          35          40          45
Gly Arg Val Tyr Thr Arg Val Ser His Pro Leu Ser Leu Gly Asp Val
          50          55          60
Val Glu Val Glu Leu Ile Glu Glu Glu Glu Pro Ser Ser Leu Ile Pro
65          70          75          80
Glu Asp Ile Pro Leu Asp Lys Val Tyr Glu Asp Asp Met Ile Leu Val
          85          90          95
Ile Asn Lys Pro Arg Asp Met Val Val His Pro Ala Pro Gly His Thr
          100          105          110
Gln Gly Thr Val Val His Ala Leu Leu His Glu Ile Gly Glu Arg Leu
          115          120          125
Lys Gln Glu Leu Pro Arg Gly Ala Met Ala Pro Arg Asp Cys Thr Ser
          130          135          140
Leu Arg
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 770:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 124 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(759871..760242)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 770:

Arg	Asn	Gly	Ser	Ser	Thr	Thr	Arg	Phe	Lys	Glu	Asn	Ala	Phe	Gly	Ile
1				5					10					15	
Gln	Arg	Leu	Met	Glu	Ile	Arg	Tyr	Phe	Leu	Ala	Arg	Pro	Leu	Leu	Glu
		20						25					30		
Glu	Glu	Val	Cys	Arg	Leu	Ala	Asn	Asn	Arg	Lys	Asn	Phe	Leu	Phe	Asp
		35					40					45			
Ala	Glu	Lys	Tyr	Leu	Ile	Pro	Ile	Cys	Tyr	Lys	Gln	Thr	Ile	Tyr	Leu
	50					55					60				
Ala	Lys	Pro	Leu	Ser	Arg	Phe	Pro	Met	Thr	Gln	Glu	Val	Trp	Glu	Leu
65					70					75					80
His	Val	Gln	His	Val	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Phe	Gly	Ile	Leu
			85						90					95	
Thr	Asp	His	Ala	Pro	Ile	Leu	Leu	Ala	Cys	Glu	Ala	Arg	Gln	Val	Val
			100					105					110		
Leu	Leu	Glu	Ser	Leu	Asp	Ser	Phe	Val	Asn	Ile	Ser				
		115						120							

(2) INFORMATIONS POUR LA SEQ ID NO: 771:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 117 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(760188..760538)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 771:

Lys	Ile	Leu	Leu	Thr	Gln	Val	Lys	Tyr	Arg	Lys	Ile	Phe	Val	Leu	Gly
1				5					10					15	
Glu	Ser	Leu	Val	Met	Asp	Thr	Gln	Phe	Ile	Ala	Ser	Arg	Ser	Val	Arg
		20						25					30		
Asn	Gln	Gly	Val	Thr	Ser	Val	Ser	Gly	Gln	Val	Lys	Glu	Glu	Leu	Met
		35					40					45			
Ser	Pro	Ser	Asn	Met	Thr	Phe	Glu	Gly	Pro	Val	Arg	Ser	Leu	Asp	Gln
	50					55					60				
Leu	Arg	Gln	Ala	Leu	Ile	Ala	Lys	Met	Gly	Glu	Gln	Lys	Gly	Gln	Glu
65					70					75					80
Met	Tyr	Asp	Arg	Phe	Ile	Gln	Ser	Leu	Leu	Ile	Ser	Thr	Phe	Thr	Thr
			85					90						95	
Val	His	Lys	Glu	Met	Asp	Arg	Ala	Gln	Arg	Ala	Ser	Lys	Lys	Met	Arg
			100					105					110		
Ser	Val	Tyr	Arg	Asp											
			115												

(2) INFORMATIONS POUR LA SEQ ID NO: 772:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 269 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 760966..761772

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 772:

```

Met Phe Pro Glu Asn Lys Met Leu Leu Ile Ala Gly Pro Cys Val Ile
1      5      10
Glu Asp Asn Ser Val Phe Glu Thr Ala Arg Arg Leu Lys Glu Ile Val
20      25      30
Ala Pro Tyr Ala Ser Ser Val His Trp Ile Phe Lys Ser Ser Tyr Asp
35      40      45
Lys Ala Asn Arg Ser Ser Val His Asn Tyr Arg Gly Pro Gly Leu Arg
50      55      60
Leu Gly Leu Gln Thr Leu Ala Lys Ile Lys Glu Glu Leu Asp Val Glu
65      70      75      80
Ile Leu Thr Asp Val His Ser Pro Asp Glu Ala Arg Glu Ala Ala Lys
85      90      95
Val Cys Asp Ile Ile Gln Val Pro Ala Phe Leu Cys Arg Gln Thr Asp
100     105     110
Leu Leu Val Thr Ala Gly Glu Thr Gln Ala Ile Val Asn Ile Lys Lys
115     120     125
Gly Gln Phe Leu Ser Pro Trp Glu Met Gln Gly Pro Ile Asp Lys Val
130     135     140
Leu Ser Thr Gly Asn Asn Lys Ile Ile Leu Thr Glu Arg Gly Cys Ser
145     150     155     160
Phe Gly Tyr Asn Asn Leu Val Ser Asp Met Arg Ser Ile Glu Val Leu
165     170     175
Arg Arg Phe Gly Phe Pro Val Val Phe Asp Gly Thr His Ser Val Gln
180     185     190
Leu Pro Gly Ala Leu His Ser Gln Ser Gly Gly Gln Thr Glu Phe Ile
195     200     205
Pro Val Leu Thr Arg Ser Ala Ile Ala Ala Gly Val Gln Gly Leu Phe
210     215     220
Ile Glu Thr His Pro Asn Pro Ser Ser Ala Leu Ser Asp Ala Ala Ser
225     230     235     240
Thr Leu Ser Leu Lys Asp Leu Glu Arg Leu Leu Pro Ala Trp Val Gln
245     250     255
Leu Phe Thr Tyr Ile Gln Glu Met Asp Ala Val Ser Val
260     265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 773:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 761759..762142

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 773:

Met	Leu	Phe	Leu	Tyr	Asp	Xaa	Xaa	Leu	Phe	His	Gly	Ile	Trp	Cys	Val	1	5	10	15
Val	Val	Leu	Ile	Leu	Cys	Ala	Cys	Val	Thr	Ala	Leu	Ala	Val	Val	Lys	20	25	30	
Met	Gly	Asp	Phe	Thr	Asn	Pro	Thr	Leu	Val	His	Gln	Asp	Ser	Val	Thr	35	40	45	
Pro	Ala	Pro	Pro	Phe	Leu	Lys	Ile	Lys	Lys	Leu	Gly	Val	Arg	Lys	Arg	50	55	60	
Ile	Ile	Ser	Pro	Glu	Lys	Gln	Leu	Phe	Tyr	Cys	Thr	Ile	Asp	Lys	Ser	65	70	75	80
Cys	Met	Glu	Leu	His	Phe	Ser	Asn	Thr	Ser	Leu	His	Cys	Arg	Glu	Leu	85	90	95	
Leu	Ser	His	Leu	Thr	Gly	Cys	Leu	Gln	Thr	Glu	Xaa	Ala	Asp	Pro	Leu	100	105	110	
Cys	Phe	Leu	Glu	Val	Leu	Glu	Asp	Phe	Leu	Ile	Thr	Lys	Ile	Ile	Leu	115	120	125	

(2) INFORMATIONS POUR LA SEQ ID NO: 774:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 239 acides aminés

(B) TYPE: acide aminé.

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 762267..762983

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 774:

Met	Ser	Val	Leu	Ser	Val	Cys	Asn	Leu	Ile	Lys	Lys	Tyr	Asn	Lys	Lys	1	5	10	15
Pro	Val	Thr	Asn	Asp	Val	Ser	Phe	Gln	Val	Asn	Ala	Gly	Glu	Ile	Val	20	25	30	
Gly	Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Ala	Phe	Tyr	Gln	35	40	45	
Thr	Val	Gly	Leu	Ile	Arg	Pro	Asp	Ser	Gly	Lys	Ile	Leu	Phe	Lys	Asn	50	55	60	
Thr	Asp	Ile	Thr	Lys	Lys	Pro	Met	Asp	Tyr	Arg	Ala	Arg	Leu	Gly	Ile	65	70	75	80
Gly	Tyr	Leu	Ala	Gln	Glu	Pro	Thr	Ile	Phe	Lys	Glu	Leu	Thr	Val	Lys	85	90	95	
Glu	Asn	Leu	Ile	Cys	Val	Leu	Glu	Ile	Tyr	Lys	Thr	Arg	Lys	Glu		100	105	110	
Gln	Thr	His	Leu	Leu	Asn	Ala	Leu	Ile	Asp	Asp	Leu	Gln	Leu	Thr	Thr	115	120	125	
Ser	Leu	His	Lys	Lys	Ala	Gly	Ser	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg	130	135	140	
Leu	Glu	Ile	Ala	Cys	Val	Leu	Ala	Leu	Asn	Pro	Ser	Val	Leu	Leu	Leu	145	150	155	160
Asp	Glu	Pro	Phe	Ala	Asn	Val	Asp	Pro	Leu	Val	Ile	Gln	Asn	Val	Lys	165	170	175	
Tyr	Leu	Ile	Lys	Ile	Leu	Ala	Ser	Arg	Gly	Ile	Gly	Ile	Leu	Ile	Thr	180	185	190	

Asp His Asn Ala Lys Glu Leu Leu Ser Ile Ala Asp Arg Cys Tyr Leu
 195 200 205
 Ile Ile Asp Gly Lys Ile Phe Phe Glu Gly Ser Ser Ala Gln Met Ile
 210 215 220
 Ala Asn Pro Met Val Arg Gln His Tyr Leu Gly Asp Ser Phe Ser
 225 230 235

(2) INFORMATIONS POUR LA SEQ ID NO: 775:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 377 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(763335..764465)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 775:

Ile Gly Gly Thr Phe Pro Arg Thr Pro Leu Ile Phe Glu Glu Ile Ala
 1 5 10 15
 Leu Leu Ser Glu Glu Gln Asn Gln Val Leu Lys Thr Val Leu Asn Ser
 20 25 30
 Cys Phe Ser Leu Val Cys Gly Gly Pro Gly Thr Gly Lys Thr Phe Leu
 35 40 45
 Ala Val Gln Met Ile Xaa Leu Ile Leu Ala Gln Ile Pro Ser Ala Gln
 50 55 60
 Ile Met Val Ala Ser Pro Thr Gly Lys Ala Ser Ala His Leu His Ser
 65 70 75 80
 Val Leu Thr Ser Gln Gly Ile Val Gly Asp Ser Val Glu Val Val Thr
 85 90 95
 Ile His Lys Phe Leu Lys Asp Met Arg Arg Gly Arg Ser Pro Val Asp
 100 105 110
 Leu Leu Leu Val Asp Glu Gly Ser Met Val Thr Met Asn Leu Leu His
 115 120 125
 Gly Leu Ile Lys Thr Ile Arg Gly Glu Ser Arg Gly Glu Thr Ile Tyr
 130 135 140
 Ala Asp Arg Met Val Ile Phe Gly Asp Ala Asn Gln Leu Ser Pro Ile
 145 150 155 160
 Gly Ile Gly Val Gly Asn Pro Phe His Glu Val Val Ser Glu Phe Ser
 165 170 175
 Lys Gln Ala Cys Phe Leu Ser Thr Ser His Arg Ala Lys His Lys Glu
 180 185 190
 Leu Gln Glu Leu Ala Ser Ala Val Leu Arg Lys Glu Leu Ile Pro Phe
 195 200 205
 Gln Pro Leu Pro Ser Arg Gln Glu Ala Ile Arg Arg Leu Ser Phe Ala
 210 215 220
 Phe Thr Gln Ala Ala Lys Glu Gly Val Ser Leu Cys Ala Leu Thr Pro
 225 230 235 240
 Met Arg Gln Gly Leu Trp Gly Phe Leu Gln Leu Asn Arg Leu Leu Phe
 245 250 255
 Asn Glu Met Gln Glu Lys His Pro Arg Ala Pro Ile Pro Ile Ile Val
 260 265 270
 Thr Glu Arg Tyr Glu Thr Trp Gly Leu Thr Asn Gly Asp Thr Gly Val
 275 280 285
 Leu Asp Pro Val Thr Glu Gln Leu Arg Phe Met Asn Gly Glu Ile Leu

290		295		300											
His	Gln	Ala	Asp	Phe	Pro	Tyr	Tyr	Ser	Tyr	Asn	Tyr	Val	Met	Ser	Val
305					310					315					320
His	Lys	Ser	Gln	Gly	Ser	Glu	Tyr	Asp	Arg	Val	Ile	Val	Ile	Leu	Pro
			325							330				335	
Lys	Gly	Ser	Glu	Val	Phe	Asp	Ser	Ala	Ile	Leu	Tyr	Thr	Ala	Ile	Thr
			340					345					350		
Arg	Thr	Lys	Gln	His	Val	Glu	Ile	Trp	Ala	Asp	Arg	Glu	Ala	Leu	Glu
		355					360					365			
Ala	Ile	Ile	Leu	Lys	Arg	Gly	Arg	Tyr							
	370					375									

(2) INFORMATIONS POUR LA SEQ ID NO: 776:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(764438..764857)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 776:

Ile	His	Ser	Thr	Thr	Ala	Lys	Arg	Lys	Ile	Phe	Pro	Val	Asn	Val	Asn
1			5					10					15		
Gln	His	Val	Gln	Asp	Ile	Val	Pro	Ser	Leu	Leu	Ala	Gln	His	Ile	Leu
		20					25					30			
Leu	Pro	Phe	Asp	Ile	Ala	Phe	Ala	Gln	Lys	His	Leu	Ser	Gln	Glu	Glu
		35				40					45				
Phe	Ser	Gln	Glu	Ala	Glu	Ala	Phe	Leu	Ala	Thr	Ala	Ser	Ala	Leu	Leu
	50				55					60					
Arg	Cys	Gly	Tyr	Pro	Tyr	Phe	Ser	Ile	Cys	Asp	Glu	Thr	Ile	His	Pro
65				70				75					80		
Thr	Leu	Pro	Gly	Ile	Ser	Asn	Lys	Gln	Leu	Phe	Gln	Trp	Phe	Gln	Leu
		85					90				95				
Leu	Ser	Ser	Arg	Ile	Lys	Glu	Glu	Leu	Phe	Glu	Val	Val	Asn	His	Lys
		100					105				110				
Ile	Tyr	Leu	Arg	Ser	Leu	Phe	Leu	Leu	Arg	Glu	Lys	Val	Phe	His	Lys
	115					120				125					
Leu	His	Arg	Leu	Ala	Gly	Arg	Phe	His	Val	His	Leu				
	130					135				140					

(2) INFORMATIONS POUR LA SEQ ID NO: 777:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 416 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(764821..766068)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 777:

```

Lys Leu Ile Gly Ala Arg Arg Tyr Ala Glu Gly Arg Ile Val Ile Asn
1      5      10      15
Ser Ile Phe Asn Lys Ile Phe Ser Arg Glu Tyr Ala Trp Ser Val Asp
      20      25      30
Met Tyr Asn Arg Leu Val Leu Met Leu Gly Gln Ser Tyr Leu Leu Glu
      35      40      45
Leu Gln Glu Gly Val Arg Ser Asp Leu Leu Pro Glu Tyr Tyr Glu Thr
      50      55      60
Ile Leu Phe Tyr Gln Lys Gln Met Lys Gly Phe Asp Ala Gly Ala Tyr
65      70      75      80
Lys Thr Phe Phe Pro Glu Ser Met Leu Val Pro Thr Ile Met Gln His
      85      90      95
Ile Phe Val Ile Pro Glu Thr Gln Leu Pro Leu Phe Met Asp Ala Leu
      100      105      110
Leu Met Trp Glu Asn Ser Tyr Val His Pro Asp Tyr Ser Leu Val Leu
      115      120      125
Glu Arg Met Lys Pro Ala Val Leu Gln Asp Gly Ile His Thr Gln Lys
      130      135      140
Ile Cys Gln Ala Ile Ala Asp Ser Lys Ile Lys Lys Leu Lys Glu Lys
145      150      155      160
Leu Ile Glu Leu Phe Ser Asp Glu Leu Val Phe Cys Val Ser Gln Gly
      165      170      175
Asn Thr Val Cys Ala Asp Gln Tyr Leu Ala Leu Leu Lys Thr Leu Asp
      180      185      190
Pro Arg Ser Ser Trp Gly His Lys Leu Leu Leu Ser Glu Lys Glu Ile
      195      200      205
Val Asn Met Val Cys Glu Asp Asp Ala Gln Tyr Ser Arg Leu Lys Asp
      210      215      220
Tyr Leu Leu Leu Trp Glu Glu Gln Asp Ile Ala Asp Val Asp Arg Gln
225      230      235      240
Gln Leu Val His Tyr Leu Phe Phe Ser Ala Lys His Leu Trp Arg Gly
      245      250      255
Gly Gln Glu Glu Ala Cys Leu Arg Leu Leu Lys Glu Ile Leu Leu Phe
      260      265      270
Ser Gln Asn Glu Lys Ala Cys Leu Asn Arg Thr Leu Arg Leu Val Lys
      275      280      285
Asp Phe Tyr Thr Gln Ala Leu Ala Met Arg Asn Phe Thr His Leu Val
      290      295      300
Trp Ile Glu Asn Phe Leu Asp Glu Val Gly Leu Pro Lys Thr Leu Ala
305      310      315      320
Ser Asp Ala Glu Ile Ala Asn Cys Leu Ala Asp Ala Gln Tyr Leu Phe
      325      330      335
Ser Lys Gly Asp Tyr Arg Leu Cys Ile Val Tyr Ser Ser Trp Leu Ala
      340      345      350
Arg Val Ala Pro Ser Thr Glu Ala Leu Gln Leu Leu Gly Leu Ser Leu
      355      360      365
Val Glu Gln Lys Glu Tyr Thr Glu Ala Leu Glu Val Phe Gln Lys Leu
      370      375      380
Pro Leu Gly Glu Asp Ala Trp Asn Ser Gln Val His Lys Ala Ser Leu
385      390      395      400
Leu Cys Tyr Lys Tyr Ile Ala Arg Gln Gln Lys Glu Lys Ser Phe Pro
      405      410      415

```

(2) INFORMATIONS POUR LA SEQ ID NO: 778:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(766065..766475)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 778:

Met	Glu	Gln	Glu	Gln	Met	Tyr	Leu	Leu	Cys	Cys	Gln	Gly	Phe	Ser	Leu
1				5					10					15	
Gln	Ile	Gln	Arg	Lys	Phe	Gln	Glu	Ser	Lys	Glu	Ile	Phe	Ser	Arg	Ile
		20					25					30			
Asp	Lys	Arg	Lys	Thr	Ser	Ala	Pro	Phe	Val	Leu	Gln	Arg	Glu	Leu	Leu
		35				40					45				
Glu	Gly	Arg	Ile	Leu	Asn	Ala	Tyr	Phe	Leu	Asn	Asn	Leu	Ser	Leu	Met
	50				55					60					
Ala	Glu	Cys	Ile	Ala	Glu	Leu	Glu	Arg	Val	Ser	Gly	Ser	Glu	Ala	His
65				70					75					80	
Leu	Leu	Phe	Phe	Lys	Ala	Leu	His	Ala	His	Arg	Thr	Lys	Gln	Tyr	Asn
			85				90						95		
Leu	Ala	Val	Asp	Val	Leu	Ser	Arg	Trp	Phe	Gly	His	Val	Asp	Gln	Thr
		100					105					110			
Lys	Pro	Leu	Cys	Leu	Asp	Thr	Asn	Val	Tyr	Glu	Leu	Phe	Ser	Pro	Tyr
		115				120						125			
Val	Leu	Glu	Glu	Ile	Ala	Ala	Glu	Ser							
	130					135									

(2) INFORMATIONS POUR LA SEQ ID NO: 779:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(766934..767989)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 779:

Met	Ser	Val	Pro	Asp	Arg	Lys	Arg	Ala	Leu	Glu	Ala	Ala	Ile	Ala	Tyr
1			5						10					15	
Ile	Glu	Lys	Gln	Phe	Gly	Ala	Gly	Ser	Ile	Met	Ser	Leu	Gly	Lys	His
		20					25					30			
Ser	Ser	Ala	His	Glu	Ile	Ser	Thr	Ile	Lys	Thr	Gly	Ala	Leu	Ser	Leu
		35				40					45				
Asp	Leu	Ala	Leu	Gly	Ile	Gly	Gly	Val	Pro	Lys	Gly	Arg	Ile	Val	Glu
	50				55				60						
Ile	Phe	Gly	Pro	Glu	Ser	Gly	Lys	Thr	Thr	Leu	Ala	Thr	His	Ile	
65			70					75					80		
Val	Ala	Asn	Ala	Gln	Lys	Met	Gly	Gly	Val	Ala	Ala	Tyr	Ile	Asp	Ala
		85					90						95		
Glu	His	Ala	Leu	Asp	Pro	Asn	Tyr	Ala	Ala	Leu	Ile	Gly	Ala	Asn	Ile
		100					105					110			

```

Asn Asp Leu Met Ile Ser Gln Pro Asp Cys Gly Glu Asp Ala Leu Ser
      115      120      125
Ile Ala Glu Leu Leu Ala Arg Ser Gly Ala Val Asp Val Ile Val Ile
      130      135      140
Asp Ser Val Ala Ala Leu Val Pro Lys Ser Glu Leu Glu Gly Glu Ile
145      150      155      160
Gly Asp Val His Val Gly Leu Gln Ala Arg Met Met Ser Gln Ala Leu
      165      170      175
Arg Lys Leu Thr Ala Thr Leu Ala Arg Thr Asn Thr Cys Ala Ile Phe
      180      185      190
Ile Asn Gln Ile Arg Glu Lys Ile Gly Val Ser Phe Gly Asn Pro Glu
      195      200      205
Thr Thr Thr Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Ile Arg Ile
      210      215      220
Asp Ile Arg Arg Ile Gly Ser Ile Lys Gly Gly Glu Asn Phe Asp Ile
225      230      235      240
Gly Asn Arg Ile Lys Val Lys Val Ala Lys Asn Lys Leu Ala Pro Pro
      245      250      255
Phe Arg Thr Ala Glu Phe Asp Ile Leu Phe Asn Glu Gly Ile Ser Ser
      260      265      270
Ala Gly Cys Ile Ile Asp Leu Ala Val Glu Lys Asn Ile Ile Asp Lys
      275      280      285
Lys Gly Ser Trp Phe Asn Tyr Gln Asp Arg Lys Leu Gly Gln Gly Arg
      290      295      300
Glu Ala Val Arg Glu Glu Leu Lys Arg Asn Lys Glu Leu Phe His Glu
305      310      315      320
Leu Glu Arg Arg Ile Tyr Glu Ser Val Gln Ala Ser Gln Ala Pro Ala
      325      330      335
Ala Ala Cys Val Asp Ser Glu Ser Arg Glu Val Ala Glu Ala Ala Lys
      340      345      350

```

(2) INFORMATIONS POUR LA SEQ ID NO: 780:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 178 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(768252..768785)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 780:

```

Met Lys Asn Ile Val Glu Gln Lys Arg Cys Leu Arg Arg Glu Gly Leu
1      5      10      15
Ala Lys Arg Glu Gln Leu Ser Val Gln Arg Arg Asp Glu Ala Ala Arg
      20      25      30
Glu Leu Met His Phe Val Met Gln Thr Ile Xaa Gln Gly Phe Val Leu
      35      40      45
Ser Tyr Ile Pro Phe Arg Ser Glu Leu Asp Val Arg Gly Ile Asn Ala
      50      55      60
Trp Leu Ala Gln Glu Asn Arg Leu Leu Leu Pro Lys Met Gln Gly Met
      65      70      75      80
Asp Ile Val Pro Ile Ala Leu Pro Phe Thr Met Ile Glu Ser Leu Tyr
      85      90      95
Ser Pro Lys Asp Leu Asn Gln Ile Glu Gly Glu Glu Ile Glu Ala Gln

```

Leu Thr

(i) CARACTERISTIQUES DE LA SEQUENCE:

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 781:

Met 1	Cys	Val	Ser	Arg 5	Ser	Leu	Arg	Trp	Cys 10	Leu	Cys	Phe	Leu	Leu 15	Leu
Cys	Gly	Trp	Val 20	Asp	Ala	Gly	Val 25	Tyr	Asp	Lys	Leu	Arg 30	Leu	Thr	Gly
Ile	Asn 35	Ile	Ile	Asp	Arg	Asn 40	Gly	Leu	Ser	Glu	Thr 45	Ile	Cys	Ser	Lys
Glu	Lys 50	Leu	Gln	Lys	Tyr	Thr 55	Lys	Ile	Asp	Phe 60	Leu	Ser	Pro	Gln	Pro
Tyr 65	Gln	Lys	Val	Met 70	Arg	Thr	Tyr	Lys	Asn	Ala 75	Ala	Gly	Glu	Ser	Val 80
Ala	Cys	Leu	Thr 85	Thr	Tyr	Tyr	Pro	Asn 90	Gly	Gln	Ile	Arg	Gln	Tyr 95	Leu
Glu	Cys	Leu	Asn 100	Asn	Arg	Ala	Phe 105	Gly	Arg	Tyr	Arg 110	Glu	Trp	His	Ser
Asn	Gly 115	Lys	Ile	His	Ile	Gln 120	Ala	Glu	Val	Ile	Gly 125	Gly	Ile	Ala	Asp
Leu 130	His	Pro	Ser	Ala	Glu	Ala 135	Gly	Trp	Leu	Phe	Asp 140	Gly	Thr	Thr	Tyr
Ala 145	His	Asp	Ser	Glu 150	Gly	Arg	Leu	Glu	Ala 155	Val	Ile	His	Tyr	Glu	Lys 160
Gly	Leu	Leu	Glu 165	Gly	Ile	Ser	Leu	Tyr 170	Tyr	His	Ala	Asn	Gly 175	Asn	Val
Trp	Lys	Glu 180	Cys	Pro	Tyr	His	Lys 185	Gly	Val	Ala	His 190	Gly	Asp	Phe	Leu
Val	Phe 195	Thr	Glu	Glu	Gly	Ser 200	Leu	Leu	Lys	Lys	Gln 205	Thr	Phe	Cys	Lys
Gly 210	Gln	Leu	Ser	Gly 215	Cys	Ala	Leu	Arg	Tyr 220	Glu	Pro	Gly	Ser	Gln	Ser
Leu 225	Leu	Ser	Glu 230	Glu	Glu	Tyr	Lys	Gln	Gly 235	Lys	Leu	Arg	Ser	Gly	Lys 240
Tyr	Tyr	Asp	Pro 245	Leu	Thr	Lys	Glu	Glu 250	Ile	Ala	Cys 255	Val	Val	Asn	Gly

Lys Gly Lys Gln Val Ile Tyr Gly Lys Tyr Ala Ile Ile Glu Thr Arg
 260 265 270
 Gln Ile Val His Gly Val Pro His Gly Glu Val Leu Leu Phe Asp Glu
 275 280 285
 His Gly Lys Ser Leu Leu Gln Ala Tyr Ser Leu Ile Asn Gly Gln Lys
 290 295 300
 Glu Gly Glu Glu Val Phe Tyr Pro Gly Gly Glu Gly Arg Lys Met
 305 310 315 320
 Leu Leu Thr Trp Ser Gln Gly Ile Leu Gln Gly Ala Val Lys Thr Trp
 325 330 335
 Tyr Pro Asn Gly Ala Leu Glu Ser Ser Lys Glu Leu Val Gln Asn Lys
 340 345 350
 Lys Thr Gly Ile Leu Met Leu Tyr Tyr Pro Glu Gly Gln Val Met Ala
 355 360 365
 Thr Glu Glu Tyr Val Asp Asp Leu Leu Ile Lys Gly Glu Tyr Phe Arg
 370 375 380
 Pro Asn Asp Arg Tyr Pro Tyr Ala Lys Val Glu Lys Gly Ser Gly Thr
 385 390 395 400
 Ala Val Phe Phe Ser Ala Thr Gly Gly Leu Leu Lys Lys Val Leu Tyr
 405 410 415
 Glu Asp Gly Lys Pro Val Ile His
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 782:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 770138..770470

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 782:

Glu Arg Lys Thr Met Gly Ile Trp Val Tyr Leu Gly Ser Asn Asn His
 1 5 10 15
 Asn Asn Thr Gly Met Ser Ser Ser Ser Ile Trp Ser Ser Phe Trp Lys
 20 25 30
 Glu Asn Asn Val Leu Phe Ser Pro Lys Val Cys Ser Cys His Asp Lys
 35 40 45
 Arg Leu Ser Ser Lys Lys Ala Phe Arg Ser Leu Thr Ala Arg Leu Leu
 50 55 60
 Thr Thr Gln Ala Val Ala Gly Ser Leu Ala Arg Ala Ser Arg Ser Leu
 65 70 75 80
 Phe Lys Lys Thr Arg Phe Ser Pro Trp Ala Ile Gln Leu Gly Lys Leu
 85 90 95
 Ala Cys Leu Cys Ala Ala Phe Ser Arg Ala Phe Leu Ile Ala Thr
 100 105 110

(2) INFORMATIONS POUR LA SEQ ID NO: 783:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 159 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(770185..770661)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 783:

Cys	Thr	Asn	Arg	Ser	Ala	Arg	Glu	Gly	Ile	Met	Arg	Arg	Leu	Gly	Val
1				5				10					15		
Trp	Val	Leu	Leu	Leu	Ala	Ser	Gly	Ala	Ala	Ser	Leu	Pro	Ala	Ile	
		20					25					30			
Gly	Ala	Trp	Cys	Trp	Arg	Gln	Arg	Thr	Ala	Glu	Ala	Trp	Glu	Asn	Leu
	35					40						45			
Leu	Ile	Asp	Met	Arg	Asp	Phe	Gln	Ser	Lys	Arg	Glu	Arg	Ser	Ser	Gln
	50				55						60				
Val	Ala	Ile	Lys	Asn	Ala	Arg	Leu	Lys	Ala	Ala	His	Lys	Gln	Ala	Ser
65				70					75					80	
Phe	Pro	Asn	Trp	Ile	Ala	Gln	Gly	Glu	Asn	Leu	Val	Phe	Leu	Asn	Lys
			85					90					95		
Glu	Arg	Asp	Ala	Leu	Ala	Lys	Leu	Pro	Ala	Thr	Ala	Trp	Val	Val	Arg
			100				105						110		
Ser	Arg	Ala	Val	Lys	Asp	Arg	Lys	Ala	Phe	Leu	Glu	Asp	Asn	Arg	Leu
		115				120						125			
Ser	Trp	Gln	Glu	Gln	Thr	Leu	Gly	Glu	Lys	Ser	Thr	Leu	Phe	Ser	Phe
	130				135						140				
Gln	Lys	Glu	Leu	Gln	Ile	Asp	Asp	Glu	Asp	Ile	Pro	Val	Leu	Leu	
145					150					155					

(2) INFORMATIONS POUR LA SEQ ID NO: 784:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 97 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(770634..770924)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 784:

Ile	Pro	Pro	Thr	Val	Pro	Thr	Asn	Gln	Glu	Val	Met	Glu	Val	Leu	Gly
1				5				10						15	
Arg	Met	Thr	Ala	Asn	Leu	Pro	Ser	Val	Ser	Phe	Ser	His	Tyr	Leu	Tyr
		20					25						30		
Lys	Leu	Glu	Asp	Ile	Pro	Ser	Glu	Glu	Arg	Pro	Leu	Gly	Gly	Tyr	Arg
	35					40						45			
Ala	Tyr	Ile	Ser	Leu	Gln	Gly	Ala	Ala	Asn	Asp	Glu	Asp	Phe	Ala	Ser
	50				55					60					
Phe	Ile	Asp	Gln	Leu	Ser	Ala	Trp	Ile	Gly	Ala	Arg	Val	Leu	Ser	Lys
65				70					75					80	
Lys	Leu	Ala	Asp	Arg	Gln	Phe	Asp	Val	Arg	Ile	Ala	Leu	Gln	Gly	Arg
			85					90					95		

Gly

(2) INFORMATIONS POUR LA SEQ ID NO: 785:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 227 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(771330..772010)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 785:

```

Met Asp Phe Lys Leu Pro Ile Tyr Cys Ile Gly Val Thr Gln Ser Ala
1          5          10          15
Glu Asn Val Thr Arg Ile Ala Ile Leu Gln Lys Thr Cys Lys Gly Trp
          20          25          30
Ser Leu Cys Arg Cys Glu Lys Leu Thr Glu Thr Gly Ala Leu Ser Trp
          35          40          45
Pro Lys Arg Phe Leu Ser Ser Lys Val Val Leu Ser Leu Gln Gly Gln
          50          55          60
Glu Thr Leu Val Lys Ser Val Ser Ser Ser Leu Lys Ser Lys Lys Asn
65          70          75          80
Phe Leu Lys Met Val Tyr Ala Glu Gln Glu Ala Thr Ala Ala Phe Pro
          85          90          95
Leu Lys Asp Leu Val Ile Ala His Asp Leu Gly Glu Trp Asn Ser Ala
          100          105          110
Gln Glu Arg Val Val Thr Leu Trp Met Leu Gln Arg Gln Ser Val Ala
          115          120          125
Leu Ala Thr Ala Leu Leu Glu Glu Lys Gly Gly Phe Ala Thr His Ile
          130          135          140
Ser Cys Arg Ala Lys Asp Leu Phe Ser Ala Leu Gln Gln Ser Leu Leu
145          150          155          160
Arg Asn Leu Glu Thr Tyr Phe Phe Val Tyr Glu Gly Leu Asp Glu Thr
          165          170          175
Val Cys Leu Phe Val Gln Glu Gly Ser Val Leu Leu Ser Arg Ser Phe
          180          185          190
Lys Asn Asp Ser Glu Ser Leu Leu Asp Asp Leu Leu Ala Ser Phe Ala
          195          200          205
Tyr Val Gln Glu Val Tyr Thr Ala Ser Phe Ile Arg Asp Pro Arg Arg
          210          215          220
Leu Ser Ile
225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 786:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 334 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 772390..773391

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 786:

```

Met Ala Pro Ser Ile Phe Ile Lys Asn Leu Pro Leu Lys Ser Pro Val
1      5      10      15
Val Tyr Ala Pro Leu Ala Gly Phe Ser Asp Phe Pro Tyr Arg Arg Met
      20      25      30
Ser Ala Glu Tyr Arg Pro Ala Leu Met Phe Cys Glu Met Val Lys Met
      35      40      45
Glu Gly Leu His Tyr Cys Pro Gln Arg Thr Leu Arg Leu Leu Asp Phe
      50      55      60
Ala Glu Ser Met Arg Pro Ile Gly Gly Gln Leu Cys Gly Ser Arg Pro
65      70      75      80
Asp Leu Ala Gly Glu Ser Ala Lys Ile Leu Glu Gly Leu Gly Phe Asp
      85      90      95
Leu Ile Asp Leu Asn Cys Gly Cys Pro Thr Asp Arg Ile Thr Lys Asp
      100      105      110
Gly Ser Gly Ser Gly Met Leu Lys Thr Pro Glu Leu Ile Gly Lys Val
      115      120      125
Val Glu Lys Met Val Glu Val Val Ser Val Pro Val Thr Val Lys Ile
130      135      140
Arg Ser Gly Trp Asp Phe Asp His Ile Asn Val Glu Glu Thr Val Arg
145      150      155      160
Ile Ile Lys Glu Ser Gly Ala Ser Ala Val Phe Val His Gly Arg Thr
      165      170      175
Arg Ser Gln Gly Tyr Gln Gly Pro Ser Asn Leu Glu Phe Ile Ser Arg
      180      185      190
Ala Lys Gln Ala Ala Gly Asp Asp Phe Pro Val Phe Gly Asn Gly Asp
195      200      205
Val Phe Ser Pro Glu Ala Ala Lys Thr Met Leu Glu Thr Thr His Cys
210      215      220
Asp Gly Val Leu Val Ala Arg Gly Thr Met Gly Ala Pro Trp Ile Gly
225      230      235      240
Lys Gln Ile Glu Asp Tyr Leu Thr Thr Gly Thr Tyr Ser Ser Pro Ser
      245      250      255
Phe Ser Thr Arg Lys Gln Ala Phe Val Gln His Leu Gln Trp Ile Glu
      260      265      270
Glu Tyr Tyr Gln Ser Glu Glu Lys Leu Leu Thr Asp Thr Arg Lys Leu
275      280      285
Cys Gly His Tyr Leu Ile Leu Ser Pro Lys Val Arg Ser Leu Arg Ala
290      295      300
Asn Leu Ala Lys Ala Ser Ser Ser Gln Glu Val Tyr Gln Leu Ile Asp
305      310      315      320
Gly Phe Glu Glu Leu Thr Glu Glu Glu Glu Leu Leu Ser Glu
      325      330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 787:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 265 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(773427..774221)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 787:

```

Asn Arg Leu Ser Lys Cys His Lys Gly Lys Leu Val Lys Ile Trp Ala
1      5      10      15
Lys Asn Arg Tyr Phe Phe Gly Cys Ser Glu Tyr Pro Thr Cys Asp Tyr
20      25      30
Lys Thr Ser Glu Glu Glu Leu Thr Phe Asp Lys Asn Glu Tyr Ala Glu
35      40      45
Asp Thr Pro Trp Asp Ala Pro Cys Ala Leu Cys Gly Gly Glu Met Lys
50      55      60
Val Arg His Gly Lys Phe Gly Ser Phe Leu Gly Cys Glu Asn Tyr Pro
65      70      75      80
Lys Cys His Tyr Ile Val Asn Leu Phe Lys Lys Gly Glu Ala Gly Ala
85      90      95
Glu Pro Glu Ala Thr Val His Cys Pro Ala Glu Gly Cys Thr Gly His
100     105     110
Leu Val Lys Arg Arg Ser Arg Phe Asn Lys Met Phe Tyr Ser Cys Ser
115     120     125
Glu Tyr Pro Ala Cys Ser Val Ile Gly Asn Ser Val Asp Ala Val Ile
130     135     140
Glu Lys Tyr Ala Gly Thr Pro Lys Thr Pro Tyr Glu Lys Lys Pro Lys
145     150     155     160
Ala Lys Lys Ser Ile Ala Ser Thr Lys Gly Lys Ala Ala Lys Thr Val
165     170     175
Lys Lys Ser Ser Ala Thr Thr Lys Lys Arg Ala Thr Lys Ala Tyr Thr
180     185     190
Pro Ser Ala Ala Leu Ala Gly Val Ile Gly Ala Asp Pro Val Gly Arg
195     200     205
Pro Glu Ala Thr Lys Lys Leu Trp Glu Tyr Ile Lys Glu Lys Gly Leu
210     215     220
Gln Ser Pro Gln Asn Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln
225     230     235     240
Gly Val Ile Gly Ala Asp Pro Ile Asp Met Phe Ala Leu Ser Lys Lys
245     250     255
Leu Ser Ala His Leu Ile Lys Glu Glu
260     265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 788:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 602 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(774191..775996)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 788:

```

Met Lys Lys Ser Leu Ile Ile Val Glu Ser Pro Ala Lys Ile Lys Thr
1      5      10      15
Leu Arg Lys Leu Leu Gly Glu Gly Phe Ile Phe Asp Ser Ser Leu Gly
20      25      30
His Ile Val Asp Leu Pro Ala Lys Gly Phe Gly Ile Asp Ile Glu Asn
35      40      45
Gly Phe Val Pro Asp Tyr Gln Ile Leu Glu Gly Lys Glu Glu Val Ile

```


50	55	60
Arg Lys Ile Cys Ala Glu	Ala Lys Lys Cys Asp	Val Val Tyr Leu Ala
65	70	75
Pro Asp Pro Asp Arg	Glu Gly Glu Ala Ile	Ala Trp His Ile Ala Asn
85	90	95
Gln Leu Pro Lys Asp Thr	Lys Ile Gln Arg Ile	Ser Phe Asn Ala Ile
100	105	110
Thr Lys Gly Ala Val Thr	Glu Ala Leu Lys His	Pro Arg Glu Ile Asp
115	120	125
Met Ala Leu Val Asn Ala	Gln Gln Ala Arg Arg	Phe Leu Asp Arg Ile
130	135	140
Val Gly Tyr Lys Ile Ser	Pro Ile Leu Gly Arg	Lys Leu Gln Arg Trp
145	150	155
Ser Gly Val Ser Ala Gly	Arg Val Gln Ser Val	Ala Leu Lys Leu Val
165	170	175
Val Asp Arg Glu Tyr Ala	Ile Glu Arg Phe Val	Pro Val Glu Phe Trp
180	185	190
Asn Ile Arg Val His Leu	Lys Asp Pro Gln Thr	Gln Lys Thr Phe Trp
195	200	205
Ala His Leu His Ser Val	Asn Gly Lys Lys Trp	Glu Lys Glu Ile Pro
210	215	220
Glu Gly Lys Thr Ser Asp	Glu Val Ile Leu Ile	Asp Ser Lys Glu Lys
225	230	235
Ala Asp Glu Ile Val Ala	Leu Leu Glu Ser Ala	Thr Tyr Val Val Asp
245	250	255
Arg Val Glu Ser Lys Glu	Lys Lys Arg His Ala	Tyr Pro Pro Phe Ile
260	265	270
Thr Ser Thr Leu Gln Gln	Glu Ala Ser Arg His	Tyr Arg Phe Ser Ser
275	280	285
Ser Arg Thr Met Asn Ile	Ala Gln Thr Leu Tyr	Glu Gly Val Asp Leu
290	295	300
Asp Ser Gln Gly Ala Val	Gly Leu Ile Thr Tyr	Met Arg Thr Asp Ser
305	310	315
Val Arg Thr Asp Pro Glu	Ala Val Lys Gln Val	Arg Lys Tyr Ile Glu
325	330	335
Gly His Phe Gly Lys Glu	Phe Val Pro Ser Ser	Pro Asn Val Tyr Ala
340	345	350
Thr Lys Lys Met Ala Gln	Asp Ala His Glu Ala	Ile Arg Pro Thr Asp
355	360	365
Val Thr Ile Thr Pro Glu	Ser Ile Arg Ser Lys	Leu Thr Glu Asp Gln
370	375	380
Tyr Lys Leu Tyr Ser Leu	Ile Trp Lys Arg Phe	Val Ala Ser Gln Met
385	390	395
Ile Ser Ala Ile Tyr Asp	Thr Leu Ala Ile Arg	Ile Thr Thr Asn Lys
405	410	415
Gly Ile Asp Leu Arg Ala	Thr Gly Ser Cys Leu	Lys Phe Lys Gly Phe
420	425	430
Leu Ala Val Tyr Glu Glu	Lys Arg Asp Glu Glu	Gly Asp Glu Glu Glu
435	440	445
Asn Ile His Leu Pro Lys	Leu Asn Glu Arg Asp	Val Leu Thr Lys Glu
450	455	460
Glu Leu Glu Ala Glu Gln	Ser His Thr Lys Pro	Leu Pro Arg Phe Thr
465	470	475
Glu Ala Ser Leu Val Lys	Glu Leu Glu Lys Ser	Gly Ile Gly Arg Pro
485	490	495
Ser Thr Tyr Ala Thr Ile	Met Asn Lys Ile Gln	Ser Arg Glu Tyr Thr
500	505	510
Leu Lys Glu Gly Gln Arg	Leu Arg Pro Thr Glu	Leu Gly Lys Val Val
515	520	525

Cys Gln Phe Leu Glu Thr Asn Phe Pro Arg Ile Met Asp Ile Gly Phe
 530 535 540
 Thr Ala Gly Met Glu Asp Glu Leu Glu Leu Ile Ala Asp Asn Lys Lys
 545 550 555 560
 Pro Trp Lys Gln Leu Leu Gln Glu Phe Cys Glu Leu Phe Leu Pro Phe
 565 570 575
 Val Val Thr Ala Glu Lys Glu Ala Phe Ile Pro Arg Ile Val Thr Glu
 580 585 590
 Ile Asp Cys Pro Asn Val Ile Lys Gly Asn
 595 600

(2) INFORMATIONS POUR LA SEQ ID NO: 789:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 348 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 776663..777706

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 789:

Val Phe Pro Gly Pro Asn Asp Ile Gly Ser Gln Glu Asn Val Lys Asp
 1 5 10 15
 Ile Cys Ser Leu Asp Pro Thr Asn Tyr Val Asn Ser Ser Cys Tyr Ser
 20 25 30
 Arg Ser Phe Pro His Gln Pro Ile Gly Thr Pro Leu Phe Phe Gly Lys
 35 40 45
 Lys Pro Val Leu Thr Tyr Gly Glu Val Ser Lys Leu Ile Ser Ser Lys
 50 55 60
 Thr Asp Pro Glu Pro Phe Ser Tyr Cys Arg Pro Thr Phe Leu Arg Ala
 65 70 75 80
 Ala Leu Asn Thr Leu Glu Phe Leu Ser Ser Pro Pro Ser Ser Asp Pro
 85 90 95
 Tyr Asp Asp Leu Leu Gln Leu Asn Lys Glu Gly Phe Leu Ala Gly Pro
 100 105 110
 Glu Glu Glu Lys Gln Ala Phe Phe Leu Arg Val Glu Arg Thr Leu Ala
 115 120 125
 Glu Ala Pro Val His Pro Thr Pro Phe Pro Ile Glu Phe Gln Lys Leu
 130 135 140
 Phe Asp Val Asn Pro Ser Phe Leu Glu Val Val Tyr Ser Asn Glu Ser
 145 150 155 160
 Leu Asp Ala Trp Glu Ala Gly Cys Thr Trp Ile Thr Asp Asn Arg Val
 165 170 175
 Ser Ile Gln Leu Arg Lys Gly Phe Gln Lys Ala Ser Phe Trp Phe Gly
 180 185 190
 Phe Phe Ser Lys Glu Glu Val Leu Ser His Glu Ala Val His Ala Val
 195 200 205
 Arg Met Lys Phe Tyr Glu Pro Ile Phe Glu Glu Val Leu Ala Tyr Ser
 210 215 220
 Thr Ser Lys His Phe Trp Arg Arg Phe Phe Gly Pro Leu Phe Arg Ser
 225 230 235 240
 Ala Gly Glu Thr His Phe Phe Leu Phe Phe Val Leu Phe Gly Ala Phe
 245 250 255
 Leu Phe Pro Trp Phe Pro Trp Ile Gly Leu Ser Cys Ile Leu Ala Pro

```

                260                265                270
Asn Met Phe Phe Phe Phe Arg Leu Phe Arg Thr Gln Ile Leu Phe Arg
                275                280                285
Lys Ala Lys Lys Lys Ile Arg Lys Leu Leu Gly Ile Glu Pro Leu Trp
                290                295                300
Val Leu Leu Arg Leu Thr Asp Arg Glu Ile Arg Leu Phe Ala Thr Gln
305                310                315                320
Pro Leu Ala Val Ile Glu Asp Phe Ala Arg Lys Glu Lys Leu Lys Ser
                325                330                335
Val Arg Trp Arg Gln Ile Tyr Gln Ser Tyr Phe Thr
                340                345

```

(2) INFORMATIONS POUR LA SEQ ID NO: 790:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 81 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(776953..777195)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 790:

```

Ile Asp Thr Leu Leu Ser Val Ile His Val His Pro Ala Ser Gln Ala
1                5                10                15
Ser Lys Leu Ser Leu Glu Tyr Thr Thr Ser Lys Lys Glu Gly Phe Thr
                20                25                30
Ser Lys Ser Phe Trp Asn Ser Met Gly Lys Gly Val Gly Cys Thr Gly
                35                40                45
Ala Ser Ala Asn Val Leu Ser Thr Arg Arg Lys Lys Ala Cys Phe Ser
                50                55                60
Ser Ser Gly Pro Ala Arg Asn Pro Ser Leu Phe Asn Cys Asn Lys Ser
65                70                75                80
Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 791:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 497 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(777732..779222)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 791:

```

Pro Pro Phe Gln Val Val Trp Gln Ile Gly Phe Lys Arg Glu Met Ile
1                5                10                15
Ile Leu Phe Thr Arg Val Ile Glu Ile Phe Cys Ala Ile Leu Gly Val
                20                25                30

```

Tyr Phe Phe His Ile His Ser Val Val Gly Gly Tyr Phe Val Leu Val
 35 40 45
 Leu Met Ala Cys His Ser Ala Ile Phe Gly Pro Ala Lys Met Gly Ile
 50 55 60
 Leu Pro Glu Met Leu Pro Ile Glu Glu Leu Ser Lys Ala Asn Gly Ala
 65 70 75 80
 Met Thr Ala Ala Thr Tyr Ser Gly Ser Ile Leu Gly Ser Cys Leu Ala
 85 90 95
 Pro Leu Met Val Asp Leu Thr Lys Asp Phe Val Thr Asn Ser Tyr Glu
 100 105 110
 Leu Ser Ala Cys Phe Cys Val Val Ser Ser Val Leu Ser Leu Phe Ile
 115 120 125
 Ala Leu Gly Ile Arg Ala Ser Asn Val Lys Asn Lys Gly Gln Lys Ile
 130 135 140
 Ala Tyr Val Ser Phe Arg Asn Leu Trp Gln Val Phe Gln Glu Thr Arg
 145 150 155 160
 Asn Ile Ala Tyr Leu Met Ile Ser Val Phe Leu Val Ala Phe Phe Leu
 165 170 175
 Phe Val Gly Ala Tyr Val Gln Leu Gln Ile Ile Pro Phe Val Glu Phe
 180 185 190
 Thr Leu Gly Tyr Ser Lys His Tyr Gly Ala Tyr Leu Phe Pro Ile Val
 195 200 205
 Ala Val Gly Met Gly Val Gly Ser Tyr Met Ala Gly Trp Ile Ser Gly
 210 215 220
 Lys Asp Ile Lys Leu Gly Phe Ser Pro Leu Ala Ala Ile Gly Val Gly
 225 230 235 240
 Leu Ser Met Met Val Leu Cys Leu Leu Ser Phe Ser Ile Thr Ala Val
 245 250 255
 Leu Ile Leu Leu Phe Cys Leu Gly Leu Val Gly Gly Ile Tyr Gln Val
 260 265 270
 Pro Leu His Ala Tyr Ile Gln Phe Val Ser Pro Glu His Lys Arg Gly
 275 280 285
 Gln Val Leu Ala Leu Asn Asn Phe Leu Asp Phe Ser Gly Val Leu Leu
 290 295 300
 Ala Ala Gly Phe Val Arg Leu Leu Gly Ala Gly Leu Arg Leu Thr Pro
 305 310 315 320
 Asp Gln Ser Phe Leu Tyr Met Gly Ser Leu Val Val Cys Phe Ala Ile
 325 330 335
 Leu Ser Leu Trp Met Leu Lys Glu His Val Tyr Arg Leu Leu Leu Thr
 340 345 350
 Arg Val Leu Lys Arg Gln Leu Gly Thr Ser Phe Ser Ser Pro Lys Ala
 355 360 365
 Glu Glu Val Trp Cys Phe Phe Val Pro Ala Thr Ser Tyr Lys Glu Thr
 370 375 380
 Arg Arg Ile Leu Ala Leu Phe Pro Lys Thr Val Arg Ser Cys Val Phe
 385 390 395 400
 Ile Leu Asp Lys Ala Leu Gln Pro Gly Trp Thr Ser Tyr Leu Ile Pro
 405 410 415
 His Cys Val Pro Thr Ile Phe Ser Tyr Gly Val Glu Gly Gln Ala Phe
 420 425 430
 Ala Gln Trp Ile Asp Arg Gln Val Val Glu Val Lys Ala Leu Leu Lys
 435 440 445
 Arg Gln Pro Ser Leu Gly Val Val Cys Leu Gly Asn Gln Ala Gln Ser
 450 455 460
 Gln Phe Phe Phe Ser Gln Leu Gln Ala Ser Gly Leu Ala Val Gln Ser
 465 470 475 480
 Gly Thr Leu Val Gln Asp Ser Glu Leu Lys Tyr Ser Leu His Leu Ala
 485 490 495

Asn

(2) INFORMATIONS POUR LA SEQ ID NO: 792:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 744 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 779321..781552

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 792:

Lys	Lys	Leu	Ile	Glu	Ile	Val	Ile	Tyr	Asn	Cys	Lys	Lys	Met	Cys	Asn
1				5					10					15	
Asp	Gln	Cys	Thr	Glu	Arg	Ser	Phe	Pro	Arg	Asn	Asn	Thr	His	Glu	Cys
			20					25					30		
Lys	Pro	Met	Asn	Glu	Leu	Ser	His	Ser	Gln	Ser	Thr	Phe	Ser	Asn	Tyr
		35					40					45			
Pro	Glu	Val	Leu	Leu	Ala	Lys	Leu	Ala	Gln	Asp	Leu	Phe	Ser	Ile	Asn
	50					55					60				
Gln	Thr	Pro	Met	Thr	Lys	Arg	Trp	Ile	Leu	Val	Pro	Ser	Ser	Asp	Thr
65				70						75					80
Asp	His	Trp	Leu	Arg	Arg	Glu	Leu	Val	Lys	Ala	Ser	Ser	Asn	His	Ile
			85						90					95	
Phe	Met	Gly	Thr	His	Ile	Phe	Ala	Ser	Phe	Asp	Ala	Phe	Val	Lys	Tyr
			100					105					110		
Leu	Phe	Thr	Gly	Thr	Arg	Leu	Val	Asp	Leu	Ser	Thr	Pro	Asp	His	Ile
		115					120					125			
Thr	Leu	Pro	Leu	Thr	Ile	Tyr	Asn	Leu	Leu	Lys	Glu	Ser	Ser	Phe	Asn
	130					135					140				
Ser	Ser	Ser	Glu	Val	Ser	Tyr	Ser	His	Leu	Gln	Lys	Leu	Ser	Ser	Ile
145				150						155					160
Phe	Lys	Lys	Phe	Tyr	Thr	Phe	Ser	Gln	Glu	Pro	Ser	Thr	Asn	Asn	Pro
			165						170					175	
Tyr	Tyr	Lys	Asn	Leu	Phe	Ala	Gln	Leu	Lys	Asp	Ser	Tyr	Thr	Pro	Leu
			180					185					190		
Glu	Thr	Ile	Phe	Ser	Ser	Ile	Leu	Asp	His	Pro	Pro	Glu	Tyr	Pro	Cys
		195					200					205			
Ser	Leu	His	Ile	Phe	Gly	Tyr	Pro	Gln	Leu	Pro	Gln	His	Val	Ala	Ser
	210				215						220				
Phe	Phe	Val	Ala	Leu	Gly	Lys	Tyr	Phe	Pro	Val	His	Phe	Tyr	Cys	Phe
225				230						235					240
Ser	Pro	Ser	Ala	Ala	Tyr	Phe	Gly	Asp	Leu	Leu	Ser	Asp	Lys	Ala	Met
			245						250					255	
Ala	Ala	Leu	Ser	Pro	Arg	Ile	Pro	Glu	Pro	His	Gln	Glu	Thr	Trp	Glu
			260					265					270		
Lys	Tyr	Val	Leu	Thr	Asp	Arg	Leu	Ala	Leu	Leu	Ala	Asn	Leu	Ala	His
		275					280					285			
Lys	Ser	Gln	Ser	Leu	Gln	Asn	Phe	Phe	Leu	Asp	Tyr	Ser	Val	Pro	Tyr
	290					295					300				
Glu	Glu	Leu	Phe	Gln	Pro	Tyr	Glu	Lys	Leu	Ser	Ser	Leu	His	Ile	Val
305				310						315					320
Lys	Asp	Ser	Phe	Phe	His	Leu	Gln	Pro	Ile	Asp	Gln	Lys	Leu	Phe	Ser
				325					330					335	

Asn Ser Pro Gln Thr Ile Phe Val Arg Gln Ala Pro Ser Ala Ser Arg
 340 345 350
 Glu Val His Gln Leu Phe Ser Leu Val Ser Gln Leu Leu His Ser Gly
 355 360 365
 Val Pro Ala Gln Glu Ile Phe Ile Leu Ser Ser Asn Leu Ser Lys Tyr
 370 375 380
 Glu Thr Leu Leu Arg Gly Ile Phe Glu Pro His Leu Pro Leu Tyr Leu
 385 390 395 400
 Thr Lys Thr Glu Lys Thr Gln Thr Arg Thr Leu Lys Asn Lys Leu Leu
 405 410 415
 Leu Val Val Thr Phe Leu Phe Ser Lys Gly Ser Leu Asn Asp Leu Leu
 420 425 430
 Arg Ile Leu Ser His Pro Asp Leu Leu Ser Pro Leu Glu Thr Thr Lys
 435 440 445
 Met Gly Phe Leu Thr His Lys Leu Thr His Tyr Trp Lys Ser Leu Ser
 450 455 460
 Gln Lys Asp Ser Pro Leu Thr Gln Leu Ile His Arg Ile Leu Asp Glu
 465 470 475 480
 Tyr Pro Phe Ile Asp Asp Thr Gly Ser Val Asn Glu Ala Glu Thr Trp
 485 490 495
 Glu Val Val Val Pro Leu Leu His Thr Leu Gln Gln Val Thr Ala Ser
 500 505 510
 Tyr Ile Glu Ser Lys Asp Lys Thr Tyr Glu Glu His Ser Arg Leu Ile
 515 520 525
 Phe Ser Ala Leu Glu Asn Ile Phe Phe Leu Ser Thr Glu Glu Tyr Ala
 530 535 540
 Leu Leu Val Ser Leu Ser Lys Thr Leu Gln Pro Phe Val Arg Ser Ser
 545 550 555 560
 Cys Ser Leu Thr Ile Phe Ile Glu Phe Cys Leu Asp Phe Leu Ser His
 565 570 575
 Ile Pro Gly His Ser Gln Leu Tyr Asn Gln Pro Gly Pro Phe Val Gly
 580 585 590
 Ser Leu Asn Ser Leu Ser Leu Ile Pro Lys Gly Tyr Thr Phe Ile Leu
 595 600 605
 Gly Ala Asn Lys Lys Asp His Ser Leu Asp Thr Ser Phe Leu Ile Asp
 610 615 620
 Pro Ser Leu Ile Gln Glu Asp Phe Leu Phe Ser Ser Thr Glu Asp Glu
 625 630 635 640
 Asp Asn Leu His Phe Leu Gln Thr Ile Val Ser Thr Lys His Gln Leu
 645 650 655
 His Ile Ser Tyr Leu Ser Ser Ser Lys Asn Pro Ala Leu Pro Ser Ser
 660 665 670
 Ala Leu Gln Asn Ile Cys Trp Met Leu Cys Leu Phe Lys Lys Asn Ile
 675 680 685
 Phe Leu Gly Asn Phe Met Leu Lys Lys Thr Phe Leu Leu Asn Arg Cys
 690 695 700
 Ile Ser Leu Thr Arg Phe Thr Thr Gly Trp Leu Lys Ser Pro Arg Tyr
 705 710 715 720
 Lys Thr Arg Pro His Pro Cys Leu Ser Leu Ile Gln Leu Arg Arg Tyr
 725 730 735
 Leu His Thr Tyr Pro Tyr Asn Ile
 740

(2) INFORMATIONS POUR LA SEQ ID NO: 793:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 382 acides aminés
- (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 781297..782442

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 793:

Leu	Ser	Leu	Phe	Ile	Gln	Glu	Ser	Ser	Ile	Thr	Glu	Leu	Cys	Phe	Ala
1				5					10					15	
Lys	His	Leu	Leu	Asp	Ala	Val	Pro	Ile	Gln	Glu	Glu	His	Leu	Ser	Gly
			20					25					30		
Lys	Leu	Tyr	Ala	Lys	Glu	Asn	Phe	Ser	Ser	Glu	Pro	Leu	His	Gln	Ser
		35					40					45			
Tyr	Gln	Val	Tyr	Tyr	Arg	Met	Ala	Gln	Val	Ser	Pro	Leu	Gln	Asn	Lys
	50					55					60				
Ala	Pro	Ser	Leu	Phe	Lys	Ser	Asp	Thr	Thr	Lys	Thr	Leu	Pro	Ser	His
65					70					75					80
Leu	Ser	Leu	Gln	His	Leu	Ile	Lys	Ala	Phe	Lys	Asp	Pro	Leu	Asn	Phe
				85					90					95	
Phe	Leu	Ser	Thr	Gln	His	Gly	Phe	Ser	Phe	His	Pro	Lys	Ala	Leu	Phe
			100					105					110		
Ser	Lys	Ser	Glu	Lys	Val	Phe	Pro	Ser	Pro	His	Asp	Ala	Lys	Ala	Phe
		115					120					125			
Trp	Asn	His	Leu	Leu	Ser	Ser	Lys	Thr	Pro	Leu	Pro	Thr	Thr	Asn	Tyr
	130					135					140				
Leu	Ser	Ala	Phe	Thr	Glu	Ser	Leu	Tyr	Thr	Asp	Val	Gln	Asp	Ser	Val
145					150					155					160
Ser	Lys	Arg	Leu	Glu	Thr	Leu	Gln	Lys	Asp	Pro	Ala	Thr	Thr	Pro	Phe
			165						170					175	
Ser	Val	Val	Phe	Ser	Asp	Gln	Leu	Phe	His	Asp	Pro	Leu	His	Pro	Asn
			180					185					190		
Asp	Gln	Gln	Val	Pro	Pro	Leu	Leu	Leu	Ser	Leu	Pro	Leu	Lys	Asn	Ile
		195				200						205			
His	Leu	Gln	Gly	Thr	Ile	His	Gly	Val	Cys	Ser	Lys	Gly	Val	Tyr	Leu
	210					215					220				
Phe	Ser	Met	His	Pro	Gly	Glu	Ala	Phe	Lys	Lys	Thr	Gln	Lys	Thr	His
225					230					235					240
Gly	Phe	Pro	Lys	Asp	Ala	Phe	Glu	Leu	Glu	Ser	Tyr	Leu	Glu	Ser	Tyr
			245						250					255	
Leu	Ser	Leu	Ala	Leu	Leu	Gln	Ala	Ser	His	Leu	Leu	Pro	Lys	Glu	Ala
			260					265					270		
Thr	Ile	Leu	Arg	Val	Thr	Pro	His	Asp	Ile	Glu	Pro	Ile	Leu	Pro	Pro
		275					280					285			
Phe	Ser	Ser	Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Ala	Ile	His	Leu	Tyr	Asp
	290					295					300				
Leu	Leu	Gln	Asn	Gln	Ala	Val	Pro	Leu	Pro	Ser	Ala	Gln	Ala	Trp	Glu
305					310					315					320
Tyr	Ile	Lys	Lys	Thr	Asp	Ser	Ala	Ser	Gln	Cys	Ile	Lys	Lys	Leu	Leu
			325						330					335	
Asp	Ser	Glu	Glu	Asp	Pro	Leu	Thr	Ser	Ser	Phe	Trp	Trp	Phe	His	Asn
			340					345					350		
Arg	Asp	Thr	Glu	Glu	Ile	Cys	Ser	Glu	Leu	Ser	Asn	Asp	Val	Leu	Ser
		355					360					365			
Gln	Leu	Leu	Ser	Leu	Phe	Ile	Asn	Gln	Asp	Ser	Gln	Gln	Asn		
	370					375					380				

(2) INFORMATIONS POUR LA SEQ ID NO: 794:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1026 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 782447..785524

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 794:

Met	Ser	Ser	Phe	Asp	Ile	Phe	Ser	Pro	Thr	Ala	Ser	Val	Ser	Gly	Lys	1	5	10	15
Phe	Phe	Leu	Glu	Ala	Ser	Ala	Gly	Thr	Gly	Lys	Thr	Phe	Thr	Ile	Glu	20	25	30	35
Gln	Val	Ile	Leu	Arg	Ser	Leu	Leu	Glu	Gly	Ser	Ile	Glu	Gln	Thr	Lys	40	45	50	55
Asn	Ile	Leu	Val	Val	Thr	Phe	Thr	Asn	Ala	Ala	Thr	Asn	Glu	Leu	Lys	60	65	70	75
Leu	Arg	Ile	Gln	Ala	Ser	Leu	Lys	Gln	Ala	Leu	Ser	Leu	Phe	Ser	Gln	80	85	90	95
Ala	Leu	Ser	His	Pro	Gly	Thr	Pro	Leu	Pro	Pro	Tyr	Ile	Ser	Ser	Ser	100	105	110	115
Glu	Thr	Lys	Val	Lys	Gln	Leu	Tyr	Met	Lys	Ile	Arg	Asn	Ser	Leu	Ala	120	125	130	135
Thr	Leu	Asp	Glu	Met	Asn	Ile	Phe	Thr	Ile	His	Gly	Phe	Cys	Arg	Phe	140	145	150	155
Thr	Leu	Glu	Gln	His	Phe	Pro	Trp	Ile	Gln	Pro	Ile	Gln	Pro	Ser	Ser	160	165	170	175
Ile	Phe	Ser	Glu	Pro	Gln	Thr	Ile	Gln	Gln	Tyr	Ile	Leu	Asp	Tyr	Leu	180	185	190	195
Arg	Lys	Asn	Leu	Trp	Asp	Thr	Val	Leu	Ser	Pro	Lys	Gln	Tyr	Ala	Phe	200	205	210	215
Leu	Ser	Tyr	His	His	Arg	Ala	Thr	Thr	Gln	Gln	Thr	Arg	His	Leu	Ile	220	225	230	235
Glu	Arg	Leu	Leu	Gln	Asp	Tyr	Thr	Ser	Thr	Pro	Asn	Leu	Ala	Leu	Ser	240	245	250	255
Pro	Leu	Ser	Ile	Thr	Leu	Gln	Lys	Leu	Lys	Ala	Trp	Val	Ser	Cys	Tyr	260	265	270	275
Gln	His	Leu	Ala	Pro	Leu	Ser	Leu	Glu	Glu	Met	Gln	Ala	Phe	Ser	Leu	280	285	290	295
Arg	Phe	Lys	Gln	Ser	Asp	Leu	Ser	Ile	Glu	Arg	Glu	Leu	Pro	Ala	Phe	300	305	310	315
Val	Gln	Gln	Phe	Glu	Thr	Asn	Pro	Tyr	Ser	Leu	Asp	Met	Leu	Phe	Phe	320	325	330	335
Pro	Gly	Met	Val	Gln	Lys	Phe	Gln	Glu	Glu	Asn	Arg	Asn	Lys	Lys	Lys	340	345	350	355
Leu	Ser	Ala	Pro	Ala	Ser	Pro	Leu	Asp	Pro	Phe	Phe	Gln	Asp	Trp	Ile	360	365	370	375
Gln	Leu	Ala	His	Pro	Phe	Cys	Gln	Lys	Glu	Pro	Ile	Phe	His	Thr	Leu	380	385	390	395
Leu	Lys	Ser	Val	Gln	His	Leu	Lys	Thr	His	Cys	Ala	Gln	Ser	Tyr		400	405	410	415
Ser	His	Asp	Glu	Ser	Ile	Ala	Thr	Leu	Glu	Ser	Leu	Leu	Asp	His	Asn	420	425	430	435
Asp	Thr	Val	Val	Ser	Gln	Leu	Arg	Lys	Gln	Phe	Gln	Leu	Val	Leu	Ile	440	445	450	455

355					360					365					
Asp	Glu	Phe	Gln	Asp	Thr	Asp	Lys	Arg	Gln	Xaa	Gln	Ile	Phe	Ser	Lys
370						375					380				
Leu	Phe	Ala	Ser	Pro	Asp	Tyr	Ser	Gly	Ser	Leu	Phe	Leu	Ile	Gly	Asp
385					390					395					400
Pro	Lys	Gln	Ser	Ile	Tyr	Glu	Trp	Arg	Asn	Ala	Asp	Leu	Pro	Thr	Tyr
				405					410					415	
Leu	Gln	Ala	Lys	His	Ser	Phe	Pro	Lys	Glu	Ala	Xaa	Leu	Ile	Leu	Asp
			420					425					430		
Thr	Asn	Tyr	Arg	Ser	Thr	Pro	Xaa	Leu	Met	Gln	Gly	Leu	Asn	His	Leu
	435					440						445			
Phe	Ser	Leu	Pro	Thr	Pro	Phe	Leu	Glu	Thr	Pro	Gln	Asn	Ile	Leu	Tyr
	450					455					460				
His	Pro	Leu	His	Ser	Lys	Gly	Ser	Ser	Glu	Ile	Ser	Tyr	Ser	Glu	Phe
465					470					475					480
Ser	Pro	Ile	His	Phe	Phe	Ser	Ser	Glu	Asp	Ile	Gln	Glu	Glu	Thr	Leu
				485					490					495	
Trp	Ile	Ser	Lys	Thr	Ala	Ser	Tyr	Leu	Arg	Ser	Ala	Tyr	Ser	Ile	Pro
			500					505					510		
Phe	Gly	Asn	Met	Ala	Val	Leu	Val	Gln	Asp	Tyr	Pro	Gln	Ala	Leu	Lys
	515						520					525			
Leu	Ile	Thr	His	Ser	Thr	Ile	Pro	Met	Ala	Tyr	Cys	Lys	Glu	Lys	Arg
	530					535					540				
Ile	Phe	Asp	Arg	Thr	Glu	Ser	Pro	Tyr	Leu	Leu	Ile	Leu	Leu	Leu	Glu
545					550					555					560
Ala	Leu	Leu	Tyr	Pro	Glu	Asn	Gln	Gln	Lys	Ile	Gln	Ala	Ile	Leu	Met
				565					570					575	
Ser	Arg	Leu	Phe	Gln	Leu	Ser	Ser	Thr	Glu	Ile	His	Gln	His	Leu	Lys
			580					585				590			
Thr	Phe	Ser	Ser	Leu	Phe	Phe	Thr	Leu	Asn	Arg	His	Leu	Tyr	His	Tyr
	595						600					605			
Ser	Leu	Leu	Ala	Thr	Phe	Tyr	Lys	Leu	Met	Gly	Glu	Asn	Val	Leu	Ser
	610					615					620				
Gln	Thr	Ile	Gly	Glu	Thr	Leu	Leu	Gln	Thr	Pro	Leu	Gly	Asp	Ile	Ile
625					630					635					640
Phe	Gln	Glu	Leu	Glu	Ala	Leu	Cys	Leu	Tyr	Leu	Asp	Lys	Thr	Thr	Glu
				645					650					655	
Asn	Pro	His	His	Lys	Leu	Leu	His	Leu	Ile	Asn	Ile	Leu	Ile	Thr	Gly
			660				665					670			
Lys	Tyr	Asp	Glu	Glu	Leu	Ser	Phe	Ser	Ser	Gln	Ser	Asn	Asp	Glu	Asn
		675					680					685			
Met	Ile	Lys	Ile	Thr	Thr	Val	His	Ser	Ser	Lys	Gly	Leu	Glu	Tyr	Asp
	690					695					700				
Val	Val	Phe	Cys	Ser	Cys	Leu	Asn	Lys	Ala	Lys	Glu	Lys	Thr	Pro	Ser
705					710					715					720
Val	His	Met	Arg	Glu	Met	Tyr	Val	Ala	Cys	Thr	Arg	Ala	Lys	Lys	Phe
				725					730					735	
Leu	Phe	Ile	Pro	Phe	Ser	Pro	Ile	Glu	Lys	Arg	Ser	Leu	Ser	Thr	Lys
			740					745				750			
Lys	Leu	Ser	Ala	Leu	Ala	Asn	Tyr	Ala	Asn	Val	Thr	Lys	His	His	Ser
		755					760					765			
Val	Pro	His	Leu	Val	Glu	Thr	Leu	Thr	Ser	Ser	Ser	Pro	Glu	Leu	Phe
	770					775					780				
Ser	Ser	Ser	Phe	Gln	Pro	Glu	Ser	Ser	Leu	Thr	Pro	Asp	Arg	Glu	
785					790					795					800
Arg	Leu	Pro	Gln	Gln	Thr	Tyr	Phe	Ser	Leu	Pro	His	Leu	Pro	Ser	Arg
				805					810					815	
Thr	Ile	His	Ser	Phe	Ser	Ser	Thr	Val	Glu	Asn	Leu	His	Phe	Ser	Glu
			820					825					830		

Pro Ile Gln Glu Leu Ser Pro Ser Leu Leu Phe Pro Gly Gly Ser Leu
 835 840 845
 Thr Gly Thr Leu Ile His Lys Leu Leu Glu Ser Leu Ala Gly Asn Phe
 850 855 860
 Ala Ala Cys Phe Glu Glu Ile Phe Asn Lys Ala Gln Thr Leu Leu Lys
 865 870 875 880
 Asn Thr Pro Leu Glu Gly Tyr Glu Ser Ile Ile Ala Glu Lys Ile Tyr
 885 890 895
 Thr Val Phe Ser Thr Thr Leu Pro Phe Ser Ser Gly Ser Phe Ala Leu
 900 905 910
 Arg Asn Ile His Pro His Asn Ile Arg Val Glu Glu Thr Phe Leu Leu
 915 920 925
 Gln Glu Glu Gly Glu Leu Trp Gln Gly Ile Val Asp Leu Phe Phe Glu
 930 935 940
 His Lys Gly Arg Phe Phe Ile Ile Asp Trp Lys Thr Ser Phe Leu Gly
 945 950 955 960
 Asp Glu Thr Ser Cys Tyr Ser Pro Asp Gln Leu His Leu Tyr Ile Gln
 965 970 975
 Arg Gln Gly Leu Asp Arg Gln Glu Arg Leu Tyr Arg Lys Ala Ala Lys
 980 985 990
 Arg Phe Leu His Gln Phe Asn Ser Ser Leu Gln Val Glu Met Ala Phe
 995 1000 1005
 Val Phe Ile Arg Gly Leu Asp Asp Lys Gly Asn Gly Phe Leu Gln Pro
 1010 1015 1020
 Gly Arg
 1025

(2) INFORMATIONS POUR LA SEQ ID NO: 795:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 785532..786002

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 795:

Thr Pro Ser Asn Tyr Ser Gln Ile Lys Pro Lys Ile Ser Gly Arg Ser
 1 5 10 15
 Leu Gly Leu Lys Ser Ile Gly Gly Asn Thr Lys Lys Ser Thr Val Glu
 20 25 30
 Gln Ser Gly Ala Lys Asp Cys Ala Phe Ile Phe Lys Glu Gln Asp Pro
 35 40 45
 Ser Leu Leu Gly Arg Thr Ser Leu Thr Val Ala Thr Arg Ser Pro Gly
 50 55 60
 Gly Lys Thr Pro Ser Asn Pro Val Val Thr Arg Thr Ser Pro Thr Ser
 65 70 75 80
 Ile Val Phe Pro Ser Thr Lys Pro Lys Ser Leu Pro Leu Ser Ile Glu
 85 90 95
 Ala Ser Gly Phe Gln Ile Gly Ser Pro Arg Pro Gln Thr Ile Pro Arg
 100 105 110
 Arg Ala Lys Ser Phe Cys Ser Asp Arg Asp Lys Glu Ser Ser Arg Ala
 115 120 125
 Cys Lys Arg Cys Lys Ala Ser Cys Leu Ser Leu Ser Ala Lys Ala Asp

(2) INFORMATION POUR LA SEQ ID NO: 796:

(A) LONGUEUR: 289 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(785546..786412)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 796:

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 797:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 377 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(786611..787741)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 797:

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Arg Gly Phe Ile Val Ser Leu Phe Glu Gln Leu Pro Ser Phe Ser Pro
1      5      10      15
Asp Ser Ile Leu Gly Leu Ala Gln Ala Phe Gln Glu Asp Pro Arg Glu
20     25     30
Asp Lys Ile Asn Leu Leu Leu Gly Thr Tyr Glu Arg Glu Lys Lys Arg
35     40     45
Tyr Gly Gly Phe Ser Ser Val Arg Lys Ala Gln Ser Val Phe Phe Asp
50     55     60
Asp Glu Lys Asp Lys Asn Tyr Leu Pro Ile Lys Gly Ser Ser Thr Phe
65     70     75     80
Leu Glu Glu Met Ala Ala Leu Cys Phe Gly Glu Leu Asp Ala Asn Arg
85     90     95
Trp Val Gly Val Gln Ala Ile Gly Gly Thr Gly Ala Leu His Leu Gly
100    105    110
Ala Ser Val Tyr Ala Asn Ala Ser Leu Ala Gly Lys Val Tyr Ile Pro
115    120    125
Ser Gln Thr Trp Gly Asn His Ser Arg Ile Phe Ser His Gln Gly Leu
130    135    140
Ala Leu Glu Tyr Tyr Pro Tyr Tyr Asp Gln Glu Thr Lys Glu Leu Asp
145    150    155    160
Leu Gln Gly Leu Lys Ala Val Leu Arg Ser Ala Pro Glu Thr Ser Leu
165    170    175
Val Leu Leu His Cys Cys Cys His Asn Pro Thr Gly Lys Asp Ile Pro
180    185    190
Leu Ser Glu Trp Pro Glu Ile Ile Thr Ile Ile Lys Glu Arg Asp Leu
195    200    205
Ile Pro Phe Phe Asp Met Ala Tyr Leu Gly Phe Ala Ser Gly Ile Glu
210    215    220
Glu Asp Arg Arg Pro Val Gln Leu Cys Ile Glu Ala Gly Val Thr Thr
225    230    235    240
Phe Val Ala Gly Ser Ala Ser Lys Asn Phe Ser Leu Tyr Gly Ser Arg
245    250    255
Val Gly Phe Phe Gly Ala Ile His Gln Asp Lys Gln Asp Leu Asn Arg
260    265    270
Ile Leu Ser Phe Leu Glu Glu Gln Ile Arg Gly Glu Tyr Ser Ser Pro
275    280    285
Ala Arg Glu Gly Val Ala Ile Val Thr Ser Ile Leu Ser Asn Pro Tyr
290    295    300
Leu Arg Gln Glu Trp Glu Leu Glu Leu Asn Gly Ile Arg Gln Ser Leu
305    310    315    320
Glu Glu Ile Arg Ser Ser Phe Val Ile Ala Met Arg Asn Val Ala Gly
325    330    335
His Ser Phe Asp Phe Ile Ala Ser Gln Lys Gly Phe Phe Gly Tyr Pro
340    345    350
Gly Phe Ser Lys Glu Gln Val Leu Phe Leu Arg Glu Glu Leu Gly Ile

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(2) INFORMATION POUR LA SEQ ID NO: 798:

(A) LONGUEUR: 134 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 787620..788021

[illegible]

(A) LONGUEUR: 735 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(787920..790124)

Cys	Asn	Ile	Ala	Leu	Phe	Cys	Tyr	Ser	Ala	Tyr	Ile	Ser	Gly	Leu	Lys
1				5					10					15	
Arg	Gly	Ala	Ile	Val	Asp	Tyr	Leu	Glu	Asn	Leu	Gln	Ser	Leu	Ile	Glu
			20					25					30		
Asn	His	Pro	Ser	Asp	Phe	Phe	Ser	Leu	Trp	Glu	Glu	Tyr	Cys	Phe	Asn
		35					40					45			

Asp Val Val Lys Gly Asp Glu Leu Val Val Leu Leu Glu Lys Ile Lys
 50 55 60
 Gly Ser Thr Ile Ala Pro Ala Phe Gly Lys Ile Ala Glu Ser Val Ile
 65 70 75 80
 Pro Leu Trp Glu Gln Leu Pro Glu Gly Glu Glu Lys Asp Lys Val Leu
 85 90 95
 Ser Leu Val Phe Asp Val Gln Thr Thr Asn Ser Lys Asn Leu Leu Glu
 100 105 110
 Ile Ala Leu Gln Gln Val Lys Lys Tyr Glu Asp Ser Ala Asn Tyr Lys
 115 120 125
 Glu Ala Leu Arg Ile Val Gly Leu Arg Asp Gly Ile Thr Phe Ser His
 130 135 140
 Cys Leu Gly Arg Phe Ala Leu Leu Met His Leu Ser Glu Gly Asn Phe
 145 150 155 160
 Val Phe His Gln Gly Gly Trp Gly Val Gly Glu Ile Met Gly Val Ser
 165 170 175
 Phe Leu Gln Gln Lys Val Leu Val Glu Phe Glu Gly Val Leu Thr Ala
 180 185 190
 Lys Asp Ile Ser Phe Glu Thr Ala Phe Arg Met Leu Val Pro Leu Arg
 195 200 205
 Lys Asp His Phe Leu Ala Arg Arg Phe Gly Asp Pro Asp Ala Phe Glu
 210 215 220
 Ala Phe Ala Arg Lys Glu Pro Val Ala Ala Ile Glu Cys Leu Leu Lys
 225 230 235 240
 Asp Leu Gly Pro Lys Asn Ala Lys Glu Ile Arg Asn Glu Leu Val Glu
 245 250 255
 Leu Val Ile Pro Glu Glu Asp Trp Ser Arg Trp Trp Gln Ser Ala Lys
 260 265 270
 Ile Lys Met Lys Lys Asp Ala Arg Ile Leu Ala Pro Ala Ser Ser Lys
 275 280 285
 Asp Pro Tyr Val Phe Asp Pro Lys Gly Phe Ser Phe Val Ser Gln Leu
 290 295 300
 Gln Ala Ser Leu Ser Gly Ser Asn Asp Ala Asn Lys Lys Ile Thr Ser
 305 310 315 320
 Cys Tyr Ala Phe Val Arg Asp Leu Gly Ser Glu Leu Lys Asp Glu Ser
 325 330 335
 Asn Arg Gln Ser Val Ile Lys Glu Leu Lys Ala Leu Asp Leu Pro Ala
 340 345 350
 Asp Ser Ala Leu Leu Ile Gln Arg Ala Met Leu Leu Ser Glu Phe Leu
 355 360 365
 Gly Glu Lys Ala Pro Glu Leu Glu Tyr Glu Asn Ile Ala Lys Leu Ser
 370 375 380
 Glu Asp Gln Leu Phe Asp Ile Val Asn Asn Ile Glu Ile Leu Ser Leu
 385 390 395 400
 Gln Lys Ser Phe Leu Ala Leu Ile His Ser Cys Ser Pro Val Trp Val
 405 410 415
 Pro Val Tyr Thr Lys Leu Phe Leu Thr Thr Ser Thr Ser Met Leu Arg
 420 425 430
 Glu Gln Val Phe Lys Val Leu Asn Ala Asp Lys Glu Ala Arg Glu Asn
 435 440 445
 Ile Leu Lys Lys Val Phe Ala Met Ile Glu Gln Pro Leu Leu Tyr Pro
 450 455 460
 Glu Leu Phe Val Trp Leu Phe Ala Arg Val Val Asp Gly Glu Asp Gly
 465 470 475 480
 Leu Phe Ala Glu Ser Asp Lys Lys Glu Ile Glu Arg Gln Met Leu Ala
 485 490 495
 Ser Ala Leu Glu Leu Met His Lys Val Ala Thr Thr Pro Gln Lys Asp
 500 505 510
 Leu Gly Lys Lys Leu Tyr Ser Phe Leu Val Gly Gln Arg Phe Leu Val

(2) INFORMATION POUR LA SEQ ID NO: 800:

(A) LONGUEUR: 150 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 790160..790609

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 800:

Asn	Ile	Glu	Ile	Phe	Val	Met	Lys	Asn	Asn	Ser	Ala	Gln	Lys	Ile	Ile
1				5					10					15	
Asp	Ser	Ile	Lys	Gln	Ile	Leu	Ser	Ile	Tyr	Lys	Ile	Asp	Phe	Asp	Pro
			20					25					30		
Ser	Phe	Gly	Ala	Thr	Leu	Thr	Asp	Asp	Asn	Asp	Leu	Asp	Tyr	Gln	Met
		35					40					45			
Leu	Ile	Glu	Lys	Thr	Gln	Glu	Lys	Ile	Gln	Glu	Leu	Asp	Lys	Arg	Ser
	50					55					60				
Gln	Glu	Ile	Leu	Gln	Gln	Thr	Gly	Met	Thr	Arg	Glu	Gln	Met	Glu	Val
65					70					75					80
Phe	Ala	Asn	Asn	Pro	Asp	Asn	Phe	Ser	Pro	Glu	Glu	Trp	Arg	Ala	Leu
				85					90					95	
Glu	Asn	Ile	Arg	Ser	Ser	Cys	Asn	Glu	Tyr	Lys	Lys	Glu	Thr	Glu	Glu
			100				105						110		
Leu	Ile	Lys	Glu	Val	Thr	Asn	Asp	Ile	Gly	His	Ser	Ser	His	Lys	Ser
		115					120					125			

Pro Thr Pro Lys Lys Thr Lys Ser Ser Ser Gln Lys Lys Ser Lys Lys
 130 135 140
 Lys Asn Trp Ile Pro Leu
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 801:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 461 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 790634..792016

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 801:

Met Lys Ile Val Val Ser Arg Gly Leu Asp Leu Ser Leu Lys Gly Ala
 1 5 10 15
 Pro Lys Glu Ser Gly Phe Cys Gly Lys Val Asp Pro Thr Tyr Val Ser
 20 25 30
 Val Asp Leu Arg Pro Phe Ala Pro Leu Pro Leu Glu Val Lys Val Thr
 35 40 45
 Pro Gly Asp Gln Val Thr Ala Gly Ser Pro Leu Ala Glu Tyr Lys Leu
 50 55 60
 Phe Ser Gly Val Phe Ile Thr Ser Pro Val Asp Gly Glu Val Val Glu
 65 70 75 80
 Ile Arg Arg Gly Asn Lys Arg Ala Leu Leu Glu Ile Val Ile Lys Lys
 85 90 95
 Lys Pro Gly Ile Ser Gln Thr Lys Phe Ser Tyr Asp Leu Gln Ser Leu
 100 105 110
 Thr Gln Lys Asp Leu Leu Glu Val Phe Lys Lys Glu Gly Leu Phe Ala
 115 120 125
 Leu Phe Lys Gln Arg Pro Phe Asp Ile Pro Ala Leu Pro Thr Gln Ser
 130 135 140
 Pro Arg Asp Val Phe Ile Asn Leu Ala Asp Asn Arg Pro Phe Thr Pro
 145 150 155 160
 Ser Val Glu Lys His Leu Ser Leu Phe Ser Ser Lys Glu Asp Gly Tyr
 165 170 175
 Tyr Ile Phe Val Val Gly Val Gln Ala Ile Ala Lys Leu Phe Gly Leu
 180 185 190
 Lys Pro His Ile Ile Ser Thr Asp Arg Leu Thr Leu Pro Thr Gln Asp
 195 200 205
 Leu Val Ser Ile Ala His Leu His Thr Ile Asp Gly Pro Phe Pro Ser
 210 215 220
 Gly Ser Pro Ser Thr His Ile His His Ile Ala Arg Ile Arg Asn Glu
 225 230 235 240
 Arg Asp Val Val Phe Thr Ile Ser Phe Gln Glu Val Leu Ser Ile Gly
 245 250 255
 His Leu Phe Leu Lys Gly Phe Val Leu Gly Gln Gln Ile Val Ala Leu
 260 265 270
 Ala Gly Ser Ala Leu Pro Pro Ser Gln Arg Lys Tyr Leu Ile Thr Ala
 275 280 285
 Lys Gly Ala Ser Phe Ser Asp Leu Leu Pro Lys Asp Ile Phe Ser Ser
 290 295 300
 Asp Glu Ile Thr Leu Ile Ser Gly Asp Pro Leu Thr Gly Arg Leu Cys


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305          310          315          320
Lys Lys Glu Glu Asn Pro Cys Leu Gly Met Arg Asp His Thr Ile Thr
          325          330          335
Leu Leu Pro Asn Pro Lys Thr Arg Glu Ser Phe Ser Phe Leu Arg Leu
          340          345          350
Gly Trp Asn Lys Leu Thr Val Thr Arg Thr Tyr Leu Ser Gly Phe Phe
          355          360          365
Lys Arg Lys Arg Val Phe Met Asp Met Asp Thr Asn Met His Gly Glu
          370          375          380
Lys Arg Pro Ile Ile Asp Ala Glu Ile Tyr Glu Arg Val Ser Ala Ile
385          390          395          400
Pro Val Pro Val Ala Leu Ile Ile Lys Ala Leu Glu Thr Gln Asn Phe
          405          410          415
Glu Glu Ala Cys Arg Leu Gly Leu Leu Glu Val Ala Pro Glu Asp Phe
          420          425          430
Ala Leu Pro Thr Phe Ile Asp Pro Ser Lys Thr Glu Met Phe Ser Ile
          435          440          445
Val Lys Glu Ser Leu Leu Arg Thr Gln Lys Arg Met Trp
          450          455          460

```

(2) INFORMATIONS POUR LA SEQ ID NO: 802:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 342 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(792059..793084)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 802:

```

Val Tyr Asn Phe Met Thr Arg Leu Pro Leu Leu Lys Arg Pro Arg Arg
1          5          10          15
Asn Arg Lys Ser Ala Ala Val Arg Ser Ile Ile Gln Glu Thr Gln Leu
          20          25          30
Cys Ser Ser Asp Leu Ile Trp Pro Ile Phe Leu Lys Asp Gly Ser Gly
          35          40          45
Ile Arg Glu Glu Ile Glu Ser Met Pro Gly Val Tyr Arg Trp Ser Leu
          50          55          60
Asp Met Val Ser Lys Glu Leu Glu Arg Leu Cys Thr Ile Gly Leu Lys
65          70          75          80
Ala Val Ile Leu Phe Pro Val Ile Asp Ala Asn Lys Lys Glu Gln Phe
          85          90          95
Gly Ser Tyr Ala Ser His Pro Tyr Asn Ile Val Cys Lys Gly Ile Gln
          100          105          110
Ala Ile Lys Lys Ser Phe Pro Glu Leu Cys Val Ile Ser Asp Ile Ala
          115          120          125
Leu Asp Pro Phe Thr Thr Ser Gly His Asp Gly Ile Phe His Asn Asn
          130          135          140
Tyr Val Ile Asn Asp Glu Ser Val Arg Val Tyr Gly Gly Ile Ala Val
145          150          155          160
Met His Ala Glu Met Gly Ala Asp Ile Val Ala Pro Ser Asp Met Met
          165          170          175
Asp Gly Arg Val Lys His Ile Arg Glu Gln Met Asp Gln Met Gly Phe
          180          185          190

```

Val Asn Thr Gly Ile Leu Ser Tyr Ser Ala Lys Tyr Ala Ser Ala Leu
 195 200 205
 Tyr Gly Pro Phe Arg Asp Ala Leu Ser Ser His Leu Gln Ser Gly Asp
 210 215 220
 Lys Arg Thr Tyr Gln Met Asp Pro Ala Asn Val Gln Glu Ala Leu Leu
 225 230 235 240
 Glu Cys Gln Leu Asp Glu Glu Glu Gly Ala Asp Met Val Met Ile Lys
 245 250 255
 Pro Ala Gly Phe Tyr Leu Asp Val Ile Val Lys Ala Arg Glu Asn Thr
 260 265 270
 His Leu Pro Val Val Ala Tyr Gln Val Ser Gly Glu Phe Ser Met Ile
 275 280 285
 Met Ala Ala Cys Leu His Gly Trp Leu Asn Lys Glu Ser Val Ile Lys
 290 295 300
 Glu Ser Leu Leu Ala Ile Lys Arg Ala Gly Ala Thr Ala Ile Ile Ser
 305 310 315 320
 Tyr Ala Thr Pro Trp Val Leu Glu Trp Leu Ala Lys Asp Ala Leu Pro
 325 330 335
 Phe Glu Arg Ser Val Leu
 340

(2) INFORMATIONS POUR LA SEQ ID NO: 803:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 238 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 793343..794056

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 803:

Ala Asn Leu Leu Tyr Arg Ser Phe Leu Met Leu Ser Lys Glu Gly Gly
 1 5 10 15
 Phe Ser Glu Glu Gln Arg Ala Arg Leu Ser His Phe Val Thr Asn Leu
 20 25 30
 Asp Ser Pro Ile Phe Ala Leu Lys Asn Leu Pro Glu Val Val Lys Gly
 35 40 45
 Ala Leu Phe Ser Lys Tyr Ser Arg Ser Thr Leu Gly Leu Arg Thr Leu
 50 55 60
 Leu Leu Lys Glu Phe Leu Asp Gly Glu Gly Gly Asn Phe Leu Asp Asp
 65 70 75 80
 Asp Gln Gln Asp Cys Glu Leu Gly Ile Gln Lys Ala Val Asp Phe Tyr
 85 90 95
 Arg Arg Val Leu Asp Asn Phe Gly Asp Asp Ser Val Gly Glu Leu Gly
 100 105 110
 Gly Ala His Leu Ala Leu Glu Gln Val Ser Met Leu Ala Lys Ile
 115 120 125
 Leu Glu Asp Ala Arg Ile Gly Gly Ser Pro Leu Glu Lys Ser Ser Arg
 130 135 140
 Tyr Val Tyr Phe Asp Gln Lys Val Asn Gly Glu Tyr Leu Tyr Tyr Arg
 145 150 155 160
 Asp Pro Ile Leu Met Thr Ser Ala Phe Lys Asp Val Phe Leu Asp Thr
 165 170 175
 Cys Asp Phe Leu Phe Asn Thr Tyr Ser Asp Leu Ile Pro Gln Val Arg

(2) INFORMATION POUR LA SEQ ID NO: 804:

(A) LONGUEUR: 304 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 794046..794957

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 804:

Gly 1	Phe	Phe	Gly	Asn 5	Gly	Arg	Phe	Trp	Gln 10	Asn	Leu	Leu	His	Arg 15	Leu
Gln	Asp	Asn	Ser 20	Leu	Val	Glu	Val	Arg 25	Asn	Ile	Gly	Glu	Gln 30	Ser	Leu
Thr	Glu	Leu	Met 35	Lys	Ile	Ile	Pro 40	Ser	Phe	Val	Ser	Arg 45	Ala	Glu	Ser
His	His 50	Tyr	His	His	Gln	Ala 55	Met	Val	Asp	Tyr	Arg 60	Arg	Ala	Leu	Lys
Glu 65	Gln	Leu	Lys	Ser	Phe 70	Ala	His	Arg	Tyr	Gly 75	Glu	Glu	Arg	Glu	Ile 80
Ser	Lys	Glu	Ala	Gly 85	Val	Lys	Leu	Val	Tyr 90	Gly	Asp	Pro	Asp 95	Gly	Leu
Tyr	Lys	Ile	Ala 100	Ala	Ala	Tyr	Met	Phe 105	Pro	Tyr	Ser	Glu	His 110	Thr	Tyr
Ala	Glu	Leu	Leu 115	Asp	Ile	Cys	Arg	Asn 120	Ile	Pro	Asn	Glu 125	Asp	Leu	Met
Arg	Ile 130	Leu	Glu	Ser	Gly	Ala 135	Ser	Phe	Arg	Glu	Asn 140	Arg	Arg	His	Lys
Ser 145	Pro	Arg	Gly	Leu	Glu 150	Cys	Ala	Glu	Phe	Ala 155	Phe	Asp	Ile	Thr	Ala 160
Asp	Phe	Gly	Ala	Tyr	Arg 165	Asp	Leu	Gln	Arg	His 170	Arg	Ile	Leu	Thr 175	Gln
Glu	Arg	Gln	Leu 180	Leu	Thr	Lys	Lys	Leu 185	Gly	Tyr	Thr	Met	Pro 190	Ser	Gln
Leu	Ile	Asp 195	Thr	Pro	Met	Glu	Ala 200	Pro	Phe	Arg	Gly	Ala 205	Met	Glu	Lys
Ala	Asp 210	Gln	Ala	Tyr	Arg	Leu 215	Ile	Ala	Glu	Glu	Phe 220	Pro	Glu	Glu	Ala
Gln 225	Tyr	Val	Val	Pro	Leu 230	Ala	Tyr	Asn	Ile	Arg 235	Trp	Leu	Phe	His	Ile 240
Asn	Ala	Arg	Gly	Leu 245	Gln	Trp	Leu	Cys	Glu 250	Leu	Arg	Ser	Gln	Pro 255	Gln
Gly	His	Glu	Ser 260	Tyr	Arg	Lys	Ile	Ala 265	Ile	Asp	Met	Ala	Arg 270	Glu	Val
Ile	Gln	Phe 275	His	Pro	Ala	Tyr	Glu 280	Leu	Phe	Leu	Lys	Phe 285	Val	Asp	Tyr

Ser Glu Thr Asp Leu Gly Arg Leu Gln Gln Glu Ser Arg Lys Lys Ser
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 805:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 86 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(795144..795401)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 805:

Glu Lys Met Lys Thr Leu Ile Asp Asn Asn Ile Val Arg Phe Lys Asn
 1 5 10 15
 Ile Ser Lys Thr Lys Gln Gly Ile Phe Val Asn Phe Gln Val Lys Gly
 20 25 30
 Glu Arg Gly Gly Ala Ser Phe Thr Ala Ser Ile Ala Val Asp Ile Asp
 35 40 45
 Ala Ala Asp Val Ser Ala Gly Asp Ser Leu Glu Thr Ile Ile Glu Arg
 50 55 60
 Cys Ala Leu Ile Gly Ile Arg Glu Phe Gln Lys Cys Glu Phe Gln Phe
 65 70 75 80
 Asp Gly Ile Ile Cys Leu
 85

(2) INFORMATIONS POUR LA SEQ ID NO: 806:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 227 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 795575..796255

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 806:

Met Ala Gly Pro Lys His Val Leu Leu Val Ser Glu His Trp Asp Leu
 1 5 10 15
 Phe Phe Gln Thr Lys Glu Leu Leu Asn Pro Glu Glu Tyr Arg Cys Thr
 20 25 30
 Ile Gly Gln Gln Tyr Lys Gln Glu Leu Ser Ala Asp Leu Val Val Cys
 35 40 45
 Glu Tyr Ser Leu Leu Pro Arg Glu Ile Arg Ser Pro Lys Ser Leu Glu
 50 55 60
 Gly Ser Phe Val Leu Val Leu Leu Asp Phe Phe Asp Glu Glu Thr Ser
 65 70 75 80
 Val Asp Leu Leu Asp Arg Gly Phe Trp Tyr Leu Ile Arg Pro Ile Thr
 85 90 95
 Pro Arg Ile Leu Lys Ser Ala Ile Ser Leu Phe Leu Ser Gln His Ser

			100					105					110				
Leu	His	Ser	Val	Pro	Glu	Ser	Ile	Arg	Phe	Gly	Pro	Asn	Val	Phe	Tyr		
		115					120					125					
Val	Leu	Lys	Leu	Thr	Val	Glu	Thr	Pro	Glu	Gly	Ser	Val	His	Leu	Thr		
		130					135					140					
Pro	Ser	Glu	Ser	Gly	Ile	Leu	Lys	Arg	Leu	Leu	Ile	Asn	Lys	Gly	Gln		
145					150					155					160		
Leu	Cys	Leu	Arg	Lys	His	Leu	Leu	Glu	Glu	Ile	Lys	Asn	His	Ala	Lys		
				165					170						175		
Ala	Ile	Val	Ala	Arg	Asn	Val	Asp	Val	His	Ile	Ala	Ser	Leu	Arg	Lys		
			180					185					190				
Lys	Leu	Gly	Ala	Tyr	Gly	Ser	Arg	Ile	Val	Thr	Leu	Arg	Gly	Val	Gly		
		195					200					205					
Tyr	Leu	Phe	Ser	Asp	Asp	Gly	Asp	Lys	Lys	Phe	Ser	Gln	Gln	Asp	Thr		
	210					215					220						
Lys	Leu	Ser															
225																	

(2) INFORMATIONS POUR LA SEQ ID NO: 807:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 246 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 796278..797015

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 807:

Ile	Pro	Ser	Tyr	Ala	Cys	Ile	Arg	Ser	Leu	Val	Met	Val	Leu	Ser	Ala		
1				5					10					15			
Ser	Leu	Phe	Ser	Pro	Glu	Glu	Phe	Leu	Tyr	Pro	Glu	Ile	Val	Ser	Gln		
			20					25					30				
Ala	Glu	Phe	Val	Trp	Ser	Ile	Leu	Thr	Leu	Leu	Glu	Glu	Lys	Leu	Ala		
		35				40					45						
Ser	His	Thr	Phe	Ser	Gly	Ile	His	Gly	His	Leu	Glu	Glu	Gly	Val	Tyr		
	50				55					60							
Leu	Lys	Asn	Lys	Glu	Thr	Ile	Glu	Ile	Gln	Glu	Gly	Ala	Tyr	Val	Glu		
65				70					75					80			
Ser	Gly	Ala	Tyr	Ile	Cys	Gly	Pro	Cys	Ile	Ile	Gly	Pro	Tyr	Thr	Gln		
			85					90					95				
Val	Arg	His	Gly	Ala	Tyr	Ile	Arg	Gly	Gly	Val	Ile	Thr	Ser	Ser	His		
		100						105					110				
Cys	Val	Ile	Gly	His	Cys	Ser	Glu	Ile	Lys	Asn	Ser	Tyr	Leu	Gly	His		
		115					120					125					
His	Ala	Lys	Ala	Ala	His	Phe	Ala	Tyr	Val	Gly	Asp	Ser	Val	Phe	Gly		
	130				135						140						
Ser	Arg	Val	Asn	Leu	Gly	Ala	Gly	Val	Arg	Cys	Ala	Asn	Phe	Arg	Leu		
145				150						155					160		
Asp	Gly	Lys	Thr	Ile	Phe	Phe	His	His	Ser	Gly	Glu	Arg	Tyr	Asp	Thr		
			165						170					175			
Lys	Arg	Lys	Lys	Leu	Gly	Ala	Phe	Leu	Gly	Arg	Gly	Val	Ser	Val	Gly		
		180						185					190				
Cys	Asn	Thr	Val	Leu	Asn	Pro	Gly	Cys	Tyr	Val	Ala	Ser	Ala	Thr	Lys		
	195						200					205					

Ile Leu Pro Lys Ser Asn His Leu Leu Arg Asn Asn Leu Cys Gln Thr
 210 215 220
 Lys Val Asp Glu Lys Lys Lys Ala Val Ala Trp Ile Trp Ile Ile Ser
 225 230 235 240
 Ala Phe Ile Asp Arg Lys
 245

(2) INFORMATIONS POUR LA SEQ ID NO: 808:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 127 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 796985..797365

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 808:

Met Asp Tyr Phe Ser Val Tyr Arg Ser Lys Val Glu Lys Lys Leu Arg
 1 5 10 15
 Asp Ser Leu Gly Asp Phe Gly Asn Thr Gln Gly Gly Leu Arg Asp Pro
 20 25 30
 Ile Glu Tyr Ala Leu Leu Gly Gly Gly Lys Arg Val Arg Pro Leu Leu
 35 40 45
 Val Gly Leu Phe Ala Glu Gly Ile His Lys Glu Arg Asp Val Leu Asp
 50 55 60
 Thr Ala Ile Ala Ile Glu Tyr Ile His Thr Ser Thr Leu Ile Ala Asp
 65 70 75 80
 Asp Leu Pro Cys Met Asp Asp Asp Asp Met Arg Arg Gly Lys Leu Arg
 85 90 95
 Phe Thr Lys Leu Leu Met Lys Leu Arg Leu Ser Trp Leu Arg Met Leu
 100 105 110
 Leu Phe Gln Leu Leu Met His Glu Phe Val Arg Met Gln Lys Arg
 115 120 125

(2) INFORMATIONS POUR LA SEQ ID NO: 809:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 199 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 797260..797856

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 809:

Arg Gln Ala Ser Val His Lys Ala Phe Asp Glu Ala Ser Ala Leu Leu
 1 5 10 15
 Ala Ser Tyr Ala Leu Ile Pro Ala Ala Tyr Ala Arg Ile Arg Lys Asn
 20 25 30
 Ala Lys Ala Leu Lys Ala Val Val Ser Cys Glu Gln Asp Val Glu Glu

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(797935..798426)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 811:

Pro	Lys	Ser	Ile	Asp	Pro	Ala	Lys	Thr	Pro	Val	Met	Met	Tyr	Cys	Thr
1				5					10					15	
Gly	Gly	Ile	Arg	Cys	Glu	Leu	Tyr	Ser	Ala	Leu	Leu	Leu	Glu	Lys	Gly
			20					25					30		
Phe	Lys	Glu	Val	Tyr	Gln	Leu	Asp	Gly	Gly	Val	Ile	Ala	Tyr	Gly	Leu
		35					40					45			
Lys	Met	Gly	Thr	Gly	Lys	Trp	Arg	Gly	Lys	Leu	Phe	Val	Phe	Asp	Asp
	50					55					60				
Arg	Met	Ala	Met	Pro	Ile	Asp	Glu	Ala	Asp	Pro	Asn	Val	Ser	Pro	Ile
65					70					75					80
Ala	Arg	Cys	Ser	Leu	Cys	Asn	Thr	Asp	Ser	Asp	Thr	Tyr	Tyr	Asn	Cys
				85					90					95	
Ala	Asn	Thr	Asp	Cys	Asn	Asn	Leu	Phe	Ile	Cys	Cys	Glu	Ser	Cys	Ile
			100					105					110		
Ala	Thr	His	Lys	Gly	Cys	Cys	Ser	Glu	Glu	Cys	Ser	Gln	Ala	Pro	Arg
		115					120					125			
Ile	Arg	Ala	Phe	Ser	Ala	Glu	Arg	Gly	Asn	Lys	Pro	Phe	Arg	Arg	Lys
	130					135					140				
His	Leu	Cys	Pro	Thr	Ile	Glu	Gln	Ser	Cys	Cys	Leu	Lys	Glu	Gln	Glu
145					150					155					160
Asn	Gln	Pro	Ala												

(2) INFORMATIONS POUR LA SEQ ID NO: 812:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(798416..798925)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 812:

Asp	Val	Phe	Met	Glu	Lys	Asn	Tyr	Tyr	Ala	Leu	Ala	Tyr	Tyr	Tyr	Phe
1				5					10					15	
Gly	Pro	Val	Ser	Asn	Pro	Tyr	Glu	Glu	Ile	Ala	Leu	His	Lys	Gln	Leu
			20					25					30		
Phe	Lys	Thr	Met	Asp	Val	Ser	Cys	Arg	Ile	Tyr	Ile	Ser	Glu	Glu	Gly
		35					40					45			
Ile	Asn	Gly	Gln	Phe	Ser	Gly	Tyr	Gln	Pro	Asp	Ala	Glu	Arg	Tyr	Met
	50					55					60				
Ala	Trp	Leu	Lys	Gln	Arg	Pro	Asp	Phe	Ala	Ser	Ile	Lys	Phe	Lys	Ile
65					70				75						80
His	His	Ile	Glu	Glu	Asn	Ile	Phe	Pro	Arg	Val	Thr	Val	Lys	Tyr	Arg
				85					90				95		
Lys	Glu	Leu	Val	Ala	Leu	Gly	Cys	Ser	Val	Asp	Thr	Thr	Lys	Gln	Gly

(2) INFORMATION POUR LA SEQ ID NO: 813:

(A) LONGUEUR: 209 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 799301..799927

[illegible]

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(800029..800862)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 814:

```

Leu Leu Gly Ala His Thr Ser Ala Ala Gly Gly Leu His Asn Ala Leu
1      5      10      15
Tyr Glu Gly Arg Asp Ile Gly Ala Thr Thr Val Gln Leu Phe Thr Ala
20      25      30
Asn Gln Arg Gln Trp Lys Arg Arg Ala Leu Thr Gln Glu Met Val Asp
35      40      45
Gln Phe Arg Ile Ala Leu Asn Glu Thr Ser Leu Ser Tyr Ile Met Ser
50      55      60
His Ala Gly Tyr Leu Asn Asn Pro Gly Ala Pro Asn Pro Glu Ile Leu
65      70      75      80
Glu Lys Thr Arg Val Cys Met His Gln Glu Ile Ala Asp Cys Ile Ser
85      90      95
Leu Gly Ile Ser Phe Val Asn Phe His Pro Gly Ala Ala Leu Ser Asp
100     105     110
Ser Lys Glu Ser Cys Leu Asp Arg Ala Ile Thr Ser Phe Ser Gln Met
115     120     125
Ala Pro Leu Phe Glu Asn His Pro Pro Leu Val Val Leu Leu Glu Thr
130     135     140
Thr Ala Gly Gln Gly Ser Leu Ile Gly Ser Ser Phe Glu Glu Leu Ala
145     150     155     160
Tyr Leu Ile Gln Gly Ile Lys Ala Leu Ile Pro Ile Gly Val Cys Leu
165     170     175
Asp Thr Cys His Ile Phe Ala Ala Gly Tyr Asp Ile Ser Ser Val Ala
180     185     190
Gly Trp Glu Gln Val Leu Lys His Phe Asp Ala Val Ile Gly Leu Ser
195     200     205
Phe Leu Arg Ala Ile His Leu Asn Asp Ser Val Phe Ala Leu Gly Lys
210     215     220
Asn Lys Asp Arg His Ala Pro Ile Gly Glu Gly Cys Ile Gly Ser Asp
225     230     235     240
Ser Phe Cys Phe Leu Met Gln Asp Glu Arg Thr Arg Met Leu Pro Lys
245     250     255
Tyr Leu Glu Thr Pro Gly Gly Pro Asp Leu Trp Thr Lys Glu Ile Arg
260     265     270
Tyr Leu Gln Lys Val Cys
275

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(2) INFORMATIONS POUR LA SEQ ID NO: 815:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 355 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 801065..802129

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 815:

```

Met Arg Lys Asp Asp Glu Gly Ser Leu Val Arg Ser Leu Phe Asn Leu
1      5      10      15
Leu Ser Gly Thr Phe Phe Ser Arg Leu Thr Gly Met Leu Arg Glu Ile
20      25      30
Val Met Ala Thr Tyr Phe Gly Ala Asp Pro Leu Val Ala Ser Phe Trp
35      40      45
Leu Ala Phe Arg Thr Ile Phe Phe Leu Arg Lys Leu Leu Gly Gly Pro
50      55      60
Ile Leu Gly Leu Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala Gln
65      70      75      80
Asn Ile Ser Arg Ala Thr Phe Phe Phe Lys Ser Phe Ser Arg Phe Phe
85      90      95
Cys Tyr Ser Ala Ile Leu Phe Thr Leu Ile Ile Glu Leu Gly Leu Cys
100     105     110
Val Trp Cys Ser Cys Val Thr Gly Ser Leu Phe Asp Thr Leu Phe Leu
115     120     125
Thr Ile Ile Leu Leu Pro Ser Gly Ile Phe Leu Met Met Tyr Thr Val
130     135     140
Asn Ser Thr Leu Leu His Cys Glu Lys Lys Phe Phe Ser Val Gly Leu
145     150     155     160
Ala Pro Ser Val Val Asn Val Leu Trp Ile Gly Thr Val Phe Leu Ala
165     170     175
Arg Asn Tyr Asp Pro Arg Asn Arg Ile Phe Gly Leu Ala Val Val Leu
180     185     190
Val Val Gly Phe Ile Leu Glu Trp Ala Ile Thr Leu Pro Gly Val Met
195     200     205
Lys Phe Leu Gly Gln Ser Lys Glu Val Pro Gln Glu Arg Asp Ser Ile
210     215     220
Arg Ala Leu Ile Ala Pro Leu Ser Leu Gly Leu Leu Ser Met Gly Ile
225     230     235     240
Phe Gln Leu Asn Leu Leu Cys Asp Met Trp Leu Ala Arg Tyr Ile Asn
245     250     255
Glu Val Gly Pro Leu Tyr Leu Met Tyr Ser Val Arg Ile Gln Gln Leu
260     265     270
Pro Val His Leu Phe Gly Leu Gly Val Phe Thr Val Leu Leu Pro Ala
275     280     285
Ile Ser Arg Cys Val Gln Asp Gln Glu His Gln Gln Gly Tyr Asp Leu
290     295     300
Leu Arg Phe Ser Leu Lys Leu Thr Val Ala Val Met Val Val Ile Thr
305     310     315     320
Met Gly Leu Leu Leu Phe Ala Leu Pro Gly Val Arg Val Leu Tyr Glu
325     330     335
His Gly Val Phe Pro Tyr Asn Ser Cys Ala Arg Tyr Cys Arg Ser Ser
340     345     350
Lys Arg Val
355

```

(2) INFORMATIONS POUR LA SEQ ID NO: 816:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 217 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 802023..802673

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 816:

```

Arg Trp Gly Tyr Cys Phe Leu Leu Cys Leu Gly Tyr Glu Cys Tyr Met
1      5      10      15
Ser Thr Glu Cys Phe Leu Thr Thr Ala Val His Ala Ile Val Glu Val
20      25      30
Leu Arg Gly Tyr Ser Gly Ser Ile Ile Pro Met Ala Leu Ala Pro Leu
35      40      45
Val Ser Ala Leu Phe Tyr Ala Arg Arg Asn Tyr Lys Val Pro Met Leu
50      55      60
Val Gly Ile Ile Ala Ala Val Val Asn Met Val Leu Asn Val Ile Gly
65      70      75      80
Cys Leu Val Cys Lys Gln Val Ala Val Leu Ala Tyr Ala Thr Ser Leu
85      90      95
Ala Ser Trp Gly Gln Leu Ala Met Leu Trp Tyr Cys Ala Gly Lys Ser
100     105     110
Leu Pro Thr Tyr Lys Gly Leu Met Trp Arg Thr Phe Lys Glu Ser Gly
115     120     125
Lys Thr Val Ile Thr Thr Ile Leu Ala Ala Val Ile Thr Ile Gly Val
130     135     140
Asn Ile Val Thr His Thr Thr Tyr Val Val Phe Ile Glu Pro Leu Thr
145     150     155     160
Val Pro Thr Lys Pro Leu Val Ser Phe Leu Asp Gln Cys Gly Val Phe
165     170     175
Phe Ala Glu Ser Ala Leu Phe Leu Ser Val Leu Phe Gly Leu Ala Lys
180     185     190
Leu Leu Lys Thr Glu Asp Leu Val Asn Leu Thr Ser Phe Gln Tyr Trp
195     200     205
Lys Gly His Gln Ser Ile Leu Arg Asn
210     215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 817:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 109 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 802920..803246

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 817:

```

Met Lys Lys Tyr Phe Tyr Lys Gly Phe Val Gly Ala Leu Leu Leu Ala
1      5      10      15
Cys Gly Ser Thr Asn Leu Ala Phe Ala Gln Ala Ser Ser Met Asp Ser
20      25      30
Gln Leu Trp Ser Val Glu Asp Leu Asp Ser Tyr Leu Ser Ser Lys Gly
35      40      45
Phe Val Glu Thr Arg Lys Arg Arg Trp Ser Phe Thr Phe Ser Trp Arg
50      55      60
Cys Pro Arg Ser Met Asp Leu Cys Lys Arg Gly Ile Leu Arg Gln Leu

```

```

65              70              75              80
Arg Leu Leu Leu Asn Leu Phe Tyr Leu Ser Ile Val Ile Val Val Asn
      85              90              95
Ser Ile Cys Met Trp Ile Thr Pro Leu Leu Ile Val Gly
      100              105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 818:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 372 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 803105..804220

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 818:

```

Leu Glu Met Ser Ala Leu Asp Gly Phe Met Gln Lys Arg His Leu Glu
1              5              10              15
Thr Thr Gln Thr Pro Thr Lys Pro Ile Leu Pro Ile Asn Arg Tyr Arg
      20              25              30
Ser Glu Phe Asn Leu Tyr Val Asp Tyr Thr Ala Ala Asn Ser Trp Met
      35              40              45
Thr Ser Lys Met Asn Trp Val Thr Ile Ala Gly Gly Glu Ser Ser Ala
      50              55              60
Ala Gly Leu Asp Ile Asn Arg Ala Phe Leu Gly Tyr Arg Phe Tyr Lys
      65              70              75              80
Asn Pro Glu Thr Gln Ala Glu Val Phe Ala Glu Ile Gly Arg Ser Gly
      85              90              95
Leu Gly Asp Ile Phe Asp Ser Asp Val Gln Phe Asn Ser Asn Phe Asp
      100              105              110
Gly Ile His Leu Tyr Ala Ala Arg Arg Ile Ser Glu Lys Leu Pro Phe
      115              120              125
Thr Met Ile Val His Gly Gly Pro Phe Val Val Asn Met Ala Glu Lys
      130              135              140
Glu Tyr Ala Trp Val Val Glu Ala Ile Leu Asn Lys Leu Pro Gly Asn
      145              150              155              160
Phe Val Val Lys Thr Ser Val Ile Asp Trp Asn Thr Leu Thr Ala Lys
      165              170              175
Thr Asn Asp Pro Ala Asp Ala Ser Thr Ala Gln Pro Ala Lys Pro Asn
      180              185              190
Thr Lys Tyr Asp Tyr Leu Val Trp Gln Trp Leu Val Gly Lys Ser Thr
      195              200              205
Ala Met Pro Trp Phe Asn Gly Gln Thr Lys Asn Leu Tyr Thr Tyr Gly
      210              215              220
Ala Tyr Leu Phe Asn Pro Leu Ala Glu Ile Pro Glu Asn Trp Lys Gln
      225              230              235              240
Ser Thr Thr Thr Pro Ala Thr Lys Ile Thr Asn Gly Lys Glu Asn His
      245              250              255
Ala Trp Phe Ile Gly Cys Ser Leu Gly Gly Val Arg Arg Ala Gly Asp
      260              265              270
Trp Ser Ala Thr Val Arg Tyr Glu Tyr Val Glu Ala Leu Ala Ile Pro
      275              280              285
Glu Ile Asp Val Ala Gly Ile Gly Arg Gly Asn Gln Met Lys Tyr Gly
      290              295              300

```

```

Phe Ala Gln Ala Ile Lys Gln Gly Leu Asp Pro Lys Glu Ser Asn Gly
305              310              315              320
Phe Thr Asn Tyr Lys Xaa Val Ser Tyr Gln Phe Val Met Gly Leu Thr
              325              330              335
Asp Ser Val Ser Phe Arg Ala Tyr Ala Ala Tyr Ser Lys Pro Ala Asn
              340              345              350
Asp Asn Leu Gly Ser Asp Phe Thr Tyr Arg Lys Tyr Asp Leu Gly Leu
              355              360              365
Ile Ser Ser Phe
              370

```

(2) INFORMATIONS POUR LA SEQ ID NO: 819:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 350 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 804307..805356

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 819:

```

Gly Phe Phe Ile Phe Leu Tyr Cys Met Glu Ser Gly Pro Glu Ser Val
1              5              10              15
Ser Ser Asn Gln Ser Ser Met Asn Pro Ile Ile Asn Gly Gln Ile Ala
              20              25              30
Ser Asn Ser Glu Thr Lys Glu Ser Thr Lys Ala Ser Glu Ala Ser Ser
              35              40              45
Ser Ala Ser Ser Ser Val Ser Ser Trp Ser Phe Leu Ser Ser Ala Lys
              50              55              60
Asn Ala Leu Ile Ser Leu Arg Asp Ala Ile Leu Asn Lys Asn Ser Ser
65              70              75              80
Pro Thr Asp Ser Leu Ser Gln Leu Glu Ala Ser Thr Ser Thr Ser Thr
              85              90              95
Val Thr Arg Val Ala Ala Lys Asp Tyr Asp Lys Ala Lys Ser Asn Phe
              100              105              110
Asp Thr Ala Lys Ser Gly Leu Glu Asn Ala Lys Thr Leu Ala Glu Tyr
              115              120              125
Glu Thr Lys Met Ala Asp Leu Met Ala Ala Leu Gln Asp Met Glu Ala
              130              135              140
Asn Ser Asp Pro Ser Asn Asp His Thr Glu Glu Leu Asn Asn Ile Lys
145              150              155              160
Lys Ala Leu Glu Ala Gln Lys Asp Thr Ile Asp Lys Leu Asn Lys Leu
              165              170              175
Val Thr Leu Gln Asn Gln Asn Lys Ser Leu Thr Glu Ala Leu Lys Thr
              180              185              190
Thr Asp Ser Ala Asp Gln Ile Pro Ala Ile Asn Ser Arg Leu Glu Ile
              195              200              205
Asn Lys Asn Ser Ala His Gln Ile Ile Lys Glu Leu Lys Glu Gln Ile
              210              215              220
Ser Asn Tyr Lys Ala Val Leu Thr Asp Val Glu Lys Val Ile Lys Glu
225              230              235              240
Phe Ser Glu Ala Gly Ile Lys Leu Gly Gln Ala Leu Gln Ser Ile Val
              245              250              255
Asp Ala Gly Asp Gln Ser Gln Ala Ala Val Leu Gln Ala Arg Gln Ser

```

(2) INFORMATION POUR LA SEQ ID NO: 820:

(A) LONGUEUR: 331 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 805290..806282

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 820:

Trp	Phe	Gly	Tyr	Ser	Tyr	Arg	Trp	Ser	Glu	Trp	Val	Arg	Xaa	Ser	Ala
1				5					10					15	
Gly	Ser	Ala	Ala	Gly	Ala	Leu	Lys	Ser	Ser	Asn	Asn	Ser	Gly	Arg	Ile
		20						25					30		
Ser	Leu	Leu	Leu	Asp	Asp	Val	Asp	Asn	Glu	Met	Ala	Ala	Ile	Ala	Met
	35						40					45			
Gln	Gly	Phe	Arg	Ser	Met	Ile	Glu	Gln	Phe	Asn	Val	Asn	Asn	Pro	Ala
	50					55					60				
Thr	Ala	Lys	Glu	Leu	Gln	Ala	Met	Glu	Ala	Gln	Leu	Thr	Ala	Met	Ser
65					70					75				80	
Asp	Gln	Leu	Val	Gly	Ala	Asp	Gly	Glu	Leu	Pro	Ala	Glu	Ile	Gln	Ala
			85						90				95		
Ile	Lys	Asp	Ala	Leu	Ala	Gln	Ala	Leu	Lys	Gln	Pro	Ser	Ala	Asp	Gly
		100						105					110		
Leu	Ala	Thr	Ala	Met	Gly	Gln	Val	Ala	Phe	Ala	Ala	Ala	Lys	Val	Gly
	115					120						125			
Gly	Gly	Ser	Ala	Gly	Thr	Ala	Gly	Thr	Val	Gln	Met	Asn	Val	Lys	Gln
	130					135					140				
Leu	Tyr	Lys	Thr	Ala	Phe	Ser	Ser	Thr	Ser	Ser	Ser	Ser	Tyr	Ala	Ala
145					150					155				160	
Ala	Leu	Ser	Asp	Gly	Tyr	Ser	Ala	Tyr	Lys	Thr	Leu	Asn	Ser	Leu	Tyr
			165						170					175	
Ser	Glu	Ser	Arg	Ser	Gly	Val	Gln	Ser	Ala	Ile	Ser	Gln	Thr	Ala	Asn
			180					185					190		
Pro	Ala	Leu	Ser	Arg	Ser	Val	Ser	Arg	Ser	Gly	Ile	Glu	Ser	Gln	Gly
		195					200					205			
Arg	Ser	Ala	Asp	Ala	Ser	Gln	Arg	Ala	Ala	Glu	Thr	Ile	Val	Arg	Asp
	210					215					220				
Ser	Gln	Thr	Leu	Gly	Asp	Val	Tyr	Ser	Arg	Leu	Gln	Val	Leu	Asp	Ser
225					230					235				240	
Leu	Met	Ser	Thr	Ile	Val	Ser	Asn	Pro	Gln	Ala	Asn	Gln	Glu	Glu	Ile
				245					250					255	

```

Met Gln Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr
      260                265                270
Pro Ala Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln
      275                280                285
Leu Glu Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln
      290                295                300
Glu Asn Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val
305                310                315                320
Asn Ile Ala Ser Leu Phe Ser Gly Tyr Leu Ser
      325                330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 821:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 543 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 806453..808081

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 821:

```

Lys Lys Tyr Tyr Trp Asp Arg Phe Ala Thr Ser Thr Thr Val Glu Leu
1      5      10
Arg Glu Leu Ala Met Asn Arg Ile His Arg Thr Gln Gly Ser Leu Thr
      20      25      30
Asp Tyr Asn Ser Thr Leu Glu Ala Ile Ala Lys Lys Ile Ala Lys Pro
      35      40      45
Asp Ser Ala Thr Ile Val Ser Gln Val Ala Gln Tyr Glu Gln Phe Lys
      50      55      60
Met Glu Gln Glu Ala Leu Lys Ala Leu Leu Val Ser Phe Asp Gln Lys
      65      70      75      80
Ala Asp Gln Arg Tyr Arg Asn Leu Ile Gln Arg Leu Glu Gln Leu Asp
      85      90      95
Val Asp Arg Gln Thr Gly Arg Ser Ile Glu Ser Pro His Ile Gln Glu
      100     105     110
Lys Pro Met Ala Ser Leu Gln Ser Glu Asn Gln Val Val Ala Gln Ala
      115     120     125
Val Val Gln Ser Asp Ser Ser Met Pro Ile Phe Thr Gly Ile Lys Gln
      130     135     140
Ser Trp Ala Val Arg Leu Val Gln Gly Ile Arg Glu Ile Leu Asp Gln
      145     150     155     160
Leu Leu Val Asp Thr Ser Leu Phe Thr Glu Glu Glu Arg Gly Asp Leu
      165     170     175
Leu Ala Ile Arg Met Asp Ala Ala Ser Leu Gln Asp Lys Gln Glu Arg
      180     185     190
Leu Ser Ala Glu Asp Ile Arg Ser Leu Leu Ser Leu Ser Asn Asp Val
      195     200     205
Met Arg Val Leu Gln Lys Ala Ser Val Ser Ser Thr Arg Gln Leu Glu
      210     215     220
Leu Ile Gln Ser Leu Ile Asp Ile Phe Gly Thr Glu Glu Asn Leu Glu
      225     230     235     240
Gln Ser Phe Ala Gln Val Arg Leu Glu Asn Phe Gln Ala Ile Leu Ser
      245     250     255
Val Ile Lys Glu Arg Leu Thr Glu Glu Glu Phe Arg Val Phe Gln Glu

```

Val Ser Glu Glu Ile Ser Ser Ile Gln Arg Thr Ser Glu Ser His Leu
 260 275 280 285
 Ser Pro Glu His Ile Glu Ala Ile Ala Arg Val Gly Gly Tyr Leu Ser
 290 295 300
 Ala Lys Ile Val Glu Ser Glu Leu Lys Ala Ser Gln Lys Val Asp Leu
 305 310 315 320
 Cys Gln Arg Ile Ala Ala Met Tyr Gln Glu Gln Val Asp Ala Val Gln
 325 330 335
 Ala Tyr His Ser Leu Glu Gln Asp Ala Leu Phe Val Asn Ser Arg Gln
 340 345 350
 His Gly Tyr Phe Val Gln Val Ile Ser Leu Val Ser Ser Leu Met His
 355 360 365
 Ser Leu Ser Pro Thr Ser Glu Glu Glu Arg Ile Leu Leu Asn Pro Ala
 370 375 380
 Met Met Val Ser Val Leu Pro Thr Val Arg Ala Ile Gly Leu Arg Phe
 385 390 395 400
 Asp Phe Leu Thr Ala Glu Gln Gln Gln Met Val Asn Ala Ala Val Ser
 405 410 415
 Ser Leu Gln Gln Gln Gln Leu Asp Glu Phe Leu Gly Val Leu Cys Ala
 420 425 430
 His Leu Val Val Val Asn Cys Gln Asn Lys Glu Thr Gly Leu Leu Glu
 435 440 445
 Gly Leu Glu Glu Ser Phe Ser Glu Thr Leu Ser Gly Leu Ser Asn Asn
 450 455 460
 Phe Val Leu Thr Ala Lys Met Gln Asp Ile Leu Gln Val Cys Ser Leu
 465 470 475 480
 Gln Gly Phe Val Thr Leu Ala Asn Gly Asp Arg Tyr Glu Leu Phe Ser
 485 490 495
 Tyr Asn Asp Ser Gly Glu Ala Val Cys Asp Glu Ile Ala Leu Gly Asp
 500 505 510
 Gly Phe His Lys Val Leu Gly Thr Met Leu Ala Val Ala Leu Ser Gln
 515 520 525
 Ala Glu Val Phe Lys Ala Arg Val Arg Ser Ile His Ser Ala Ser
 530 535 540

(2) INFORMATIONS POUR LA SEQ ID NO: 822:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 328 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 808026..809009

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 822:

Arg Phe Leu Lys Gln Arg Tyr Leu Lys Gln Glu Cys Asp Arg Phe Ile
 1 5 10 15
 Leu Gln Ala Asp Ser Glu Lys Asn Met Ile His Lys Arg Met Val Gln
 20 25 30
 Gly Glu Gln Lys Ser Leu Phe Leu Thr Lys Met Gln Thr Glu Leu Asn
 35 40 45
 Ala Gly Lys Thr Ile Ala Gln Thr Lys Glu Val Glu Ala Ser Pro Leu
 50 55 60


```

Pro Ser Ala Val Ala Ser Val Leu Ile Asp His Tyr Met Pro Lys Glu
65      70      75      80
Val Glu Phe Leu Glu Lys Ile Ser Ser Arg Leu Tyr Tyr Gly Asn Lys
      85      90      95
Gly Ser Asp Ile Gly Asn Thr Ile Leu Asp Ala Ile Ser Leu Tyr Val
      100      105      110
Asn Ser Ala Thr Tyr Phe Gly Phe Ala Asn Tyr Ile Gly Gln Pro Pro
      115      120      125
Val Val Gly Lys Thr Gly Glu Asn Ile Phe Ala Gly Ser Ala Asp Asn
      130      135      140
Ala Lys Ala Lys Leu Asp Glu Glu Arg Lys Gln Val Asp Val Phe Leu
145      150      155      160
Glu Ile Thr Lys Ala Ala Lys Thr Thr Val Thr Asn Gln Gln Ser Ala
      165      170      175
Val Thr Asp Asp Asp Lys Leu Ser Thr Glu Gln Lys Ala Lys Ile Asn
      180      185      190
Ala Glu Leu Thr Gln Tyr Thr Asp Met Leu Asn Ala Ile Asn Asn Ser
      195      200      205
Leu Thr Ser Leu Lys Thr Gln Leu Ala Pro Leu Ser Val Ser Thr Val
      210      215      220
Glu Gly Val Asp Gly Val Phe Glu Val Lys Asn Gly Lys Pro Gly Glu
225      230      235      240
Asn Gly Lys Asn Trp Arg Leu Val Leu Gln Thr Leu Glu Asp Thr Val
      245      250      255
Val Ser Gly Glu Val Gly Ser Pro Thr Asn Ile Gly Met Phe Gln Met
      260      265      270
Gln Ala Leu Val His Ser Asn Gln Gln Ala Tyr Ala Asp Met Gly Gln
      275      280      285
Asn Phe Gln Leu Glu Leu Gln Met His Leu Thr Ser Met Gln Gln Glu
      290      295      300
Trp Met Val Val Ala Thr Ser Leu Gln Leu Leu Asn Gln Ile Tyr Leu
305      310      315      320
Gly Leu Ala Arg Asn Leu Leu Arg
      325

```

(2) INFORMATIONS POUR LA SEQ ID NO: 823:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 461 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(809079..810461)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 823:

```

Leu Leu Asn Arg Lys Ile Ser Ser Met Lys Arg Ser Arg Asn Leu Met
1      5      10      15
Thr Ser Gln Glu Val Thr Thr Ser Val Pro Phe Gly Leu Thr Leu Arg
      20      25      30
Leu Gln Gln Ser Ser Arg Leu Lys Thr Val Thr Thr Asp Glu Val Lys
      35      40      45
Gln Ala Leu Thr Ser Gln Ala Asn Thr Ile Val Ser Asp Phe Ser Leu
      50      55      60
Ala Gln Thr Leu Lys Ser Thr Ile Asn Lys Ile Val Gln Glu Asn Gly

```

(2) INFORMATION POUR LA SEQ ID NO: 824:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 426 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(810328..811605)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 824:

Lys	Thr	Leu	Val	Glu	Met	Cys	Ser	Met	Asn	Ile	Phe	Asn	Lys	Ile	Asn
1				5					10					15	
Ser	Val	Ser	Lys	Asp	Tyr	Thr	Lys	Ile	Glu	Glu	Leu	Phe	Leu	Pro	Thr
			20					25					30		
His	Lys	Asn	Lys	Thr	Phe	Cys	Met	Asn	Gln	Val	Met	Gln	Phe	Gln	Lys
		35					40					45			
Thr	Glu	Ile	Glu	Arg	Ser	Ala	Ile	Gln	Asn	Val	Leu	Ser	Leu	Leu	Asp
	50					55					60				
Leu	Asp	Asn	Asp	Val	Lys	Gly	Lys	Tyr	Glu	Gln	Leu	Val	Ala	Ser	Leu
65					70					75					80
Ser	Ser	Ser	Ala	Pro	Thr	Thr	Thr	Ser	Gln	Pro	Ser	Asp	Glu	Ser	Ala
				85					90					95	
Val	Ile	Thr	Tyr	Asp	Pro	Pro	Ser	Ser	Asn	Pro	Leu	Tyr	Asn	Ala	Ser
			100						105				110		
Lys	Gln	Ala	Trp	Val	His	Asn	Val	Leu	Val	Gly	Phe	Leu	Ser	Val	Val
		115					120					125			
Asn	Glu	Ala	Lys	Thr	Lys	Ala	Thr	Glu	Ile	Ala	Gly	Gln	Gln	Asn	Pro
	130					135					140				
Pro	Gln	Thr	Asp	Leu	Lys	Pro	Leu	Thr	Asp	Leu	Phe	Asp	Ser	Leu	Thr
145					150					155					160
Thr	Leu	Val	Asp	Lys	Ala	Asn	His	Arg	Glu	Leu	Ser	Asn	Glu	Asp	Leu
				165					170					175	
Glu	Thr	Phe	Tyr	Leu	Leu	Pro	Asp	Gln	Ile	Phe	Ser	Ala	Ile	Gln	Thr
			180					185					190		
Phe	Pro	Phe	Glu	Gly	Asn	Gln	Lys	Val	Leu	Phe	Ser	Asn	Gln	Leu	Leu
		195					200					205			
Asp	Ser	Phe	Gly	Glu	Asp	Ala	Ser	Ile	Glu	Gln	Val	Phe	Ala	Asp	Ile
	210					215					220				
Arg	Ile	Glu	Gly	Leu	Gln	Asp	Thr	Leu	Asn	Met	Val	Gln	Ser	Arg	Leu
225					230					235					240
Ser	Ala	Thr	Glu	Phe	Glu	Ser	Phe	Lys	Glu	Leu	Gln	Met	Ile	Ile	Asp
				245					250					255	
Thr	Leu	Arg	Glu	Tyr	Val	Glu	Pro	Phe	Asn	Asp	Glu	Gly	Phe	Asp	Thr
			260					265					270		
Ile	Leu	Gln	Thr	Ser	Lys	Asp	Leu	Ser	Ser	Ala	Ile	Ile	Asn	Ser	Ser
	275						280					285			
Leu	Ser	Ser	Asn	Asp	Lys	Ile	Glu	Leu	Cys	Arg	Asn	Ile	Ala	Asp	Leu
	290				295					300					
Tyr	Arg	Asp	Gln	Val	Leu	Ser	Ile	Lys	Asn	Leu	Asp	Asn	Val	Leu	Asn
305					310					315					320
Glu	Thr	Ile	Tyr	Ile	Asn	Ala	Arg	Asn	Ser	Ser	Leu	Phe	Ser	Asn	Ile
				325					330					335	
Cys	Ser	Leu	Val	Glu	Phe	Ile	Met	Gly	Ser	Phe	Ala	Pro	Ile	Gly	Leu
			340					345					350		
Asn	Glu	Thr	Thr	Ile	Glu	Val	Thr	Asn	Ala	Ser	Ile	Ala	Gly	Ala	Leu
	355						360					365			
Gln	Ala	Val	Arg	Ala	Ile	Asp	Thr	Arg	Phe	His	Glu	Leu	Thr	Pro	Glu
	370					375					380				
Gln	Lys	Asn	Leu	Val	Asn	Glu	Thr	Val	Lys	Lys	Leu	Asp	Asp	Phe	Ser
385					390					395					400
Gly	Gly	Asn	Tyr	Ile	Gly	Ala	Phe	Trp	Ala	Tyr	Phe	Thr	Ser	Ala	Thr
				405					410					415	
Val	Val	Ser	Ser	Lys	Asp	Cys	Asp	Asn	Arg						

420

425

(2) INFORMATIONS POUR LA SEQ ID NO: 825:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 811725..812342

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 825:

Ile	Leu	Gly	Gln	Leu	Leu	Tyr	Leu	Glu	Arg	Val	Tyr	Leu	Arg	Leu	Asn	15
1				5				10								
Ser	Ala	Asn	Pro	Cys	Ser	Asp	Phe	Lys	Asn	Gln	Ala	Arg	Pro	Ala	Ile	30
		20						25								
Asp	Met	Glu	Glu	Leu	Asn	Ser	Gly	Leu	Tyr	Val	Leu	Arg	Arg	Leu	Ala	45
		35					40									
Val	Ala	Leu	Glu	Ala	Gly	Tyr	Xaa	Gly	Val	Xaa	Ser	Val	Val	Asn	Pro	60
		50				55										
Ser	Asn	Arg	Val	Phe	Pro	Gly	Gly	Asp	Trp	Gly	Val	Arg	Arg	Ala	Ala	80
65					70					75						
Gly	Gly	Ser	Thr	Pro	Ala	Ala	Gly	Thr	Ile	Ser	Gly	Ser	Thr	Xaa	Ala	95
				85					90							
Asp	Ile	Lys	Gln	Ser	Thr	Ala	Lys	Val	Leu	Val	Thr	Thr	Ile	Thr	Asp	110
			100					105								
Ser	Leu	Asn	Ala	Leu	Ile	Glu	Asp	Val	Pro	Glu	Val	Pro	Met	Thr	Gln	125
		115					120									
Val	Thr	Gly	Val	Ser	Ser	Asn	Leu	Val	Leu	Met	Glu	Ser	Tyr	Gln	Gln	140
		130				135										
Lys	Asp	Ser	Leu	Asn	Asp	Thr	Glu	Gln	Ala	Ser	Val	Phe	Ala	Ser	Ala	160
145				150						155						
Tyr	Ala	Pro	Ser	Asp	Glu	Ser	Ile	Lys	Thr	Val	Ile	Lys	Lys	Glu	Gln	175
				165					170							
Glu	Lys	Glu	Leu	Gln	Glu	Gly	Lys	Asp	Arg	Val	Thr	Ala	Gln	Leu	Thr	190
			180					185								
Ala	Gln	Gly	Ala	Ser	Asp	Gln	Val	Ile	Glu	Lys	Ser	Leu	Gly			205
			195				200									

(2) INFORMATIONS POUR LA SEQ ID NO: 826:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 398 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 812329..813522

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 826:

```

Arg Ser Leu Trp Ala Asp Tyr Glu Lys Tyr Tyr Val Asp Glu Tyr Phe
1      5      10      15
Asp Thr His Val Lys Glu Ala Leu Trp Lys His Arg Ala Ser Ile Gly
      20      25      30
Glu Asn Ile Gln Glu Met Leu Asp Gln Cys Leu Asn Leu Gly Leu Asp
      35      40      45
Val Pro Asp Ser Leu Thr Lys Glu Asn Ile Asn Asp Ala Asn Ala Lys
      50      55      60
Leu Val Leu Gln Ala Trp Met Glu Ala Phe Asn Asn Ala Met Glu Val
65      70      75      80
Glu Pro Ala Leu Gly Gly Ser Lys Glu Val Ile Asp Ser Val Leu Lys
      85      90      95
Met Ile Pro Phe Ala Lys Gln Ser Ser Asn Leu Ser Asp Thr Asp Ile
      100      105      110
Asn Thr Ile Tyr Thr Gln Ala Ala Leu Pro Pro Pro Glu Val Met Asp
      115      120      125
Tyr Tyr Leu Thr Arg Gln Asp Ala Gly Ile Cys Lys Gly Glu Val Val
130      135      140
Lys Ala Phe Gln Gln Ala Thr Gln Asn Leu Gln Ser Val Arg Ser Asn
145      150      155      160
Val Glu Glu Gln Ile Lys Glu Leu Glu Val Lys Lys Thr Ser Phe Leu
      165      170      175
Gln Ala Gln Ala Ser Leu Glu Ser Met Leu Glu Gly Val Lys Arg Leu
      180      185      190
Asn Asp Asn Gln Lys Phe Thr Ser Val Arg Leu Thr Ser Val Met Glu
      195      200      205
Cys Tyr Ala Gly Leu Ile Ala Leu Ser Gln Ile Thr Asp Val Leu Asp
210      215      220
Ser Ala Gly Ile Ser Leu Ile Thr Gln Tyr Val Asp Lys Phe Leu Lys
225      230      235      240
Leu Asn Asn Ala His Thr Ala Gln Thr Leu Ala His Val Ile Ser Tyr
      245      250      255
Met Ala Ala Tyr Cys Glu Val Ala Glu Cys Thr Met Ala Ser Thr Ile
      260      265      270
Val Ser Glu Asp Thr Val Leu Gln Lys Val Lys Asp Lys Trp Asn Glu
      275      280      285
Leu Lys Lys Glu Lys Phe Phe Glu Ser Phe Thr Leu Pro Asp Asp Asn
290      295      300
Glu Leu Lys Thr Asn Tyr Ile Thr Ser Thr Asn Asn Val Cys Arg Ala
305      310      315      320
Asn Phe Ser Asn Phe Val Asn Thr Val Ile Thr Glu Lys Ile Asn Leu
      325      330      335
Thr Val Ala Val Arg Glu Ala Gln Ser Leu Leu Thr Glu Phe Gln Gly
      340      345      350
Lys Ala Ser Glu Tyr Leu Asn Thr Phe Gln Ser Glu Ile Asn Thr Leu
      355      360      365
Asn Gln Thr Tyr Asp Thr Leu Asp Pro Ala Lys Ala Ser Phe Asn Tyr
370      375      380
Phe Tyr Arg Glu Tyr Thr Phe Phe Thr Cys Thr Gly Cys Arg
385      390      395

```

(2) INFORMATIONS POUR LA SEQ ID NO: 827:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 106 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 813455..813772

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 827:

```

Ile Gln Pro Lys Leu Leu Leu Ile Thr Ser Thr Gly Ser Thr Pro Ser
1      5      10      15
Leu Arg Ala Gln Ala Val Asp Ser Trp Ile Asp Ser Thr Ser Leu Gly
20      25      30
Ser Ala Phe Ile His Leu Ile Leu Asn Thr Gln Ile Pro Lys Gln Glu
35      40      45
Asn Phe Leu Asn Pro Leu Ile Gln Glu Val Asn Phe Asn Asn Val Ala
50      55      60
Ala Asn Ala Val Asn Asp Leu Leu Ser Ile Thr Asn Asn Phe Ser Thr
65      70      75      80
Ser Ser Val Tyr Tyr Asn Leu Ser Ser Tyr Leu Val Glu Ser Lys Ala
85      90      95
Arg Lys Arg Phe Ile Leu Trp Gly Phe Leu
100      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 828:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 201 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 813732..814334

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 828:

```

Lys Ala Arg Gln Gly Lys Asp Leu Phe Cys Gly Asp Phe Phe Glu Phe
1      5      10      15
Met Gly Ala Leu Ala Lys Glu His Glu Tyr Ile Val Arg Asp Ile Lys
20      25      30
Ser Cys Tyr Arg Ala Glu Val Phe Gly Glu Ala Leu Leu Ala Arg Val
35      40      45
Glu Ala Leu Ala Gln Gly His Lys Val Thr Asp Ala Lys Ala Asn Ser
50      55      60
Met Arg Thr Gln Ala Asn Leu Tyr Leu Ser Phe Ile Arg Ile Ile Val
65      70      75      80
Glu Gln Leu Ala Val Leu Asp Ser Leu Leu Arg Ser Leu Asn Tyr Glu
85      90      95
Val Glu Lys Lys Asp Asn Asn Tyr Asp Lys Asp Lys Tyr Lys Ile Thr
100      105      110
Gly Pro Thr Asp Trp Ile Ser Thr Leu Ala Ser Leu Glu Gly Tyr Ala
115      120      125
Val Asn Gly Phe Asp Asn Ala Ser Leu Ser Gly Gly Leu Gly Pro Met
130      135      140
His Thr Leu Val Gln Thr Asp Gln His Asp Tyr Leu Thr Gln Ser Gln
145      150      155      160
Thr Gln Gln Leu Asn Leu Gln Asn Gln Met Thr Asn Ile Gln Gln Glu
165      170      175

```

Trp Thr Leu Val Ser Thr Ser Met Gln Val Leu Asn Gly Ile Leu Ser
 180 185 190
 His Leu Ala Ala Glu Ile Tyr Ser Asn
 195 200

(2) INFORMATIONS POUR LA SEQ ID NO: 829:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 300 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(814314..815213)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 829:

Phe Phe Leu Glu Val Ser Thr Met Ala Ala Thr Val Pro Ile Ala Ser
 1 5 10 15
 Pro Val Gly Arg Leu Leu Ser Ser Ala Thr Ala Thr Thr Leu Arg Gly
 20 25 30
 Asn Ala Thr Ser Leu Arg Ser Lys Leu Ser Ser Val Asn Asp Leu Phe
 35 40 45
 Asp Leu Ile Ser Ser Ser Cys Thr Leu Ala Arg Val Thr Pro Arg Thr
 50 55 60
 Thr Val Ser Xaa Thr Gln Gln Gln Gln Leu Ser Thr Ile Glu Thr Thr
 65 70 75 80
 Leu Gly Ser Ala Lys Ser Ala Ser Asn Ala Val Gln Ala Xaa Cys Gly
 85 90 95
 Ile Val Gln Leu Leu Thr Gly Gly Leu Phe Phe Lys Thr Asn Pro Asp
 100 105 110
 Gly Ser Phe His Leu Asp Leu Val Ser Gln Gln Arg Thr Leu Leu Ser
 115 120 125
 Pro Leu Ser Leu Val Ser Lys Val Thr Arg Leu Ala Ser Lys Val Leu
 130 135 140
 Gly Thr Val Lys Phe Met Gly Ser Gln Thr Phe Pro Val Tyr Gln Leu
 145 150 155 160
 Gly Ala His Ala Thr Gly Ile Gly Leu Ser Ala Ser Ala Phe Gly Thr
 165 170 175
 Val Ser Pro Pro Ser Met Ser Gln Lys Thr Gln Glu Lys Phe Ser Gly
 180 185 190
 Thr Ser Asn Arg Ile Asn Leu Gln Lys Glu His Leu Lys Lys Thr Ala
 195 200 205
 Ser Trp His Val Leu Lys Glu Leu Val Gln Val Cys Ser Thr Cys Phe
 210 215 220
 Ala Ala Ser Trp Thr Cys Trp Leu Arg Leu Ser Val Ser Ser Ala Met
 225 230 235 240
 Gln Phe Leu Gln His Leu Trp Glu Cys Thr Pro Leu Leu Leu Trp Val
 245 250 255
 Ser Ser Ala Ser Tyr Leu Leu Trp Glu Met Leu Phe Phe Leu Ser Leu
 260 265 270
 Phe Lys Val Cys Lys His His Ile Leu Glu Ala Arg Arg Tyr Ile Ser
 275 280 285
 Ala Ser Xaa Phe Leu Ile Arg Ile Asn Phe Arg Cys
 290 295 300

(2) INFORMATIONS POUR LA SEQ ID NO: 830:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 161 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(814396..814878)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 830:

```

Trp Ile Phe Pro Pro Arg Ser Cys Phe Ala Thr Lys Asn Pro Pro Val
1      5      10      15
Ser Thr Ile Thr Cys Gln Gln Ser Asn Ser Phe Ser Gln Gln Ser Ser
20      25      30
Arg Asn Arg Glu Ile His Gly Leu Pro Asn Phe Pro Cys Leu Pro Val
35      40      45
Gly Cys Thr Arg Asn Trp Tyr Trp Leu Ile Cys Phe Cys Val Trp Asn
50      55      60
Cys Gln Ser Ala Phe Asp Val Ala Glu Asn Ser Arg Glu Val Leu Gly
65      70      75      80
Asn Leu Lys Gln Asn Lys Pro Thr Glu Gly Thr Ser Lys Glu Asn Gly
85      90      95
Phe Met Ala Arg Leu Lys Arg Ala Arg Ala Ser Met Phe Asn Leu Leu
100     105     110
Cys Ser Ile Leu Asp Leu Leu Ala Gln Ala Phe Cys Phe Ile Ser Asp
115     120     125
Ala Val Ser Thr Ala Phe Met Gly Val His Thr Ala Phe Ile Val Gly
130     135     140
Ile Phe Cys Phe Leu Ser Ala Leu Gly Asn Val Ile Leu Ser Ile Ala
145     150     155     160
Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 831:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 87 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(815428..815688)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 831:

```

Pro Gln Lys Arg Pro Ser Ala Glu Lys Arg Val Ile Thr Ser Lys Lys
1      5      10      15
Lys Gln Leu Arg Asn Gln Ser Phe Lys Ser Lys Val Arg Thr Ile Leu
20      25      30
Lys Lys Phe Glu Leu Ala Val Gln Ser Gly Asp Val Glu Ser Ile Ser
35      40      45

```


Ala Gly Leu Arg Ser Val Tyr Ser Ile Ala Asp Lys Ala Val Lys Arg
 50 55 60
 Gly Ile Phe Lys Lys Gly Lys Ala Asp Arg Val Lys Ser Arg Ala Ser
 65 70 75 80
 Glu Arg Ala Cys Pro Ala Ala
 85

(2) INFORMATIONS POUR LA SEQ ID NO: 832:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 447 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 816116..817456

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 832:

Ser	Ile	Pro	Lys	Phe	Ala	Ile	Cys	Arg	Asp	Ile	Val	Trp	Gly	Cys	Thr	1	5	10	15
Ala	Gly	Met	Gln	Tyr	Val	Met	Gly	Arg	Thr	Asn	Ser	Met	Thr	Arg	Gly	20	25	30	
Phe	Leu	Asn	Lys	Arg	Arg	Val	Leu	Glu	Lys	Cys	Arg	Thr	Ala	Lys	Gln	35	40	45	
Lys	Ile	His	Tyr	Cys	Ile	Ser	Arg	Tyr	Phe	His	Tyr	Leu	Pro	Pro	Val	50	55	60	
Leu	Ala	Ile	Leu	Leu	Pro	Ile	Gly	Ser	Trp	Pro	Phe	Leu	Ser	Glu	Gln	65	70	75	80
Gln	Trp	Trp	Cys	Gly	Ser	Phe	Leu	Phe	Pro	Val	Val	Ser	Ser	Leu	Gly	85	90	95	
Trp	Leu	Phe	Ala	Ile	Gly	Arg	Arg	Glu	Arg	Gln	Leu	Arg	Ala	Ala	Ala	100	105	110	
Gly	Gln	Leu	Glu	Ala	Lys	Ile	Arg	Lys	Leu	Thr	Glu	Gln	Asp	Glu		115	120	125	
Gly	Leu	Lys	Asn	Ile	Arg	Glu	Thr	Ile	Glu	Lys	Arg	Gln	Lys	Glu	Thr	130	135	140	
Asp	Arg	Leu	Lys	Leu	His	Asn	Asp	Lys	Leu	Val	Glu	Gln	Leu	Gly	Gln	145	150	155	160
Ala	Arg	Glu	Val	Phe	Ile	Gln	Ala	Lys	Gly	Arg	Tyr	Asp	His	Met	Glu	165	170	175	
Glu	Leu	Ser	Arg	Arg	Leu	Lys	Glu	Glu	Asn	Gln	Gln	Leu	Gln	Met	Gln	180	185	190	
Leu	Glu	Ala	Ala	Val	Arg	Glu	Arg	Asn	Glu	Lys	Ile	Leu	Glu	Asn	Gln	195	200	205	
Glu	Leu	Leu	Gln	Glu	Leu	Lys	Glu	Thr	Leu	Ala	Tyr	Gln	Gln	Glu	Leu	210	215	220	
His	Asp	Glu	Tyr	Gln	Ala	Thr	Phe	Val	Glu	Gln	His	Ser	Met	Leu	Asp	225	230	235	240
Lys	Arg	Gln	Ala	Tyr	Ile	Gly	Asn	Leu	Glu	Ala	Lys	Val	Gln	Asp	Leu	245	250	255	
Met	Cys	Glu	Leu	Arg	Asn	Leu	Leu	Gln	Leu	Glu	Met	Gly	Ala	Lys	Thr	260	265	270	
Asn	Leu	Pro	Gly	Lys	Pro	Val	Ala	Ser	Arg	Asp	Val	Val	Ala	Gln	Leu	275	280	285	
Val	Leu	Glu	Phe	Arg	Lys	Ile	Val	Phe	Arg	Val	Glu	Thr	Thr	Glu	Ala				

(2) INFORMATION POUR LA SEQ ID NO: 833:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 571 acides aminés

(A) LONGUEUR: 571 g/mol
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 817608..819320

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 833:

(x1)	DESCRIPTION OF THE SEQUENCE																	
Met	Arg	Met	Asp	Thr	Leu	Asp	Ser	Gln	Ala	Ala	Glu	Ala	Ala	Gln	Glu			
1				5					10					15				
Glu	Glu	Ile	Gln	Arg	Lys	Leu	Glu	Glu	Leu	Val	Thr	Leu	Ala	Lys	Asp			
			20					25					30					
Gln	Gly	Phe	Ile	Thr	Tyr	Glu	Glu	Ile	Asn	Glu	Ile	Leu	Pro	Pro	Ser			
		35					40					45						
Phe	Asp	Thr	Pro	Glu	Gln	Ile	Asp	Gln	Val	Leu	Ile	Phe	Leu	Ala	Gly			
	50					55					60							
Met	Asp	Val	Gln	Val	Leu	Asn	Gln	Ala	Asp	Val	Glu	Arg	Gln	Lys	Glu			
65					70				75						80			
Arg	Lys	Lys	Glu	Ala	Lys	Glu	Leu	Glu	Gly	Leu	Ala	Lys	Arg	Ser	Glu			
			85						90					95				
Gly	Thr	Pro	Asp	Asp	Pro	Val	Arg	Met	Tyr	Leu	Lys	Glu	Met	Gly	Thr			
			100					105					110					
Val	Pro	Leu	Leu	Thr	Arg	Glu	Glu	Glu	Val	Glu	Ile	Ser	Lys	Arg	Ile			
		115					120					125						
Glu	Lys	Ala	Gln	Val	Gln	Ile	Glu	Arg	Ile	Ile	Leu	Arg	Phe	Arg	Tyr			
	130					135					140							
Ser	Thr	Lys	Glu	Ala	Val	Ser	Ile	Ala	Gln	Tyr	Leu	Ile	Asn	Gly	Lys			
145					150				155					160				
Glu	Arg	Phe	Asp	Lys	Ile	Val	Ser	Glu	Lys	Glu	Val	Glu	Asp	Lys	Thr			
				165					170					175				
His	Phe	Leu	Asn	Leu	Leu	Pro	Lys	Leu	Ile	Ser	Leu	Leu	Lys	Glu	Glu			
			180					185					190					

Asp	Ala	Tyr	Leu	Glu	Glu	Arg	Leu	Leu	Ala	Leu	Lys	Asp	Pro	Ala	Leu	195	200	205
Ser	Lys	Pro	Asp	Gln	Ala	Arg	Leu	Asn	Asp	Glu	Leu	Glu	Lys	Cys	Arg	210	215	220
Ile	Arg	Thr	Gln	Ala	Tyr	Leu	Arg	Cys	Phe	His	Cys	Arg	His	Asn	Val	225	230	235
Thr	Glu	Asp	Phe	Gly	Glu	Val	Val	Phe	Lys	Ala	Tyr	Asp	Ser	Phe	Leu	245	250	255
Gln	Leu	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Lys	Ala	Arg	Ala	Glu	Arg	Asn	260	265	270
Lys	Phe	Ala	Ala	Ala	Lys	Leu	Ala	Ala	Ala	Arg	Arg	Lys	Leu	His	Lys	275	280	285
Arg	Glu	Val	Ala	Ala	Gly	Arg	Thr	Leu	Glu	Glu	Phe	Lys	Lys	Asp	Val	290	295	300
Arg	Met	Leu	Gln	Arg	Trp	Met	Asp	Lys	Ser	Gln	Glu	Ala	Lys	Lys	Glu	305	310	315
Met	Val	Glu	Ser	Asn	Leu	Arg	Leu	Val	Ile	Ser	Ile	Ala	Lys	Lys	Tyr	325	330	335
Thr	Asn	Arg	Gly	Leu	Ser	Phe	Leu	Asp	Leu	Ile	Gln	Glu	Gly	Asn	Met	340	345	350
Gly	Leu	Met	Lys	Ala	Val	Glu	Lys	Phe	Glu	Tyr	Arg	Arg	Gly	Tyr	Lys	355	360	365
Phe	Ser	Thr	Tyr	Ala	Thr	Trp	Trp	Ile	Arg	Gln	Ala	Val	Thr	Arg	Ala	370	375	380
Ile	Ala	Asp	Gln	Ala	Arg	Thr	Ile	Arg	Ile	Pro	Val	His	Met	Ile	Glu	385	390	395
Thr	Ile	Asn	Lys	Val	Leu	Arg	Gly	Ala	Lys	Lys	Leu	Met	Met	Glu	Thr	405	410	415
Gly	Lys	Glu	Pro	Thr	Pro	Glu	Glu	Leu	Gly	Glu	Glu	Leu	Gly	Phe	Thr	420	425	430
Pro	Asp	Arg	Val	Arg	Glu	Ile	Tyr	Lys	Ile	Ala	Gln	His	Pro	Ile	Ser	435	440	445
Leu	Gln	Ala	Glu	Val	Gly	Asp	Gly	Gly	Glu	Ser	Ser	Phe	Gly	Asp	Phe	450	455	460
Leu	Glu	Asp	Thr	Ala	Val	Glu	Ser	Pro	Ala	Glu	Ala	Thr	Gly	Tyr	Ser	465	470	475
Met	Leu	Lys	Asp	Lys	Met	Lys	Glu	Val	Leu	Lys	Thr	Leu	Thr	Asp	Arg	485	490	495
Glu	Arg	Phe	Val	Leu	Ile	His	Arg	Phe	Gly	Leu	Leu	Asp	Gly	Arg	Pro	500	505	510
Lys	Thr	Leu	Glu	Glu	Val	Gly	Ser	Ala	Phe	Asn	Val	Thr	Arg	Glu	Arg	515	520	525
Ile	Arg	Gln	Ile	Glu	Ala	Lys	Ala	Leu	Arg	Lys	Met	Arg	His	Pro	Ile	530	535	540
Arg	Ser	Lys	Gln	Leu	Arg	Ala	Phe	Leu	Asp	Leu	Leu	Glu	Glu	Glu	Lys	545	550	555
Ile	Gly	Ser	Gly	Lys	Ile	Lys	Ser	Tyr	Lys	Asn						565	570	

(2) INFORMATIONS POUR LA SEQ ID NO: 834:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 130 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 819324..819713

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 834:

```

Ser Cys Cys Leu Gln Gly Val Leu Leu Tyr Arg Leu Asp Ile Ala Asp
1          5          10          15
Phe Arg Val Trp Val Ser Ile Gly Val Ser Glu Gln Glu Arg His Tyr
20          25          30
Pro Gln Pro Val Leu Val Ser Leu Ser Leu Phe Phe Lys Glu Glu Pro
35          40          45
Lys Ala Trp Ser Thr Asp Lys Val Ser Asp Ser Val Cys Tyr Ala Glu
50          55          60
Leu Val Ser Leu Ile Glu Glu Val Ala Thr Asn Asn Pro Cys Ala Leu
65          70          75          80
Ile Glu Arg Leu Ala Lys Val Leu Leu Glu Lys Ile Glu Lys Ala Leu
85          90          95
Ala Gly Gln Val Ser Arg Ile Asp Leu Arg Val Ser Lys Glu Arg Pro
100          105          110
Pro Ile Pro Asp Leu Leu Ser Pro Val Ser Phe Ser Ile Ser Arg Glu
115          120          125
Val Pro
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 835:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 233 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 819704..820402

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 835:

```

Arg Gly Ala Met Thr Ser Trp Asn Phe Val Cys Leu Ser Leu Gly Ser
1          5          10          15
Asn Leu Gly Asn Arg His Glu His Ile Arg Arg Ala Tyr Ala Ser Leu
20          25          30
Lys Lys Ala Gly Ile Arg Asn Leu Lys Ser Ser Val Ile Leu Glu Thr
35          40          45
Lys Ala Leu Leu Leu Glu Gly Ala Pro Lys Glu Trp Asp Leu Pro Tyr
50          55          60
Phe Asn Ser Val Val Ile Gly Glu Thr Gln Leu Ser Pro Asp Glu Leu
65          70          75          80
Ile Glu Glu Ile Lys Met Ile Glu Ser Arg Phe Gly Gln Asp Ala Ser
85          90          95
Leu Lys Trp Gly Pro Arg Pro Ile Asp Ile Asp Val Leu Phe Tyr Gly
100          105          110
Asp Glu Ala Phe Ser Tyr His Ser Asp Lys Cys Thr Ile Pro His Pro
115          120          125
Lys Val Leu Glu Arg Pro Phe Ile Leu Ser Met Met Ala Ser Leu Cys
130          135          140
Pro Tyr Arg Arg Phe Arg Leu Glu Gly Ser Ser Cys Asn Gly Lys Thr
145          150          155          160

```

```

Phe Ala Glu Leu Ala Ala Ile Tyr Pro Leu Thr Glu Glu Asp Ala Leu
      165      170      175
Gly Ser Phe Gly Ser Ala Thr Gln Ile Met Gly Ile Val Asn Ile Thr
      180      185      190
Asp Asn Ser Ile Ser Asp Thr Gly Leu Phe Leu Glu Ala Ser Arg Ala
      195      200      205
Ala Ala His Ala Glu Arg Leu Phe Ala Glu Gly Ala Ser Ile Ile Asp
      210      215      220
Leu Gly Ala Gln Gln Pro Ile Leu Val
225      230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 836:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 229 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 820375..821061

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 836:

```

Phe Arg Gly Ala Thr Thr Asn Pro Arg Val Lys Asp Leu Gly Ser Val
1      5      10      15
Glu Gln Glu Trp Glu Arg Leu Glu Pro Val Leu Arg Leu Leu Ala Glu
      20      25      30
Gly Trp Gly Ala Ala Gln Gln Cys Pro Asp Val Ser Ile Asp Thr Phe
      35      40      45
Arg Pro Glu Ile Ile Arg Arg Ala Val Glu Val Phe Pro Ile Arg Trp
      50      55      60
Ile Asn Asp Val Ser Gly Gly Ser Leu Glu Met Ala His Leu Ala Lys
      65      70      75      80
Glu Phe Gly Leu Arg Leu Leu Ile Asn His Ser Cys Ser Leu Pro Pro
      85      90      95
Arg Pro Asp Cys Val Leu Ser Tyr Glu Glu Ser Pro Ile Glu Gln Met
      100      105      110
Leu Arg Trp Gly Glu Ser Gln Leu Glu Gln Phe Ala Gln Val Gly Leu
      115      120      125
Asp Thr Ser Trp Gln Val Val Phe Asp Pro Gly Ile Gly Phe Gly Lys
      130      135      140
Thr Pro Val Gln Ser Met Leu Leu Met Asp Gly Val Lys Gln Phe Lys
      145      150      155      160
Arg Val Leu Glu Cys Pro Val Leu Ile Gly His Ser Arg Lys Ser Cys
      165      170      175
Leu Ser Met Leu Gly Arg Phe Asn Ser Asp Asp Arg Asp Trp Glu Thr
      180      185      190
Ile Gly Cys Ser Val Ser Leu His Asp Arg Gly Val Asp Tyr Leu Arg
      195      200      205
Val His Gln Val Glu Gly Asn Arg Arg Ala Leu Ala Ala Ala Trp
      210      215      220
Ala Gly Met Phe Val
225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 837:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 159 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 821061..821537

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 837:

```

Met Ile Gln Ala Thr Gly Ile Val Ala Ile Asp Pro Arg Gly Val Met
1      5      10
Gly Ala Leu Gly Lys Leu Pro Trp Ser Tyr Pro Glu Asp Leu Arg Phe
20     25     30
Phe Ala Glu Thr Ile Arg Asn His Pro Ile Ile Met Gly Arg Lys Thr
35     40     45
Trp Glu Ser Leu Pro Asp Lys Tyr Lys His Gly Arg Asp Ile Val Val
50     55     60
Phe Ser Arg Arg Met His Pro Pro Gln Cys Ile Gly Val Ser Ser Phe
65     70     75     80
Ala Glu Tyr Gly Thr Leu Ser Leu Asn His Pro Phe Leu Ile Gly Gly
85     90     95
Ala Glu Leu Phe Glu Ser Phe Phe Gln Gln Asn Leu Leu Lys Ala Cys
100    105    110
Phe Val Thr His Ile Lys Lys Lys Tyr Trp Gly Asp Thr Phe Phe Pro
115    120    125
Ile Thr Arg Leu Ser Gly Trp Lys Lys Glu Cys Ile Cys Asn Thr Glu
130    135    140
Asp Phe Ser Ile Tyr Tyr Tyr Glu Asn Asn Ser Asp Gln Asn Thr
145    150    155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 838:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 198 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 821646..822239

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 838:

```

Ser Ala Val Ala Asp Ala Arg Met Cys Lys Ala Glu Leu Ile Lys Lys
1      5      10
Glu Ala Asp Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile Tyr Leu Thr
20     25     30
Lys Lys Glu Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn
35     40     45
Thr Asp Gln Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu Gly Ser Cys
50     55     60
Asn Arg Ile Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val Lys Glu Leu
65     70     75     80

```

Gly	Val	Ile	Ile	Thr	Asp	Ser	His	Thr	Thr	Pro	Met	Arg	Arg	Gly	Val
				85					90					95	
Leu	Gly	Ile	Gly	Leu	Cys	Trp	Tyr	Gly	Phe	Ser	Pro	Leu	His	Asn	Tyr
			100					105					110		
Ile	Gly	Ser	Leu	Asp	Cys	Phe	Gly	Arg	Pro	Leu	Gln	Met	Thr	Gln	Ser
		115					120					125			
Asn	Leu	Val	Asp	Ala	Leu	Ala	Val	Ala	Ala	Val	Val	Cys	Met	Gly	Glu
		130				135					140				
Gly	Asn	Glu	Gln	Thr	Pro	Leu	Ala	Val	Ile	Glu	Gln	Ala	Pro	Asn	Met
145					150					155					160
Val	Tyr	His	Ser	Tyr	Pro	Thr	Ser	Arg	Glu	Glu	Tyr	Cys	Ser	Leu	Arg
				165					170					175	
Ile	Asp	Glu	Thr	Glu	Asp	Leu	Tyr	Gly	Pro	Phe	Leu	Gln	Ala	Val	Thr
			180					185					190		
Trp	Ser	Gln	Glu	Lys	Lys										
			195												

(2) INFORMATIONS POUR LA SEQ ID NO: 839:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 822182..822931

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 839:

Asn	Arg	Gly	Leu	Ile	Arg	Thr	Phe	Phe	Ala	Ser	Gly	Tyr	Val	Glu	Ser
1				5					10					15	
Arg	Lys	Glu	Met	Met	Glu	Val	Phe	Met	Asn	Phe	Leu	Asp	Gln	Leu	Asp
			20					25					30		
Leu	Ile	Ile	Gln	Asn	Lys	His	Met	Leu	Glu	His	Thr	Phe	Tyr	Val	Lys
		35					40					45			
Trp	Ser	Lys	Gly	Glu	Leu	Thr	Lys	Glu	Gln	Leu	Gln	Ala	Tyr	Ala	Lys
	50					55					60				
Asp	Tyr	Tyr	Leu	His	Ile	Xaa	Ala	Phe	Pro	Lys	Tyr	Leu	Asp	Ala	Ile
65					70					75					80
His	Ser	Arg	Cys	Asp	Asp	Leu	Glu	Ala	Arg	Lys	Leu	Leu	Leu	Asp	Asn
			85						90					95	
Leu	Met	Asp	Glu	Glu	Asn	Gly	Tyr	Pro	Asn	His	Ile	Asp	Leu	Trp	Lys
			100					105					110		
Gln	Phe	Val	Phe	Ala	Leu	Gly	Val	Thr	Pro	Glu	Glu	Leu	Glu	Ala	His
		115					120					125			
Glu	Pro	Ser	Glu	Ala	Ala	Lys	Ala	Lys	Val	Ala	Thr	Phe	Met	Arg	Trp
		130				135					140				
Cys	Thr	Gly	Asp	Ser	Leu	Ala	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Ser	Tyr
145					150					155					160
Glu	Ser	Gln	Ile	Pro	Arg	Ile	Ala	Arg	Glu	Lys	Ile	Arg	Gly	Leu	Thr
			165						170					175	
Glu	Tyr	Phe	Gly	Phe	Ser	Asn	Pro	Glu	Asp	Tyr	Ala	Tyr	Phe	Thr	Glu
			180					185					190		
His	Glu	Glu	Ala	Asp	Xaa	Arg	His	Ala	Arg	Glu	Glu	Lys	Ala	Leu	Ile
		195					200					205			
Glu	Met	Leu	Leu	Lys	Asp	Asp	Ala	Asp	Lys	Val	Leu	Glu	Ala	Ser	Gln

(2) INFORMATION POUR LA SEQ ID NO: 840:

(i) CARACTERISTIQUES DE LA
(A) LONGUEUR: 437 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(823045..824355)

(xi) DESCRIPTION DE LA SÉRIE

Pro Met Leu His Gln His Gln Thr Ala Ser Val Ala Leu Cys Pro Ala	15
1	5
Leu His Leu Gln Gln Gly Leu Asp Met Leu Gln Met Pro Val Ala Glu	10
	20
Leu Ala Thr Phe Val Ser Gln Gln Ile Thr Ile Asn Pro Cys Phe Asp	25
	30
Leu Asp Ser Leu Asp Ser Pro Pro Glu Ser Phe Ser Phe Phe Pro Ile	35
	40
Ser Glu Gln His Pro Phe Thr Glu Thr Leu Ser Ala Tyr Leu Leu Arg	45
65	50
Gln Ile Asp Thr Asn Phe Ala Ser Ser Gln Glu Arg Thr Ile Ala Gln	55
	60
Tyr Ile Val Gly Asn Leu Ser Pro Glu Gly Leu Phe Leu Glu Asn Pro	65
	70
Ser Leu Val Ala Ala Asp Leu Asn Val Ser Glu His Leu Phe His Lys	75
	80
Val Trp Gln Arg Ile Gln Gln Leu His Pro Leu Gly Val Gly Ala Pro	85
	90
Ser Leu Gln Ser Tyr Trp Val Ser Leu Leu Gln Thr Ser Pro His Lys	95
145	100
Glu Ala Leu Ala Ile Ile Arg Asn His Phe Pro Arg Leu Ala Arg Cys	105
	110
Asp Phe Thr Thr Ile Ala Arg Lys Met His Ala Thr Thr Thr Glu Ile	115
	120
Leu Thr Phe Leu Arg His Ala Phe Ala Ser Ile Pro Trp Cys Pro Ala	125
	130
Ala Gly Phe Ser Glu Thr Leu His Pro Pro Ala Pro Ala Leu Pro Asp	135
	140
Ala Tyr Leu Ser Phe Ser Arg Asn Ser Ser Trp Asp Val Ser Ile Asn	145
	150
Lys Asp Cys Leu Pro Ser Ile Arg Leu Asn Asp Thr Val Leu Asp Ile	155
	160
Tyr Pro Ser Leu Pro Arg Glu Glu Lys Asp His Leu Ser Gln Gln Ile	165
	170
Arg Ala Ala Lys Gln Leu Leu Arg Asn Val Lys Lys Arg Glu Glu Thr	175
	180
Leu Leu Ala Ile Leu Arg Val Leu Ile Pro Tyr Gln Glu Glu Phe Leu	185
	190
	195
	200
	205
	210
	215
	220
	225
	230
	235
	240
	245
	250
	255
	260
	265
	270
	275
	280
	285
	290
	295
	300

Leu Lys Lys Arg Thr Ser Pro Lys Ala Phe Ser Val Lys Gln Ile Ala
 305 310 315 320
 Arg Glu Leu Ser Leu His Glu Ala Thr Val Cys Arg Ala Ile Asp Asn
 325 330 335
 Lys Thr Leu Ala Thr Pro Val Gly Leu Leu Pro Met Arg Ser Leu Phe
 340 345 350
 Pro Gln Ala Val Gly Ser Cys Pro Asp Gln Ser Lys Ala Thr Ile Leu
 355 360 365
 His Trp Ile His Gln Trp Ile Ser Thr Glu Lys His Pro Leu Ser Asp
 370 375 380
 Ala Ala Ile Ser Gln Lys Ile Ile Glu Lys Gly Ile Pro Cys Ala Arg
 385 390 395 400
 Arg Thr Val Ala Lys Tyr Arg Ser Gln Leu Asn Ile Pro Pro Ala His
 405 410 415
 Gln Arg Lys His Leu Cys Ser Val Leu Thr Thr Thr Arg Thr Glu Asn
 420 425 430
 Ser Arg His Thr Ile
 435

(2) INFORMATIONS POUR LA SEQ ID NO: 841:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 512 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(824359..825894)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 841:

Ala Xaa Leu Arg Lys Leu Asn Leu Asp Lys Lys Leu Cys Asn Ala Met
 1 5 10 15
 Gln Phe Thr Ile Ser Gln Ala Lys Asn Arg Leu Gln Ser Pro Glu Asp
 20 25 30
 Leu Asp Ser Lys Glu Tyr Pro Asp Pro Thr Arg Thr Val Tyr Ala Glu
 35 40 45
 Tyr Gln Glu Gln Leu Arg Ala Ala Asn Ala Leu Asp Phe Asp Asp Leu
 50 55 60
 Leu Phe Leu Thr Glu Lys Leu Leu Arg Ile Pro Glu Val Gln Gln Glu
 65 70 75 80
 Tyr Ala Asn His Trp Lys Ala Leu Leu Ile Asp Glu Tyr Gln Asp Thr
 85 90 95
 Asn His Ala Gln Tyr Leu Ile Ala Lys Arg Leu Ala Ala Ala His Asn
 100 105 110
 Asn Ile Phe Val Val Gly Asp Pro Asp Gln Ser Ile Tyr Ser Trp Arg
 115 120 125
 Gly Ala Asn Ile Ser Asn Ile Leu Asn Phe Glu Gln Asp Tyr Ser Gln
 130 135 140
 Ala Leu Val Val Arg Leu Glu Glu Asn Tyr Arg Ser Cys Gly Thr Ile
 145 150 155 160
 Leu Glu Ala Ala Asn Ala Leu Ile Gln Asn Asn Ser Ala Arg Leu Glu
 165 170 175
 Lys Thr Leu Arg Ser Val Lys Gly Pro Gly Asp Lys Ile Phe Cys Phe
 180 185 190
 Thr Gly Lys Asn Asp Arg Asp Glu Ala Glu Gln Val Leu Glu Glu Ile

195 200 205
 Ser Asn Leu His Ser Tyr Lys Asp Ile Pro Leu Ser Asp Ile Cys Ile
 210 215 220
 Leu Tyr Arg Thr Asn Phe Gln Ser Gln Ser Phe Glu Ala Ala Leu Leu
 225 230 235 240
 Lys Arg Gly Tyr Pro Tyr Glu Ile Ile Gly Gly Ile Ser Phe Tyr Lys
 245 250 255
 Arg Arg Glu Ile Gln Asp Ile Leu Ala Phe Leu Arg Leu Phe Ser Asn
 260 265 270
 Asn Tyr Asp Met Ala Ala Phe Glu Arg Thr Ile Ser Leu Lys Lys Cys
 275 280 285
 Gly Ile Gly Ala Thr Thr Leu Ala Ala Leu Met Asn Tyr Ala Lys Ile
 290 295 300
 Thr Asp Leu Pro Ile Leu Gln Ala Cys Trp Asp Val Leu Glu Lys Lys
 305 310 315 320
 Ser Ile Arg Leu Thr Lys Lys Gln Gln Gln Gly Leu Phe Ser Tyr Leu
 325 330 335
 Thr His Phe His Gln Met Glu Gln Leu Tyr Gly Asn Cys Asp Leu His
 340 345 350
 Glu Phe Ile Asn Glu Thr Ile Arg Ile Thr Asp Tyr Leu Ser Ile Leu
 355 360 365
 Lys Glu Asp Pro Glu Thr Tyr Glu Asp Arg Lys Asn Asn Leu Glu Gln
 370 375 380
 Leu Leu Ala Glu Thr Gln Ile Trp Gly Lys Ser Ser Glu Asn Leu Pro
 385 390 395 400
 Gly Phe Leu Glu Asp Leu Ala Leu Lys Ser Ser Ala Asp Glu Thr Ala
 405 410 415
 Ser Ser His Asp Arg Leu Lys Leu Met Thr Ile His Asn Ser Lys Gly
 420 425 430
 Leu Glu Phe Pro Val Val Phe Leu Val Gly Leu Glu Glu Asn Leu Leu
 435 440 445
 Pro His Ala Asn Ser Lys Gly Met His Glu Asn Ile Glu Glu Glu Arg
 450 455 460
 Arg Leu Cys Tyr Val Gly Ile Thr Arg Ala Gln Glu Tyr Leu Tyr Leu
 465 470 475 480
 Ser Arg Ala Lys Thr Arg Phe Leu Trp Gly Thr Glu Arg Thr Met Val
 485 490 495
 Pro Ser Arg Phe Ile Ser Glu Leu Pro Arg Ala Leu Leu Lys Phe Val
 500 505 510

(2) INFORMATIONS POUR LA SEQ ID NO: 842:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(825879..826259)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 842:

Met Leu Thr Ser Glu Leu Asn Ala Ala Gln Val Thr Ala Val Thr Ala
 1 5 10 15
 Pro Leu Gln Pro Val Leu Val Leu Ala Gly Ala Gly Ala Gly Lys Thr
 20 25 30

```

Arg Val Val Thr His Arg Ile Leu His Leu Ile Glu Glu Ser Arg Leu
   35           40           45
Asp Pro Lys Gln Ile Leu Ala Ile Thr Phe Thr Asn Lys Ala Ala Asn
   50           55           60
Glu Leu Lys Glu Arg Ile Gln Ser Gln Cys Arg Glu Leu Gly Tyr Ser
   65           70           75           80
Asp Val Pro Met Val Ser Thr Phe His Ser Leu Ser Val Tyr Ile Leu
           85           90           95
Arg Arg Ser Ile His Leu Leu Asp Arg Gln Ser Asn Phe Val Ile Tyr
           100          105          110
Asp Gln Ser Asp Ser Xaa Lys Leu Ile Lys Gln Xaa Tyr Ala Ser
           115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 843:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 229 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 826340..827026

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 843:

```

Met His Glu Ala Phe Thr Ile Glu Gln Leu Pro Pro Ser Trp Gln Glu
 1           5           10           15
Gln Leu Lys Asp Glu Trp Ser Gln Pro Tyr Trp Ser Gln Leu Leu Ala
           20           25           30
Phe Leu Lys Ser Glu Tyr Ala Gln Ala Lys Ile Tyr Pro Lys Lys Glu
           35           40           45
Asn Ile Phe Ala Ala Leu Arg Ser Thr Pro Phe Asp Gln Val Arg Val
           50           55           60
Val Ile Leu Gly Gln Asp Pro Tyr His Gly Glu Gly Gln Ala His Gly
           65           70           75           80
Leu Ser Phe Ser Val Pro Arg Gly Gln Ala Leu Pro Pro Ser Leu Arg
           85           90           95
Asn Ile Phe Gln Glu Leu His Thr Asp Leu Gly Ile Arg Asn Glu Ser
           100          105          110
Gly Cys Leu Gln Ala Trp Ala Asp Gln Gly Val Leu Leu Leu Asn Thr
           115          120          125
Val Leu Thr Val Arg Ala Gly Glu Ala Phe Ser His Ala Gly Arg Gly
           130          135          140
Trp Glu Arg Phe Thr Asp Ala Ile Val Thr Lys Leu Ile Gln Asn Arg
           145          150          155          160
Thr His Val Ile Phe Val Leu Trp Gly Asn Ala Ala Arg Gln Lys Cys
           165          170          175
Asn Leu Leu Phe Gln Thr Lys His Gln His Ala Val Leu Ala Cys Pro
           180          185          190
His Pro Ser Pro Leu Ala Ala His Arg Gly Phe Phe Gly Cys Cys His
           195          200          205
Phe Ser Lys Ile Asn Tyr Leu Leu Lys Lys Gln Gly Lys Thr Met Ile
           210          215          220
Asn Trp Lys Ile Glu
225

```

(2) INFORMATIONS POUR LA SEQ ID NO: 844:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 79 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 827014..827250

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 844:

```

Leu Glu Asp Arg Met Ile Asp Gly Ile Gln Thr Cys Ser Phe Ser Pro
1          5          10          15
Thr His Arg Leu Thr Ala Lys Ser Ala Val Ser Ile Glu Met Pro Leu
          20          25          30
Ala Thr Gln Asn Leu Gln Glu Gly Ala Leu Val Asn Ala Lys Leu Glu
          35          40          45
Ala Asp Phe Ala Arg Ala Glu Gln Ile Leu Thr Glu Met Gln Glu Ile
          50          55          60
Arg Ser Ser Leu Glu Arg Ser Leu Glu Thr Leu Phe Pro Arg Glu
65          70          75

```

(2) INFORMATIONS POUR LA SEQ ID NO: 845:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 209 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(827230..827856)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 845:

```

Met Lys Ile Leu Ile Ala Ser Ser His Gly Tyr Lys Val Arg Glu Thr
1          5          10          15
Lys Ala Phe Leu Lys Lys Leu Gly Glu Phe Asp Ile Phe Ser Leu Val
          20          25          30
Asp Tyr Pro Ser Tyr Gln Pro Pro Lys Glu Thr Gly Glu Thr Pro Glu
          35          40          45
Glu Asn Ala Ile Gln Lys Gly Leu Phe Ala Ala Gln Thr Phe Arg Cys
          50          55          60
Trp Thr Ile Ala Asp Asp Ser Met Leu Ile Ile Pro Ala Leu Gly Gly
65          70          75          80
Leu Pro Gly Lys Leu Ser Ala Ser Phe Ala Gly Glu Gln Ala Asn Asp
          85          90          95
Lys Asp His Arg Lys Lys Leu Leu Glu Asn Met Arg Leu Leu Glu Asn
          100          105          110
Thr Ile Asp Arg Ser Ala Tyr Phe Glu Cys Cys Val Ala Leu Ile Ser
          115          120          125
Pro Phe Gly Lys Ile Phe Lys Ala His Ala Ser Cys Glu Gly Thr Ile
          130          135          140

```

Ala Phe Glu Glu Arg Gly Ser Ser Gly Phe Gly Tyr Asp Pro Leu Phe
 145 150 155 160
 Val Lys His Asp Tyr Lys Gln Thr Tyr Ala Glu Leu Pro Glu Ala Ile
 165 170 175
 Lys Asn Gln Val Ser His Arg Ala Lys Ala Leu Val Lys Leu Gln Pro
 180 185 190
 Tyr Val Glu Thr Val Leu Ala Asn His Leu Leu Ala Gly Lys Glu Ser
 195 200 205
 Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 846:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 828007..829275

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 846:

Arg Lys Ile Arg Phe Pro Leu Ser Lys Arg Asp Pro Lys Glu Ile Met
 1 5 10 15
 Lys Thr Ile Cys Lys Leu Val Ile Leu Ala Leu Leu Phe Pro Asn Val
 20 25 30
 Ser Tyr Ala Leu Val Gln Val Gly Leu Glu Arg Leu Phe Gln Glu Glu
 35 40 45
 Lys Tyr Leu Glu Lys Ile Arg Gly Lys Arg Val Ala Leu Ile Ser His
 50 55 60
 Ser Ala Ala Ile Asn Arg Gln Gly Glu His Ser Leu Cys Val Phe Asn
 65 70 75 80
 Lys His Lys Gly Val Cys Lys Leu Ser Ala Leu Cys Thr Leu Glu His
 85 90 95
 Gly Tyr Phe Gly Ala Ser Ile Ala Glu Thr Pro Gly Tyr Asp Pro Ile
 100 105 110
 Leu Glu Asp Ile Pro Val Ile Ser Leu Phe Ala Ser Lys Glu Ile Pro
 115 120 125
 Ala Glu Val Ile Glu Ala Cys Asp Val Phe Val Tyr Asp Val Gln Asp
 130 135 140
 Ile Gly Val Arg Ser Tyr Ser Phe Ile Ser Ala Leu Leu Gln Val Val
 145 150 155 160
 Lys Ala Ser Ala Ser Lys Lys Glu Leu Ile Val Leu Asp Arg Pro
 165 170 175
 Asn Pro Met Gly Gly Asn Leu Val Asp Gly Pro Leu Pro Asp Lys Glu
 180 185 190
 Ala Phe Pro Ala Ile Pro Tyr Cys Tyr Gly Met Thr Pro Gly Glu Leu
 195 200 205
 Ala Leu Leu Tyr Arg Ala Arg Tyr Ala Pro Lys Ala Ser Val Thr Val
 210 215 220
 Val Pro Met Arg Gly Trp Lys Arg Ser Met Ile Phe Ala Asp Thr Gly
 225 230 235 240
 Leu Ile Trp Val Pro Thr Ser Pro Gln Ile Pro Asp Ala Gln Ser Ala
 245 250 255
 Tyr Phe Tyr Ala Thr Thr Gly Ile Ile Gly Ala Leu Ser Val Thr Asn

```

                260                265                270
Ile Gly Ile Gly Tyr Thr Leu Pro Phe Lys Val Leu Gly Ala Pro Trp
                275                280                285
Met Asp Gly Cys Lys Val Ala Gln Glu Leu Asn Lys Ala Arg Leu Pro
                290                295                300
Gly Val His Phe Leu Pro Phe Met Tyr Glu Pro Phe Phe Gly Lys Phe
305                310                315                320
Lys Met Glu Met Cys Ser Gly Val Leu Val Val Leu Gln Asp Pro Lys
                325                330                335
Gln Phe Leu Pro Met Glu Thr Gln Ser Val Ile Leu Gly Val Leu Lys
                340                345                350
Thr Leu Tyr Pro Lys Glu Val Glu Gln Ala Phe Leu Leu Leu Asp Arg
                355                360                365
Leu Val Pro Arg Arg Lys Ala Ile Gln Asn Leu Leu Gly His Ser Glu
                370                375                380
Phe Leu Asn Val Cys Leu His Lys Lys Tyr Ile Thr Trp Pro Leu Arg
385                390                395                400
Thr Met Cys Ala Glu Gly Arg Lys Gln Phe Ile Glu Gln Arg Gln Pro
                405                410                415
Phe Leu Leu Pro Glu Tyr Ala
                420

```

(2) INFORMATIONS POUR LA SEQ ID NO: 847:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 533 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 829355..830953

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 847:

```

Gly Leu Ser Asn Ser Phe Arg Asp Gln Glu Gln Gly Leu Gln Ala Val
1      5      10      15
Leu Arg Ala Ala Arg Val Ile Ser His Met Phe Ser Gln Thr Ile Gly
20      25      30
Pro Tyr Gly Phe Ser Thr Ile Val His Asn Val Gln Asp Thr Arg Thr
35      40      45
Thr Gln Asp Ser Gln Ser Met Leu Lys Asp Ile Leu Phe Pro Asp Val
50      55      60
Phe Glu Asn Ile Gly Met Lys Leu Ile Arg Asp Thr Ala Leu Gly Thr
65      70      75      80
Arg Met Arg Phe Gly Asp Gly Ala Lys Thr Thr Ala Leu Leu Ile Glu
85      90      95
Ala Leu Leu Ala Glu Gly Met Thr Gly Ile Gln Lys Gly Leu Asp Pro
100     105     110
His Glu Ile His Arg Gly Met Leu Leu Ala Glu Lys Lys Ile Gln Glu
115     120     125
Val Phe Tyr Arg Glu Thr Phe Pro Leu Ser Asp Leu Glu His Thr Val
130     135     140
Tyr Val Ser Ser Ile Ala Arg Arg Phe Asn Ser Glu Ile Ala Ser Val
145     150     155     160
Leu Ser Ser Ala Val Gly Tyr Gly Gly Lys Asn Gly Tyr Tyr Ile Val
165     170     175

```

```

Glu Glu His Glu Glu Ser Glu Thr Tyr Trp His Ala Glu Glu His Ala
      180      185      190
Val Trp Asp Phe Gly Tyr Ala Ser Pro Tyr Phe Ile Thr His Ala Glu
      195      200      205
Thr Gly Thr Val Glu Tyr Ser Gln Val Tyr Ile Leu Val Ser Glu His
      210      215      220
Pro Leu His Tyr Ser Asn Pro Ser Phe Leu Thr Phe Leu Gln Ser Val
      225      230      235      240
Val Gln Ala Gly Lys Thr Pro Leu Val Ile Val Ala Glu Ala Phe Asp
      245      250      255
Lys Glu Leu Leu Ala Met Leu Glu Met Asn Gln Ile Glu Arg Val Phe
      260      265      270
Pro Val Cys Ala Val Lys Val Ser Gly Lys His Ala Arg Glu Ser Leu
      275      280      285
Glu Asp Ile Ala Val Leu Thr Gly Ala Thr Leu Leu Pro Glu Met Asp
      290      295      300
Phe Glu Asp Ser Glu Glu Glu Arg Ile Ala Asn Arg Leu Gly Phe Val
      305      310      315      320
Ala Gly Ile Cys Val Ser Ser Thr Ser Leu Cys Val Pro Arg Glu Thr
      325      330      335
Asp Asn Lys Gln Arg Val Ala Glu His Cys Ala Phe Leu Gln Asp Lys
      340      345      350
Leu Ser Phe His Arg Lys Lys Ser Ala Arg Leu Arg Arg Arg Leu
      355      360      365
Ala Arg Leu Ser Thr Gly Glu Val Cys Ile His Ile Ala Ala Asp Cys
      370      375      380
Ile Pro Gln Glu Glu Ile Gly Tyr Ile Thr Ser Ser Ile Arg Ala Met
      385      390      395      400
Thr Glu Ser Leu Arg Ser Gly Cys Leu Pro Gly Gly Gly Cys Ala Phe
      405      410      415
Ile Arg Ala Ala Arg Glu Ile Ser Val Pro Leu Ala Leu Ser Pro Ser
      420      425      430
Glu Arg Phe Gly Phe Leu Ala Val Leu Ser Ala Ala Glu Lys Pro Phe
      435      440      445
Arg Ala Ile Val Thr Arg Ser Gly Arg Val Glu Glu Glu Val Phe Ser
      450      455      460
Glu Val Phe Ser Gln Ala Asp Trp Arg Val Gly Phe Asn Gly Val Ser
      465      470      475      480
Gly Phe Val Glu Asp Ile Val Ser Gln Gly Ile Cys Asp Gly Ala Ser
      485      490      495
Cys Ile Gln His Ala Leu Ser His Ala Val Gly Thr Thr Gly Leu Leu
      500      505      510
Leu Thr Ser Ala Leu Phe Ile Ala Ser Gln Glu Pro Met Leu Arg Glu
      515      520      525
Glu Asn Ser Glu Glu
      530

```

(2) INFORMATIONS POUR LA SEQ ID NO: 848:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 210 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 831119..831748

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 848:

```

Val Gln Ile Leu Ser Gly Ala Leu Phe Leu Ser Arg Arg Ser Thr Met
1      5      10      15
Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys Ala Val
20      25      30
Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg Gly Lys
35      40      45
Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val Cys Pro
50      55      60
Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu Glu His
65      70      75      80
Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr His Ser
85      90      95
Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly Thr Glu
100     105     110
Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe Gly
115     120     125
Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu Ile
130     135     140
Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro Leu
145     150     155     160
Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu Ile Phe
165     170     175
Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser Gly Glu
180     185     190
Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe Gln Thr
195     200     205
Met Asp
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 849:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 134 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(831751..832152)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 849:

```

Leu Ala Cys Gly Met Lys Phe Thr Val Ala Val Phe Gly Glu Ala Glu
1      5      10      15
Glu Gly Ser Phe Glu Ser Ala Tyr Leu Cys Ser Ser Leu Thr Asp Leu
20      25      30
His Asn Asn Leu Gly His Gly Arg Asp Ser Pro Ser Gly Ile Ser Leu
35      40      45
Ala Val Gln Ala Ile Met Gln Gly Tyr Asp Ile Leu Phe Phe Arg Val
50      55      60
Lys Glu Glu Gly Phe Phe Ile Asp Ser Tyr Phe Phe Gly Leu His Phe
65      70      75      80
Leu Asn Thr Gln Thr Ser Leu Thr Asn Ile Val Ala Leu Ala Leu Pro
85      90      95

```


Gly Val Gly Asp Phe Asn Ile Ile Glu Ala Ser Leu Ala Leu Cys Arg
 100 105 110
 Lys Leu Lys Ser Leu Leu Leu Phe Ser Asp Gln Asp Leu Tyr Asp Phe
 115 120 125
 Leu Thr Phe Lys Asp Ala
 130

(2) INFORMATIONS POUR LA SEQ ID NO: 850:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(832214..832744)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 850:

Ser Ala Val Phe Ala Gly Tyr Ser Ser Arg Ser Arg Arg Thr Ser Ser
 1 5 10 15
 Arg Leu His Ala His His Asn Glu Leu Ala Met Ile Ser Glu Arg Leu
 20 25 30
 Asp Glu Gln Asp Thr Lys Leu Gln Gln Leu Ser Ser Thr Gln Asp His
 35 40 45
 Asn Leu Pro Arg Gln Val Gln Arg Leu Glu Thr Asp Gln Lys Ala Leu
 50 55 60
 Ala Lys Thr Leu Ala Ile Leu Ser Gln Ser Val Gln Asp Ile Arg Ser
 65 70 75 80
 Ser Val Gln Asn Lys Leu Gln Glu Ile Gln Gln Glu Gln Lys Lys Leu
 85 90 95
 Ala Gln Asn Leu Arg Ala Leu Arg Asn Ser Leu Gln Ala Leu Val Asp
 100 105 110
 Gly Ser Ser Pro Glu Asn Tyr Ile Asp Phe Leu Ala Gly Glu Thr Pro
 115 120 125
 Glu His Ile His Ile Val Lys Gln Gly Glu Thr Leu Ser Lys Ile Ala
 130 135 140
 Ser Lys Tyr Asn Ile Pro Val Val Glu Leu Lys Lys Leu Asn Lys Leu
 145 150 155 160
 Asn Ser Asp Thr Ile Phe Thr Asp Gln Arg Ile Arg Leu Pro Lys Lys
 165 170 175
 Lys

(2) INFORMATIONS POUR LA SEQ ID NO: 851:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(832805..833446)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 851:

```

Glu Asn Cys Tyr Arg Ile Trp Arg Glu Thr Phe Pro Met Leu Gly Ser
1      5      10      15
Ile Ser Phe Thr Thr Tyr Lys Glu Asn Leu Met Arg Lys Thr Ile Phe
20      25      30
Lys Ala Phe Asn Leu Leu Phe Ser Leu Leu Phe Leu Ser Ser Cys Ser
35      40      45
Tyr Pro Cys Arg Asp Trp Glu Cys His Gly Cys Asp Ser Ala Arg Pro
50      55      60
Arg Lys Ser Ser Phe Gly Phe Val Pro Phe Tyr Ser Asp Glu Glu Ile
65      70      75      80
Gln Gln Ala Phe Val Glu Asp Phe Asp Ser Lys Glu Glu Gln Leu Tyr
85      90      95
Lys Thr Ser Ala Gln Ser Thr Ser Phe Arg Asn Ile Thr Phe Ala Thr
100     105     110
Asp Ser Tyr Ser Ile Lys Gly Glu Asp Asn Leu Thr Ile Leu Ala Ser
115     120     125
Leu Val Arg His Leu His Lys Ser Pro Lys Ala Thr Leu Tyr Ile Glu
130     135     140
Gly His Thr Asp Glu Arg Gly Ala Ala Ala Tyr Asn Leu Ala Leu Gly
145     150     155     160
Ala Arg Arg Ala Asn Ala Val Lys Gln Tyr Leu Ile Lys Gln Gly Ile
165     170     175
Ala Ala Asp Arg Leu Phe Thr Ile Ser Tyr Gly Lys Glu His Pro Val
180     185     190
His Pro Gly His Asn Glu Leu Ala Trp Gln Gln Asn Arg Arg Thr Glu
195     200     205
Phe Lys Ile His Ala Arg
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 852:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 145 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(833368..833802)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 852:

```

Pro Asp Gly Thr Arg Leu Val Phe Val Ser Asn Lys Asp Gly Thr Pro
1      5      10      15
Arg Ile Tyr Gln Met Gln Ile Ser Pro Glu Gln His Ser Pro Arg Leu
20      25      30
Leu Thr Lys Lys Tyr Arg Asn Ser Ser Cys Pro Thr Trp Ser Pro Asp
35      40      45
Gly Lys Lys Ile Ala Phe Cys Ser Val Ile Lys Gly Val Arg Gln Ile
50      55      60
Cys Val Tyr Asp Leu Ala Ser Gly Arg Asp Glu Gln Leu Thr Thr Ser
65      70      75      80
Thr Glu His Lys Glu Ser Pro Ser Trp Ala Ala Asp Ser Asn His Leu
85      90      95

```

Val Tyr Ser Ala Gly Ser Ser Asn Thr Ser Glu Leu Phe Leu Leu Ser
 100 105 110
 Leu Ile Thr Lys Lys Ser Arg Lys Ile Val Ile Gly Ser Gly Glu Lys
 115 120 125
 Arg Phe Pro Cys Trp Gly Ala Phe Pro Ser Gln His Ile Lys Lys Thr
 130 135 140
 Ser
 145

(2) INFORMATIONS POUR LA SEQ ID NO: 853:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(833879..834679)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 853:

Thr Ala Gly Lys Phe Cys Leu Met Lys Gly Ser Val Val Phe Leu Arg
 1 5 10 15
 Ser Leu Leu Cys Leu Leu Cys Leu Leu Pro Ser Thr Leu His Cys Glu
 20 25 30
 Asp Leu Glu Ile His Val Arg Ser Glu Ser Ser Leu Leu Pro Ile Ala
 35 40 45
 Val Ser Leu Leu Ser Ser Pro Lys Asp Ser Arg Gln Ala Ser Tyr Leu
 50 55 60
 Ala Ser Leu Arg Asp Leu Phe Ala Arg Asp Leu Ala Leu Gly Asp Leu
 65 70 75 80
 Leu Ala Pro Thr Lys Glu Leu Ala Pro Gln Thr Ile Phe Ile Glu Ala
 85 90 95
 Ser Tyr Pro Glu Leu Ile Phe Ser Leu Lys Lys Glu Gly Lys Gly Ser
 100 105 110
 Gln Lys Ile Phe Ser Leu Glu Leu Ser Gly Asp Pro Ser Lys Asp His
 115 120 125
 Gln Ala Ile His Glu Ala Ala Asp Arg Ile His Phe Leu Leu Thr Arg
 130 135 140
 Val Pro Gly Ile Ser Ser Gly Lys Ile Ile Phe Ser Leu Cys Ala Thr
 145 150 155 160
 Asn Ser Ser Thr Glu Leu Lys Gln Gly Glu Leu Trp Ser Val Asp Tyr
 165 170 175
 Asp Gly Gln His Leu Tyr Pro Leu Thr Asn Glu His Ser Leu Ser Val
 180 185 190
 Thr Pro Thr Trp Met His Ile Ser His Ile Pro Ala Tyr Met Tyr Val
 195 200 205
 Ser Tyr Lys Leu Gly Val Pro Lys Ile Phe Leu Asn Thr Leu Asn Gln
 210 215 220
 Pro Ala Gly Lys Lys Ser Leu Leu Cys Lys Gly Ile Ser Leu Cys Arg
 225 230 235 240
 Leu Ser Leu Leu Lys Leu Asn Ser Ser Pro Leu Phe Leu Ile Glu Thr
 245 250 255
 Ala Ile Leu Ile Phe Leu Tyr Asn His Ser His
 260 265

(2) INFORMATIONS POUR LA SEQ ID NO: 854:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 264 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(834661..835452)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 854:

Tyr Ser Phe Gln Thr Val Ser Arg Asp Gln Ile Asp Tyr Arg Arg Ser
 1 5 10 15
 Arg Ile Ser Gly Thr Ser Tyr Cys Phe Glu Glu Leu Thr Met Pro Lys
 20 25 30
 Phe Gln Tyr Ala Pro Phe Leu Cys Ala Ser Ile Ile Ile His Ile Ala
 35 40 45
 Leu Gly Gly Met Leu Phe Phe Ser Ala Pro Gln Lys Lys Lys Pro Arg
 50 55 60
 Leu Ser Pro Phe Lys Glu Arg Ile Val Ala Leu Pro Pro Glu Pro Lys
 65 70 75 80
 Ile Thr Thr Thr Leu Gln Thr Pro Ser Pro Gln Pro Ile Arg Lys Pro
 85 90 95
 Val Lys Asn Ala Pro Ala Pro Glu Lys Lys Ala Ala Lys Pro Pro Ala
 100 105 110
 Ile Ser Asn Pro Gln Lys Ser Pro Gln Lys Pro Asn Lys Ala Ser Pro
 115 120 125
 Thr Pro Arg Asn Glu Thr Leu Glu Lys Lys Gln Ala Thr Leu Lys Lys
 130 135 140
 Leu Ala Gln Leu Ala Asn Gln Leu Ala Glu Glu Ala Glu Thr Gln Glu
 145 150 155 160
 Ser His Ile Ala Gln Phe Ser Trp Pro Ala Gln Ala Gln Val Leu Thr
 165 170 175
 Glu Asn Thr Ser Tyr Gln Gln Asp Ala Phe Cys Ala Leu Phe Gln Gln
 180 185 190
 Tyr Val Ser Leu Pro Phe Pro Gly Glu Val Arg Leu Lys Leu Glu Phe
 195 200 205
 Ser Arg Glu Gly Ala Leu Leu His Cys Ser Ile Leu Ser Thr Ile Ser
 210 215 220
 His Ala Asp Lys Gln His Ile Leu Asn Gln Ile Gln Lys Ile Pro Phe
 225 230 235 240
 Gln Ser Phe Phe Ser Ala Tyr Lys Thr Ser Lys Asn Ile Val Phe His
 245 250 255
 Ile Arg Leu Gln Gly Asn Ser Ala
 260

(2) INFORMATIONS POUR LA SEQ ID NO: 855:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 136 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(835371..835778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 855:

```

Leu Met Lys Arg Phe Val Tyr Glu Asp Leu Glu Glu Asp Pro Ser Val
1           5           10           15
Asn Leu Thr Pro Leu Ile Asp Ile Val Phe Val Ile Leu Met Ala Phe
          20           25           30
Met Ile Ala Met Pro Leu Ile Lys Ile Asp Arg Ile Ser Leu Ala Thr
          35           40           45
Gly Ser Ser Ser His Gln Ala Phe Lys Lys Gln Glu Ser Gln Gln Ala
          50           55           60
Glu Ile Lys Val Phe Arg Asn His Thr Ile Thr Leu Asn Asp Leu Pro
65           70           75           80
Val Ser Leu Gln Glu Leu Arg Ser Gln Leu Thr Val Ile His Ala Gln
          85           90           95
His Pro Asn Ile Val Pro Leu Leu Leu Gln Asp Gly Asp Thr Ala Phe
          100          105          110
Lys Leu Tyr Gln Glu Ile Lys Ser Thr Ile Glu Glu Ala Gly Phe Gln
          115          120          125
Glu Leu His Ile Ala Leu Lys Asn
          130          135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 856:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(835775..836482)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 856:

```

Val Tyr Val Leu Met Phe Gln Leu Val Asn Asn Pro Ile Ile Gln Ser
1           5           10           15
Phe Gln Glu Ala Asp Leu Phe Gly Lys Val Ile Phe Phe Ser Leu Phe
          20           25           30
Ala Leu Ser Ile Cys Thr Trp Thr Val Leu His Gln Lys Leu Ser Ile
          35           40           45
Gln Lys Lys Lys Phe Leu Lys Ser Gly Lys Ser Leu Lys Glu Phe Leu Ile
          50           55           60
Lys Asn Arg His Ser Pro Leu Ser Leu Asp Ile His Pro Glu Ser Thr
65           70           75           80
Pro Phe Thr Asp Leu Tyr Phe Thr Ile Lys Arg Gly Thr Leu Glu Leu
          85           90           95
Leu Asp Lys Asn Arg Gln Leu Ala Pro Glu Arg Thr Pro Leu Leu Ser
          100          105          110
Val Glu Asp Ile Gln Ser Leu Glu Thr Leu Phe Asn Ala Val Met Pro
          115          120          125
Lys Tyr Arg Ala Leu Leu Asn Lys Asn Asn Phe Ile Pro Ala Thr Thr
          130          135          140
Ile Ser Leu Ala Pro Phe Leu Gly Leu Leu Gly Thr Val Trp Gly Ile

```

(2) INFORMATION POUR LA SEQ ID NO: 857:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 221 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 836602..837264

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 857:

(2) INFORMATION POUR LA SEQ ID NO: 858:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 497 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 837209..838699

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 858:

```

Met Phe Leu Cys Gln Gln Gly Lys Ala Asp Arg Ala Thr Gln Ala Trp
1      5      10      15
Phe Ile Ala Glu Asn Thr Arg Asp Phe Ala Tyr Ala Gln Glu Val Pro
20     25     30
Leu Glu Gln Ala Thr Thr Tyr Ile Trp Lys Leu Lys His Pro Glu Gly
35     40     45
Asn Met Pro Lys Gly Val Gly Leu Ser Arg Ile Leu Ile Phe Lys Asp
50     55     60
Asp Ala Gly Lys Val Val Ala Ser Tyr Gln Val Glu Xaa Asn Gln Val
65     70     75     80
Glu Gln Leu Ser Ala Leu Ser Trp Gly Phe Leu Ser Ile Leu Leu Met
85     90     95
Ala Phe Ile Gly Gly Ile Leu Leu Asn Ile Met Pro Cys Val Leu Pro
100    105    110
Leu Ile Thr Leu Lys Val Phe Ser Leu Ile Lys Ser Ala Ala Asp His
115    120    125
His Ser Ser Ser Val Ile Gly Gly Ile Trp Phe Thr Leu Gly Ala Ile
130    135    140
Val Ser Phe Trp Gly Leu Ala Phe Cys Ala Phe Leu Leu Lys Val Leu
145    150    155    160
Gly Gln Asn Ile Gly Trp Gly Phe Gln Leu Gln Glu Pro Met Phe Val
165    170    175
Ala Val Leu Ile Ile Val Phe Phe Leu Phe Ala Leu Ser Ser Leu Gly
180    185    190
Val Phe Glu Met Gly Met Ile Cys Leu Ser Leu Gly Glu Lys Leu Gln
195    200    205
Glu Glu Gly Gly Ala Ser Val Arg Lys Asn Gln Ile Trp Gly Ala Phe
210    215    220
Phe Asn Gly Met Leu Thr Thr Leu Val Thr Thr Pro Cys Thr Gly Pro
225    230    235    240
Phe Leu Gly Ser Val Phe Gly Leu Val Met Ala Val Ser Phe Val Lys
245    250    255
Gln Leu Ala Ile Phe Thr Ala Ile Gly Leu Gly Met Ala Ser Pro Tyr
260    265    270
Leu Leu Phe Ala Ser Phe Pro Lys Met Leu Ala Ile Leu Pro Lys Pro
275    280    285
Gly Pro Trp Met Ser Thr Phe Lys Gln Leu Thr Gly Phe Met Leu Leu
290    295    300
Ala Thr Ala Thr Trp Leu Ile Trp Ile Phe Gly Val Glu Thr Ser Ala
305    310    315    320
Thr Ala Val Thr Ile Leu Leu Val Gly Leu Trp Leu Ala Ala Val Gly
325    330    335
Ala Trp Ile Leu Gly Arg Trp Gly Thr Leu Val Ser Pro Arg Asn Gln
340    345    350
Arg Leu Leu Ala Ser Val Val Phe Ile Phe Cys Ile Leu Ser Ser Leu
355    360    365
Val Ile Thr Ser Ile Gly Val Arg Tyr Phe Asp Glu Asn Val Pro Pro

```

370 375 380
 Ala His Ser Phe Asp Trp Gln Ser Phe Ser Pro Glu Lys Leu Ala Asp
 385 390 395 400
 Leu Arg Glu Lys Gly Ile Pro Val Phe Val Asn Phe Thr Ala Lys Trp
 405 410 415
 Cys Leu Thr Cys Gln Leu Asn Lys Pro Leu Leu His Ala Asn Met Gln
 420 425 430
 Ala Phe Ala Ala Lys Gly Val Val Thr Leu Glu Ala Asp Trp Thr Lys
 435 440 445
 Lys Asp Pro Lys Ile Thr Glu Leu Ala Arg Leu Gly Arg Ala Ser
 450 455 460
 Val Pro Ser Tyr Val Tyr Tyr Pro Ala Gly Asn Lys Ala Pro Leu Ile
 465 470 475 480
 Leu Pro Glu Arg Leu Ser Gln Ser Ala Leu Glu Glu Met Val Phe Ser
 485 490 495
 Gln

(2) INFORMATIONS POUR LA SEQ ID NO: 859:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 272 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 838760..839575

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 859:

Leu Arg Lys Ile Asp Tyr Glu Gly Ser Met Glu Ile Val Asp Ala His
 1 5 10 15
 Val His Leu Ser Ser Glu Glu Phe Ile Glu Asp Phe Gly Asp Val Val
 20 25 30
 Leu Arg Gly Lys Thr Ala Gly Val Thr Arg Val Val Asn Val Thr Thr
 35 40 45
 Thr Lys Ala Glu Leu Leu Arg Ser Phe Ala Tyr Ala Glu Ala Tyr Pro
 50 55 60
 Asp Trp Met Phe Tyr His Val Ala Gly Thr Pro Pro Gln Asp Ala Gln
 65 70 75 80
 Asp Asp Ile Glu Glu Asp Phe Gln Glu Phe Cys Arg Ala Ala Glu Asp
 85 90 95
 Gly Lys Leu Ala Ala Ile Gly Glu Val Gly Leu Asp Tyr Leu Phe Ala
 100 105 110
 Val Gln Ala Ser Glu Gln Glu Arg Gln Lys Glu Val Leu Cys Arg Tyr
 115 120 125
 Leu Gln Leu Ala Leu Gln His Glu Leu Pro Leu Val Val His Cys Arg
 130 135 140
 Gly Ala Phe Glu Asp Phe Phe His Ile Leu Asp His Val Tyr Arg Val
 145 150 155 160
 Asp Gln Arg Ala Lys Pro Gly Met Leu His Cys Phe Thr Gly Thr Tyr
 165 170 175
 Glu Glu Ala Thr Glu Leu Leu Ala Arg Asp Trp Tyr Ile Ser Ile Ser
 180 185 190
 Gly Ile Val Thr Phe Lys Asn Ala Lys Ser Leu Gln Asp Leu Val Glu
 195 200 205


```

Lys Ile Pro Leu Glu Arg Leu Leu Val Glu Thr Asp Ala Pro Tyr Leu
 210                215                220
Ala Pro Thr Pro Leu Arg Gly Lys Arg Asn Glu Pro Ala Asn Ile Val
225                230                235                240
His Thr Leu Ala Arg Ile Ala Glu Ile Lys Gly Ile Ser Val Tyr Glu
                245                250                255
Leu Gln Asp Ala Val Ser Thr Asn Val Gln Arg Trp Leu Arg Gly Ser
                260                265                270

```

(2) INFORMATIONS POUR LA SEQ ID NO: 860:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 839942..840583

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 860:

```

Leu Phe Arg Leu Val Phe Ile Pro Ser Ser Asp Leu Ala Ile Phe Phe
 1                5                10                15
Glu Gly Glu Arg Ile Phe Ser Leu Gln Met Glu Glu His Leu Arg Tyr
                20                25                30
Gly Arg Asn Leu Ala Tyr Thr Leu Gln Arg Met Thr Ala Trp Ile Leu
                35                40                45
Leu Ala Gly Leu Ala Phe His Val Ile Gln Phe Arg Phe Val Leu Tyr
 50                55                60
Pro Ile Gln Val Thr Ile Gln Gly Lys Thr Phe Tyr Ala Val Ser Phe
65                70                75                80
Asp Ala Ala Arg Tyr Pro Ser Val Val Gln Gly Thr Thr Gly Phe Phe
                85                90                95
Ile Met Asn Val Pro Phe Ala Glu Gly Gly Pro Gln Ile Thr Glu Gln
                100                105                110
Phe Leu Gln Glu Lys Asp Arg Ala Leu Phe Ala Ser His Lys Ser Tyr
                115                120                125
Ile Phe Thr Pro Glu Ala Arg Lys Ala Phe Leu Tyr Ala Val Arg Asn
130                135                140
Ala Leu Gly Ser Leu Trp Met Ala Ile Phe Tyr Thr Leu Phe Val Ile
145                150                155                160
Ala Ala Val Phe His Gly Phe Asn Gly Val Trp Thr Phe Val Ser Arg
                165                170                175
Trp Gly Ile Ile Ile Ser Ser Arg Tyr Leu Arg Leu Cys Gln Ile Leu
                180                185                190
Cys Tyr Val Gly Met Cys Val Val Met Ala Met Gly Ile Ser Val Ile
                195                200                205
Trp Asn Met Tyr Leu Leu
                210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 861:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 423 acides aminés

(B) TYPE: acide aminé

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 861:

(X1) DESCRIPTION

Trp	Ser	Met	Asp	Val	Cys	Leu	Ala	Met	Gly	Asn	His	Tyr	Leu	Phe	Pro
1				5					10					15	
Leu	Ser	Pro	Ile	Met	Ser	Asp	Leu	Met	Leu	Arg	Arg	Asp	Val	Cys	Cys
			20					25					30		
Asp	Gly	Tyr	Gly	Tyr	Gln	Arg	Asn	Leu	Glu	Tyr	Val	Phe	Val	Met	Met
			35				40					45			
Asn	Gln	Arg	Cys	Arg	Val	Ile	Ile	Ile	Gly	Gly	Gly	Leu	Ala	Gly	Leu
			50			55				60					
Ser	Ala	Ala	Met	Gln	Leu	Ala	Asp	Arg	Gly	Ile	Leu	Val	Glu	Leu	Phe
65				70					75						80
Ser	Leu	Thr	Lys	Val	Lys	Arg	Ser	His	Ser	Val	Cys	Ala	Gln	Gly	Gly
			85						90					95	
Ile	Asn	Ala	Ala	Leu	Asn	Leu	Lys	Gly	Glu	Asn	Asp	Ser	Pro	Tyr	Ile
			100					105					110		
His	Ala	Tyr	Asp	Thr	Ile	Lys	Gly	Gly	Asp	Phe	Leu	Ala	Asp	Gln	Pro
			115				120						125		
Pro	Val	Leu	Glu	Met	Cys	Leu	Thr	Ala	Ser	Arg	Ile	Ile	His	Met	Leu
			130			135					140				
Asp	Arg	Phe	Gly	Cys	Pro	Phe	Asn	Arg	Asp	Ala	Asp	Gly	Asn	Leu	Asp
145				150					155						160
Val	Arg	Arg	Phe	Gly	Gly	Thr	Leu	Tyr	His	Arg	Thr	Val	Phe	Cys	Gly
			165						170					175	
Ala	Ser	Thr	Gly	Gln	Gln	Leu	Met	Tyr	Thr	Met	Asp	Glu	Gln	Val	Arg
			180					185					190		
Arg	Arg	Glu	Trp	Gln	Gly	Lys	Ile	Ile	Lys	Arg	Glu	Asn	His	Glu	Phe
			195				200					205			
Val	Arg	Leu	Ile	Thr	Asn	Thr	Glu	Gly	Arg	Ala	Cys	Gly	Val	Val	Val
			210			215					220				
Met	Asn	Leu	Phe	Asn	His	Arg	Leu	Glu	Val	Ile	Gln	Gly	Asp	Ala	Val
225				230					235						240
Ile	Ile	Ala	Thr	Gly	Gly	Leu	Gly	Val	Ile	Phe	Gln	Met	Ser	Thr	Asn
			245						250				255		
Ser	Thr	Ile	Cys	Thr	Gly	Ala	Ala	Asn	Gly	Arg	Leu	Phe	Met	Gln	Gly
			260					265					270		
Met	His	Tyr	Ala	Asn	Pro	Glu	Phe	Ile	Gln	Ile	His	Pro	Thr	Ala	Ile
			275				280					285			
Pro	Gly	Leu	Asp	Lys	Leu	Arg	Leu	Ile	Ser	Glu	Ser	Val	Arg	Gly	Glu
			290			295					300				
Gly	Gly	Arg	Val	Trp	Val	Pro	Arg	Cys	Ser	Ser	Lys	Thr	Ile	Ile	Phe
305				310					315						320
Pro	Asp	Gly	Ser	Arg	Arg	Pro	Cys	Gly	Glu	Thr	Gly	Lys	Pro	Trp	Tyr
			325						330				335		
Phe	Leu	Glu	Glu	Met	Tyr	Pro	Ala	Tyr	Gly	Asn	Leu	Val	Ser	Arg	Asp
			340					345					350		
Val	Gly	Ala	Arg	Ala	Ile										

Gly Glu Asp Pro Lys Lys Val Pro Met Arg Ile Phe Leu Arg Cys Thr
 405 410 415
 Ile Leu Trp Glu Ala Pro Gly
 420

(2) INFORMATIONS POUR LA SEQ ID NO: 862:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 841659..842459

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 862:

Lys	Ser	Pro	Tyr	Ala	His	Phe	Ser	Ala	Val	His	Tyr	Ser	Met	Gly	Gly	1	5	10	15
Ala	Trp	Val	Asp	Trp	Pro	Ala	Ser	Asp	Asp	Arg	Asp	Arg	Asp	Ser	Arg	20	25	30	
Tyr	Arg	His	Met	Thr	Asn	Ile	Pro	Gly	Cys	Phe	Asn	Cys	Gly	Glu	Ser	35	40	45	
Asp	Phe	Gln	Tyr	His	Gly	Ala	Asn	Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	50	55	60	
Ala	Cys	Leu	Tyr	Ala	Gly	Leu	Val	Ala	Gly	Asp	Glu	Ala	Ala	Arg	Phe	65	70	75	80
Val	Glu	Ser	Phe	Gly	Ser	Cys	Ile	Tyr	Ser	Gln	Gln	Asp	Leu	Asn	Gln	85	90	95	
Ala	Leu	Gln	Gln	Glu	Gln	Glu	Ile	Ser	Arg	Glu	Ile	Leu	Ser	Arg	Gln	100	105	110	
Gly	Gly	Glu	Asn	Ala	Phe	Ala	Leu	His	Glu	Glu	Ile	Ala	Arg	Val	Met	115	120	125	
Val	Ser	Asn	Val	Thr	Val	Lys	Arg	Glu	Asn	Lys	Ala	Leu	Glu	Glu	Thr	130	135	140	
Leu	His	Lys	Leu	Lys	Glu	Phe	Arg	Glu	Arg	Ile	Lys	Lys	Val	Ser	Val	145	150	155	160
His	Asp	Ser	Ser	Arg	Phe	Ala	Asn	Lys	Thr	Phe	His	Phe	Val	Arg	Gln	165	170	175	
Met	Glu	Pro	Met	Leu	Glu	Leu	Ala	Leu	Ala	Ile	Thr	Thr	Gly	Ala	Leu	180	185	190	
Leu	Arg	Asn	Glu	Phe	Arg	Gly	Ser	His	Tyr	Lys	Pro	Glu	Phe	Ser	Lys	195	200	205	
Arg	Asp	Asp	Val	Asn	Trp	Leu	Lys	Thr	Thr	Ile	Ala	Thr	Tyr	Ser	Val	210	215	220	
Asp	Glu	Pro	Glu	Ile	Ser	Tyr	Lys	Lys	Val	Asp	Thr	Arg	His	Val	Asn	225	230	235	240
Pro	Glu	Leu	Arg	Asp	Tyr	Thr	Arg	Gln	Gly	Ala	Lys	Asp	Val	Val	Leu	245	250	255	
Glu	Asn	Ile	Pro	Ala	Asn	Ile	His	Phe	Pro	Ile						260	265		

(2) INFORMATIONS POUR LA SEQ ID NO: 863:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 863:

(2) INFORMATION POUR LA SEQ ID NO: 864:

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 864:

(X1)	DESCRIPTION														
Leu	Ala	Asn	Phe	Leu	Ala	Ile	Ala	Arg	Phe	Phe	Phe	Ala	Lys	Ala	Thr
1				5					10					15	
Leu	Leu	Tyr	Val	Val	Lys	Ser	Cys	Arg	Phe	Ser	Pro	His	Lys	Thr	Ser
			20					25					30		
Ser	Ser	Lys	Glu	Ala	Phe	Ser	Leu	Leu	Ala	Lys	Glu	Ser	Asn	Thr	Glu
		35					40					45			
Thr	Ser	Lys	Arg	Asp	Met	Thr	Lys	Lys	Gly	Val	Phe	Ser	Leu	Pro	Leu
	50					55					60				

```

Pro Trp Asn Lys Ile Ala Met Gln Ser Ser Lys Leu Lys Ser Pro His
65              70              75              80
Leu Gln Lys Thr Leu Cys Tyr Ser Ser Val Phe Phe Leu Asn Asn Glu
85              90              95
Glu Asn Asn Ala Arg Lys Glu Lys Arg Glu Thr Ser His Pro Ile Ala
100            105            110
Glu Met Leu Ser Val Lys Gly Asn Phe Leu Gly His Thr Arg Thr Gln
115            120            125
Leu Trp Ala Cys Pro Asp Pro Ser Ile Pro Arg Val Pro Ile Asn Ala
130            135            140
Arg Asn Arg Leu Ser Arg Arg Phe Ser Pro Gly
145            150            155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 865:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 986 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 843239..846196

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 865:

```

Gln Arg Val Phe Trp Arg Trp Gly Leu Leu Ser Phe Glu Asp Cys Ile
1              5              10              15
Ala Ile Leu Phe His Gly Lys Gly Arg Glu Lys Thr Pro Phe Phe Val
20            25            30
Met Ser Arg Leu Asp Val Ser Val Phe Asp Ser Leu Ala Asn Lys Glu
35            40            45
Lys Ala Ser Leu Leu Glu Glu Val Leu Cys Gly Glu Asn Leu Gln Asp
50            55            60
Phe Thr Thr Tyr Ser Lys Val Ala Leu Ala Lys Lys Asn Leu Ala Ile
65            70            75            80
Ala Arg Lys Leu Ala Ser Tyr Ile Leu Asn Glu Glu Gly Asp Leu Glu
85            90            95
Leu Ser Arg Val Val Glu Ser Ile Gln Leu Leu Thr Lys Cys Leu Tyr
100           105           110
Pro Leu Gly Pro Tyr Arg Gln Gly Glu Gly Pro Ile Arg Glu His Val
115           120           125
Leu Lys Met Leu Glu Phe Leu Arg Asp Asp Gln Glu Ile Lys Asn Arg
130           135           140
Phe Arg Arg Phe Phe Val Pro Ser Tyr Ala Arg Val Gln Asp Leu Ile
145           150           155           160
Arg Asn Thr Leu Ala Leu Pro Ala Ser Glu Thr Val Thr Val Arg His
165           170           175
Val Arg Glu Ala Ala Leu Val Ala Leu Phe Thr Tyr Leu Arg Gln Asp
180           185           190
Val Gly Ser Cys Phe Ala Thr Ala Leu Ala Ile Leu Ile His Arg Glu
195           200           205
Tyr Pro Leu Leu Phe Ile Arg Asp Leu Glu Asp Leu Leu Ser Ser Gly
210           215           220
Lys Ile Ser Arg Ile Val Gly Asp Arg Glu Ile Ser Val Pro Ile Asn
225           230           235           240
Leu Leu Pro Cys Val Gly Asp Leu Phe Lys Pro Ile Cys Val Met Asp

```

245 250 255
 Leu Tyr Pro Asn Pro Val Ala Thr Leu Ala Ala Ser Ser Asp Leu Gln
 260 265 270
 Ala Ala Phe Val Ala Ser Gly Ile Phe Pro Thr Thr Gly Asp Ile Ala
 275 280 285
 Gly Glu Val Gln Thr Leu Leu Ala Asn Glu Phe Ile Tyr Gln Lys Val
 290 295 300
 Gln Asp Ile His Gly Lys Ile Thr Ala His Asp Val Ile Gln Asp Ser
 305 310 315 320
 Leu Leu His His Tyr Gln Leu Ser Leu Ser Thr Val Gln Ala Ser Val
 325 330 335
 Leu Gln Glu Gly Phe Arg Lys Glu Arg Gly Asp Gly Thr Val Leu Leu
 340 345 350
 Ser Thr Asn Ser Gln Arg Val Leu Ser Tyr Leu Glu Ser Tyr Glu Gln
 355 360 365
 Ala Lys Leu Gly Phe Ile Arg Asp Thr Gln Asn Val Leu Leu Lys Ser
 370 375 380
 Trp Glu Tyr Thr Leu Ala Thr Leu Ala Asp Ala Ser Gln Thr Thr Thr
 385 390 395 400
 Thr Lys His Leu Gln Ile Ala Leu Gly Trp Thr Ser Asp Asp Glu Asp
 405 410 415
 Gly Leu Arg Glu Ile Ile Arg Arg Phe Leu Ala Glu Glu Val Ala Thr
 420 425 430
 Thr Gln Ala Phe Ala Gly Gln Cys Glu Glu Thr Tyr Gln Glu Ala Lys
 435 440 445
 Ala Gln Leu Glu Tyr Val Glu Ser Arg Met Arg Asn Pro Ile Asn Lys
 450 455 460
 Gln Asp Ser Gln Ile Leu Ala Met Asp His Val Arg Phe Arg Gln Glu
 465 470 475 480
 Leu Asn Gln Ala Leu Gln Asp Trp Asn Ala Ala Gln Glu Lys Leu Lys
 485 490 495
 Lys Met Ile Met Leu Pro Asp Phe Leu Leu Ser Phe Tyr Ser Arg Glu
 500 505 510
 Ile Pro Asn Tyr Phe Arg Ser Val Tyr Asp Ala Phe Ile Arg Glu Phe
 515 520 525
 Ser Gly Asn Tyr Gln Asp Val Pro Ala Gly Phe Arg Ile Leu Phe Thr
 530 535 540
 Tyr Gly Arg Ser His Pro Asn Thr Trp Glu Pro Ile Tyr Ser Ile Glu
 545 550 555 560
 Glu Phe Ile His Ala Leu Thr Glu Phe Phe Thr Ser Ile Glu Gly Asp
 565 570 575
 Leu Leu Ala Lys His Asn Val Ser Gly Leu Glu Lys Glu Thr Ser Ile
 580 585 590
 Leu Leu His Arg Ile Val Ser Ala Leu His Glu Pro Arg Phe Gln Glu
 595 600 605
 Ala Ala Met Glu Arg Ile Leu Lys Ala Tyr Asn Cys Pro Ile Pro Gln
 610 615 620
 Gly Ile Phe Gln His Leu Asp Gln Val Thr His Thr Pro Trp Val Tyr
 625 630 635 640
 Val Ser Gly Gly Thr Val Thr Thr Leu Val Gly Asp Tyr Phe Glu Asn
 645 650 655
 Ser Lys Pro Leu Val Lys Leu Glu Lys Leu Pro Ala Asp Pro His Glu
 660 665 670
 Leu Ala Ala Phe Phe Ala Asp Ala Leu Lys Asp Leu Pro Glu Ala Val
 675 680 685
 Lys Asp Tyr Val Glu Asn Gly Asp His Ser Leu Leu Ala Ala Pro
 690 695 700
 Ser His Val Phe Ser Val Thr Ala Gly Ala Pro Leu Phe Arg Asp Ala
 705 710 715 720

```

Trp Thr Asn Asp Trp Tyr Ser Tyr Thr Trp Leu Arg Asp Val Trp Leu
      725      730      735
Ser Lys His Gln Asp Phe Leu Lys Arg Thr Leu Phe Asp Lys Ser Ala
      740      745      750
Ile Tyr Ala Phe Ile Thr Arg Phe Cys Thr Arg Tyr Tyr Leu Gln Glu
      755      760      765
Leu Thr Gln Asp Leu Leu Tyr Phe Cys Asp Asp Leu Ser Leu Ser Ile
      770      775      780
Pro Glu Phe Tyr Glu Lys Ser Ser Arg Phe Phe Gln Ser Thr Val His
785      790      795      800
Asp Glu Lys Val Val Ala Thr Leu Gln Lys Tyr Leu Ala Ser Gln Phe
      805      810      815
Val His Glu Ala Pro Tyr Val Ser Glu Gln Gln Leu Pro Gln Ile Ile
      820      825      830
Ser Asp Leu Ser Ser Tyr Leu Gly Ile Ser Ser Arg Ile Ser Tyr Asp
      835      840      845
Gln Leu Ala Thr Leu Leu Glu Glu Asn Val Gly Lys His Ser Leu Leu
      850      855      860
Ser Ser Ser Asp Leu Arg His Leu Tyr Lys Gly Leu Leu Met Ala Gly
865      870      875      880
Tyr Gln Arg Val Tyr His Glu Glu Asp Leu Ser Met Arg Leu Ile Ala
      885      890      895
Ala Met Arg His Tyr Gly Leu Ala Tyr Pro Ala Pro Leu Leu Phe Gly
      900      905      910
Asp Thr Asn Trp Ala Tyr Arg Tyr Phe Gly Phe Ile Xaa His Pro Gly
      915      920      925
Thr Gln Glu Met Asp Leu Trp Glu Phe Asn Tyr Leu Gly Leu Val Gly
      930      935      940
Arg Pro Ser Glu Asn Lys Glu Arg Trp Phe Ala Val Arg Asp Pro Trp
945      950      955      960
Ala Leu Tyr Pro Glu Ser His Arg Leu Arg Asn Gly Pro Ser Thr Arg
      965      970      975
Leu Ser Lys Trp Ile Ala Glu Arg Phe Phe
      980      985

```

(2) INFORMATIONS POUR LA SEQ ID NO: 866:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 112 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(843802..844137)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 866:

```

Ile Asn Ser Leu Ala Ser Ser Val Cys Thr Ser Pro Ala Ile Ser Pro
1      5      10      15
Val Val Gly Asn Met Pro Glu Ala Thr Asn Ala Ala Cys Lys Ser Asp
      20      25      30
Glu Ala Ala Arg Val Ala Thr Gly Leu Gly Tyr Lys Ser Ile Thr Gln
      35      40      45
Ile Gly Leu Asn Lys Ser Pro Thr His Gly Arg Arg Leu Ile Gly Thr
      50      55      60
Glu Ile Ser Arg Ser Pro Thr Ile Arg Asp Ile Phe Pro Glu Asp Asn

```

(2) INFORMATION POUR LA SEQ ID NO: 867:

(A) LONGUEUR: 609 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(846217..848043)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 867:

Asn	Ile	Cys	Phe	Arg	Cys	Gly	Met	Arg	Gln	Thr	Phe	Thr	Lys	Arg	Ile
1				5					10					15	
Leu	Leu	Phe	Leu	Phe	Leu	Val	Ile	Pro	Ala	Pro	Leu	Leu	Leu	Asn	Leu
			20					25					30		
Val	Val	Leu	Ser	Phe	Phe	Ser	Phe	Ala	Ala	Val	Lys	Thr	Thr	Ile	Ile
		35					40					45			
Gln	Asp	Leu	His	Thr	Arg	Thr	Met	Asn	Phe	Asn	Leu	Glu	Leu	Glu	Lys
	50					55					60				
Lys	Ile	Ala	Ile	Gln	Asn	Ile	Phe	Leu	Lys	Arg	Leu	Ala	Glu	Thr	Leu
65					70					75					80
Ala	Leu	Lys	Thr	Leu	Thr	Thr	Ser	His	Asp	Phe	Phe	Thr	Glu	Ala	Tyr
				85					90					95	
Ser	Glu	Met	Ile	Ala	Leu	Gly	Asp	Thr	Asp	Leu	Ser	Leu	Cys	Leu	Leu
			100					105					110		
Ser	Ser	Ala	Asn	Asp	Ser	Ile	Arg	Thr	Lys	Asn	Pro	Arg	Asp	Pro	Phe
		115					120					125			
Val	Arg	Tyr	Ile	Lys	Ala	His	Pro	Glu	Ile	Arg	Asp	Lys	Leu	Ile	Gln
	130					135					140				
Asn	Pro	Gly	Asn	Ala	Ser	Leu	Ile	Ser	Ile	Ser	Glu	Arg	Pro	Asp	Thr
145					150					155					160
Glu	Asp	His	Tyr	Leu	Val	Phe	Ala	Glu	Pro	Leu	Pro	Ile	Tyr	Glu	Asp
			165						170					175	
Pro	Ser	Leu	Ala	Gly	Trp	Val	Ile	Ala	Phe	Tyr	Ser	Met	Gln	Lys	Leu
			180					185					190		
Arg	Asn	Tyr	Leu	Phe	His	Asn	Lys	Gln	Ser	Tyr	Gln	Asp	Leu	Leu	Cys
		195					200					205			
Tyr	Leu	Asn	His	Lys	Gly	Glu	Leu	Leu	Phe	Ser	Asp	Ser	Ser	Pro	Phe
	210				215						220				
Gln	Asn	Gly	Ala	Phe	Ser	Leu	Ser	Met	Glu	Gly	Tyr	Pro	Ala	Leu	Ser
225					230					235					240
Ser	Glu	Lys	Ala	Ser	Tyr	Pro	Leu	Glu	Pro	Ser	Pro	Glu	Leu	Phe	Lys
			245						250					255	
Ala	Lys	Glu	Leu	Leu	Lys	Val	Ser	Asn	Thr	Arg	Glu	Asn	Phe	Leu	Ser
			260					265					270		
Leu	Phe	Ile	Ser	Leu	Ala	Ala	Tyr	Thr	Thr	Tyr	Pro	Phe	Ser	Cys	Ala
		275					280					285			
Asp	Pro	Ser	Ile	His	Leu	His	Tyr	Thr	Ser	Leu	Arg	Leu	Pro	Ile	Asn
	290					295					300				

Val Ile Leu Phe Tyr Ile Leu Ala Phe Ser Leu Met Gly Trp Val Leu
 305 310 315 320
 Ser Cys Thr Ser Lys Arg Leu Asn Arg Pro Leu Gln Glu Leu Ser Val
 325 330 335
 Ser Met Glu Ser Ala Trp Lys Gly Asn His Asn Val Arg Tyr Glu Pro
 340 345 350
 Gln Pro Tyr Gly Tyr Glu Ile Asn Glu Leu Gly Asn Ile Phe Asn Cys
 355 360 365
 Thr Leu Leu Leu Leu Asn Val Lys Glu Lys Ala Glu Ile Glu Tyr
 370 375 380
 Ile Ser Gly Asn Leu Leu Gln Lys Glu Leu Ala Leu Leu Ser Ser Leu
 385 390 395 400
 Lys Asp Thr Leu Leu Cys Gln Arg Ser Asn Ser Leu Pro Gly Gly Thr
 405 410 415
 Phe Ser Leu His Tyr Leu Gln Gly Glu Gln Gln Thr Gly Tyr Phe Tyr
 420 425 430
 Gly Trp Val Ala Thr Pro Glu Lys Asp Arg Leu Phe Gly Val Ile Gly
 435 440 445
 Ile Ala Gly Asp Ile Gly Leu Pro Ser Tyr Leu Tyr Ala Leu Ser Ala
 450 455 460
 Arg Ser Leu Phe Leu Thr Tyr Ala Ser Leu Gly Tyr Ser Leu Pro Ser
 465 470 475 480
 Ile Cys His Lys Thr Met Arg Ser Phe Asp Glu Thr Thr Val Gly Asn
 485 490 495
 Glu Ala Ser Val Ser Ile Ala Cys Leu Glu Tyr Asp Leu Ser Ser Lys
 500 505 510
 Ser Leu Ser Val Leu Thr Glu Gly Ala Asn Pro Pro Thr Leu Phe Ile
 515 520 525
 Lys Arg Gln Glu His Leu Leu Thr Met Ser Glu Gln Gln Arg Ile Glu
 530 535 540
 Thr Gly Asp Ile Leu Val Cys Leu Thr Gly Gly Pro His Ile Ile Gln
 545 550 555 560
 Tyr Leu Lys Thr Leu Pro Ile Glu Ala Leu Leu Lys Asp Pro Leu Ala
 565 570 575
 Pro Leu Asn Ser Lys Asn Phe Ala Glu Met Leu Thr Thr Met Leu Arg
 580 585 590
 Ser Lys Asn Gln Thr Gln Ile Asp Gly Ala Val Gly Phe Leu Ser Phe
 595 600 605
 Ile

(2) INFORMATIONS POUR LA SEQ ID NO: 868:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 658 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(848150..850123)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 868:

Ala Pro Leu Gly Lys Lys Arg Glu Met Thr Ile Pro Ile His Glu Asn
 1 5 10 15
 Lys Tyr Ser Met Ile Ser Phe Thr Arg Thr Ile Gly Phe Arg Leu Trp

20 25 30
 Leu Ile Cys Val Ala Ala Ile Met Phe Pro Leu Gly Ile Asn Ile Leu
 35 40 45
 Gln Leu Asn Leu Gln Gln Tyr Lys Lys Thr Leu Ser Ser Ile Thr Ser
 50 55 60
 Asp Leu Arg Glu Asn Ala Leu Phe Lys Ala His Thr Leu Gln Gln Thr
 65 70 75 80
 Ile Pro Leu Asn Ile Asp Ile Leu Ala Leu Phe Ser Glu Ile Phe Asp
 85 90 95
 Leu Asp Arg Gly Val Pro Ala Glu Pro Asp Leu Ala Leu Ser Lys Glu
 100 105 110
 Met Glu Lys Ile Phe His Ser Thr Tyr Lys Glu Ile Ser Leu Val Lys
 115 120 125
 Lys Glu Ala Asp Gly Asn Phe Arg Val Val Ala Ser Ser Arg Ile Glu
 130 135 140
 Gln Leu Gly Lys Asn Tyr Asn Gln Glu Ile Phe Leu Ser Asp Ser Gln
 145 150 155 160
 Pro Phe Leu Ala Thr Leu Arg His Ser Gly Ser Asp Ser Gln Val Leu
 165 170 175
 Ala Val Leu Gln Thr Asn Ile Phe Asp Ile Ser Ser Gln Glu Val Leu
 180 185 190
 Gly Val Leu Tyr Thr Leu Ser Asp Thr Asn Tyr Leu Leu Asn Gly Leu
 195 200 205
 Leu Ala Ala Lys Asp Pro Leu Ser Val Lys Thr Ala Ile Leu Ser Lys
 210 215 220
 Asn Gly Ile Ile Leu Gln Ala Thr Asp Ser Ser Leu Asp Leu Val Ser
 225 230 235 240
 Ile His Lys Thr Val Ser Lys Glu Gln Phe Cys Asp Val Phe Leu Arg
 245 250 255
 Asp Asp Ile Cys Pro Pro His Leu Leu Leu Arg Pro Pro Leu Asn Leu
 260 265 270
 Asp Pro Leu Pro Tyr Gly Glu Asn Phe Val Ser Phe Cys Ile Gly Asn
 275 280 285
 Thr Glu Met Trp Gly Tyr Ile His Ser Leu Pro Glu Met Asp Phe Arg
 290 295 300
 Ile Leu Thr Tyr Glu Glu Lys Ser Ile Ile Phe Ala Ser Leu Trp Arg
 305 310 315 320
 Arg Thr Leu Leu Tyr Phe Ala Tyr Phe Cys Cys Val Leu Leu Gly Ser
 325 330 335
 Ile Thr Ala Phe Leu Val Ala Lys Arg Leu Ser Lys Pro Ile Arg Lys
 340 345 350
 Leu Ala Thr Ala Met Met Glu Thr Arg Arg Asn Gln His His Pro Tyr
 355 360 365
 Glu Pro Asp Ser Leu Gly Phe Glu Ile Asn His Leu Gly Glu Ile Phe
 370 375 380
 Asn Ser Met Val Gln Ser Leu Ser Gln Gln Gln Ser Leu Ala Glu Lys
 385 390 395 400
 Asn Phe Glu Ile Lys Gln His Ala Gln Asn Ala Leu Arg Leu Gly Glu
 405 410 415
 Glu Ala Gln Gln Arg Leu Leu Pro Asn Gln Leu Pro Asp Ser Ala Thr
 420 425 430
 Thr Glu Ile Ala Lys Ala Tyr Ile Pro Ala Val Thr Val Gly Gly Asp
 435 440 445
 Phe Phe Asp Ile Phe Val Ile Gly Glu Gly Pro Gln Ala Lys Leu Phe
 450 455 460
 Leu Ile Val Ala Asp Ala Ser Gly Lys Gly Val Asn Ala Cys Ala Tyr
 465 470 475 480
 Ser Leu Phe Leu Lys Asn Met Leu His Thr Phe Leu Ser Glu Leu Ser
 485 490 495

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Ser Ile Gln Glu Ala Val Gln Gln Thr Ala Ala Leu Phe Tyr Gln Gln
      500                      505          510
Thr Ala Glu Ser Gly Met Phe Val Thr Leu Cys Ile Tyr Cys Tyr His
      515                      520          525
Tyr Ala Thr Arg Glu Leu Glu Tyr Tyr Ser Cys Gly His Asn Pro Ala
      530                      535          540
Cys Leu Arg Ala Pro Asn Gly Asp Ile Ser Phe Leu Ser His Pro Gly
545      550                      555          560
Met Ala Leu Gly Phe Leu Pro Glu Val Pro Pro His Pro Ala Tyr Thr
      565                      570          575
Leu Val Leu Glu Glu Glu Ser Leu Leu Val Leu Tyr Thr Asp Gly Val
      580                      585          590
Thr Glu Ala Ser Asn Lys His Gly Glu Met Phe Gly Glu Glu Arg Leu
      595                      600          605
Lys Ala Leu Val Ala Ser Leu Thr Lys Gln Ser Ala Glu Glu Ala Ile
      610                      615          620
Gln Ser Ile Met Phe Ser Ile Lys Ser Phe Val Lys Asp Cys Pro Gln
625      630                      635          640
His Asp Asp Ile Thr Leu Leu Val Leu Lys Ile Pro Lys Glu Pro Ser
      645                      650          655
Ala Tyr

```

(2) INFORMATIONS POUR LA SEQ ID NO: 869:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 472 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(850230..851645)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 869:

```

Ile Pro Arg Tyr Asp Pro Phe Leu Leu Arg Glu Ser Pro Ser Glu Pro
1      5      10      15
Ser Leu Cys Ile Ala Val Ile His Ala His Arg Arg Lys Leu Asp Lys
      20      25      30
Thr Ser Glu Leu Leu Ser Leu Thr Val Leu Asp Lys Asp Leu Val Met
      35      40      45
Phe Asp Val Val Ile Ser Asp Ile Glu Ala Arg Glu Ile Leu Asp Ser
      50      55      60
Arg Gly Tyr Pro Thr Leu Cys Val Lys Val Ile Thr Asn Thr Gly Thr
      65      70      75      80
Phe Gly Glu Ala Cys Val Pro Ser Gly Ala Ser Thr Gly Ile Lys Glu
      85      90      95
Ala Leu Glu Leu Arg Asp Lys Asp Pro Lys Arg Tyr Gln Gly Lys Gly
      100      105      110
Val Leu Gln Ala Ile Ser Asn Val Glu Lys Val Leu Val Pro Ala Leu
      115      120      125
Gln Gly Phe Ser Val Phe Asp Gln Ile Thr Ala Asp Ala Ile Met Ile
      130      135      140
Asp Ala Asp Gly Thr Pro Asn Lys Glu Lys Leu Gly Ala Asn Ala Ile
145      150      155      160
Leu Gly Val Ser Leu Ala Phe Ser Lys Ser Cys Leu Gln Ile Leu Tyr

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          165          170          175
Arg Asp Leu Leu Tyr Arg Tyr Leu Gly Gly Ser Phe Ser His Val Leu
          180          185          190
Pro Cys Pro Met Met Asn Leu Ile Asn Gly Gly Met His Ala Thr Asn
          195          200          205
Gly Leu Gln Phe Gln Glu Phe Met Ile Arg Pro Ile Ser Ala Pro Ser
          210          215          220
Leu Lys Glu Ala Val Arg Met Gly Ala Glu Val Phe Asn Ala Leu Lys
          225          230          235
Lys Ile Leu Gln Asn Arg Gln Leu Ala Thr Gly Val Gly Asp Glu Gly
          245          250          255
Gly Phe Ala Pro Asn Leu Ala Ser Asn Ala Glu Ala Leu Asp Leu Leu
          260          265          270
Leu Thr Ala Ile Glu Thr Ala Gly Phe Thr Pro Arg Glu Asp Ile Ser
          275          280          285
Leu Ala Leu Asp Cys Ala Ala Ser Ser Phe Tyr Asn Thr Gln Asp Lys
          290          295          300
Thr Tyr Asp Gly Lys Ser Tyr Ala Asp Gln Val Gly Ile Leu Ala Glu
          305          310          315
Leu Cys Glu His Tyr Pro Ile Asp Ser Ile Glu Asp Gly Leu Ala Glu
          325          330          335
Glu Asp Phe Glu Gly Trp Lys Leu Leu Ser Glu Thr Leu Gly Asp Arg
          340          345          350
Val Gln Leu Val Gly Asp Asp Leu Phe Val Thr Asn Ser Ala Leu Ile
          355          360          365
Ala Glu Gly Ile Ala Gln Gly Leu Ala Asn Ala Val Leu Ile Lys Pro
          370          375          380
Asn Gln Ile Gly Thr Leu Thr Glu Thr Ala Glu Ala Ile Arg Leu Ala
          385          390          395
Thr Ile Gln Gly Tyr Ala Thr Ile Leu Ser His Arg Ser Gly Glu Thr
          405          410          415
Glu Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Phe Asn Thr Gly Gln
          420          425          430
Ile Lys Thr Gly Ser Leu Ser Arg Ser Glu Arg Ile Ala Lys Tyr Asn
          435          440          445
Arg Leu Met Ala Ile Glu Glu Met Gly Pro Glu Ala Leu Phe Gln
          450          455          460
Asp Ser Asn Pro Phe Ser Lys Ala
          465          470

```

(2) INFORMATIONS POUR LA SEQ ID NO: 870:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 676 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(851669..853696)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 870:

```

Lys Ile Leu Thr Thr Ile His Cys Val Gly Gly Gly Val Leu Lys Gln
1           5           10           15
Gln Phe Val Leu His Ala Pro Phe Leu Pro Cys Gly Asp Gln Pro Glu
          20          25          30

```

Ala	Ile	Arg	Arg	Leu	Ser	Gln	Gly	Ile	Thr	Asp	Gly	Val	Pro	Ala	Gln
		35					40					45			
Val	Leu	Leu	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Thr	Phe	Thr	Met	Ala	Asn
	50					55					60				
Val	Ile	Ala	Asn	Val	Asn	Val	Pro	Thr	Leu	Val	Leu	Ala	His	Asn	Lys
65					70					75					80
Thr	Leu	Ala	Ala	Gln	Leu	Tyr	Gln	Glu	Phe	Lys	Ala	Phe	Phe	Pro	Glu
				85					90					95	
Asn	Ala	Val	Glu	Tyr	Phe	Ile	Ser	Tyr	Tyr	Asp	Tyr	Tyr	Gln	Pro	Glu
			100					105					110		
Ala	Tyr	Ile	Ala	Arg	Ser	Asp	Thr	Tyr	Ile	Glu	Lys	Ser	Leu	Leu	Ile
			115				120					125			
Asn	Asp	Glu	Ile	Asp	Lys	Leu	Arg	Leu	Ser	Ala	Thr	Arg	Ser	Ile	Leu
	130					135					140				
Glu	Arg	Arg	Asp	Thr	Leu	Ile	Val	Ser	Ser	Ile	Ser	Cys	Ile	Tyr	Gly
145					150					155					160
Ile	Gly	Ser	Pro	Asp	Asn	Tyr	Ser	Ser	Met	Ala	Leu	Thr	Leu	Glu	Val
				165					170					175	
Gly	Lys	Glu	Tyr	Pro	Arg	Ser	Gln	Leu	Ser	Ser	Gln	Leu	Val	Arg	Met
				180				185					190		
His	Tyr	Gln	Ala	Ser	Ser	Thr	Pro	Gln	Arg	Ser	Ala	Phe	Arg	Glu	Arg
		195					200					205			
Gly	Ser	Val	Ile	Asp	Ile	Phe	Leu	Ala	Tyr	Glu	Ser	Asp	Leu	Ala	Val
	210					215					220				
Arg	Leu	Glu	Phe	Met	Asn	Asp	Thr	Leu	Ile	Ser	Ile	Glu	Tyr	Val	Asp
225					230					235					240
Pro	Leu	Thr	Met	Ile	Pro	Ser	His	Thr	Thr	Ser	Ser	Ile	Thr	Leu	Tyr
				245					250					255	
Pro	Gly	Ser	His	Tyr	Val	Thr	Pro	Glu	Ala	Val	Arg	Glu	Gln	Ala	Ile
			260					265					270		
Arg	Thr	Ile	Arg	Glu	Glu	Leu	Glu	Gln	Arg	Met	Leu	Phe	Phe	Glu	Gly
		275					280					285			
Arg	Pro	Val	Glu	Gln	Glu	Arg	Leu	Phe	Gln	Arg	Thr	Thr	His	Asp	Ile
	290					295					300				
Glu	Met	Ile	Lys	Glu	Ile	Gly	Phe	Cys	Lys	Gly	Ile	Glu	Asn	Tyr	Ser
305					310					315					320
Arg	His	Phe	Thr	Gly	Ala	Ala	Pro	Gly	Glu	Pro	Pro	Thr	Cys	Leu	Leu
				325					330					335	
Asp	Tyr	Phe	Pro	Asp	Asp	Phe	Leu	Leu	Ile	Ile	Asp	Glu	Ser	His	Gln
			340				345						350		
Thr	Leu	Pro	Gln	Leu	Arg	Ala	Met	Tyr	Arg	Gly	Asp	Gln	Ser	Arg	Lys
		355					360					365			
Gln	Ser	Leu	Val	Glu	Tyr	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Phe	Asp	Asn
	370					375					380				
Arg	Pro	Leu	Thr	Tyr	Glu	Glu	Ala	Arg	Arg	Tyr	Phe	His	Arg	Val	Ile
385					390					395					400
Tyr	Val	Ser	Ala	Thr	Pro	Gly	Asp	Leu	Glu	Ile	Gln	Glu	Ser	Arg	Gly
				405					410					415	
His	Ile	Ile	Glu	Gln	Ile	Ile	Arg	Pro	Thr	Gly	Ile	Pro	Asp	Leu	Leu
			420					425					430		
Pro	Glu	Ile	Arg	Pro	Ala	Lys	Gly	Gln	Ile	Asp	Asp	Leu	Leu	Glu	Glu
		435					440					445			
Ile	Arg	Gln	Arg	Leu	Arg	Lys	Asp	Gln	Glu	Lys	Ile	Leu	Val	Ile	Ser
	450					455					460				
Val	Thr	Lys	Lys	Leu	Ala	Glu	Asp	Ile	Ala	Ala	Phe	Leu	Ala	Glu	Leu
465					470					475					480
Gly	Ile	Ala	Ala	Ala	Tyr	Leu	His	Ser	Gly	Ile	Glu	Thr	Ala	Glu	Arg
				485					490					495	
Thr	Gln	Ile	Leu	Thr	Asp	Leu	Arg	Leu	Gly	Asn	Ile	Asp	Val	Leu	Ile

```

          500                      505                      510
Gly Val Asn Leu Leu Arg Glu Gly Ile Asp Leu Pro Glu Val Ser Leu
          515                      520                      525
Val Ala Ile Leu Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Ser Ala
          530                      535                      540
Ser Leu Ile Gln Phe Cys Gly Arg Ala Ala Arg Asn Ile His Gly Lys
545                      550                      555                      560
Val Ile Cys Tyr Ala Asp Arg Ile Thr Pro Ser Met Asp His Met Leu
          565                      570                      575
Lys Glu Thr Glu Arg Arg Arg Lys Ile Gln Leu Asp Tyr Asn Gln Gln
          580                      585                      590
His Lys Ile Thr Pro Gln Pro Ile Lys Pro Phe Leu Ala Asn Pro
          595                      600                      605
Ile Thr Lys Glu Ala Gly Gln Glu Glu Thr Arg Leu Lys Met Gln Ser
          610                      615                      620
Ser Lys Glu Leu Glu Ala Ser Ile Lys Thr Tyr Glu Glu Ala Met Tyr
625                      630                      635                      640
Gln Ala Ala Gln Glu Phe Gln Phe Asp Glu Ala Ala Lys Tyr Arg Asp
          645                      650                      655
Leu Met Asn Ala Ala Lys Lys Gln Leu Leu Phe Gln Lys Gly Glu Glu
          660                      665                      670
Glu Asn Gly Asp
          675

```

(2) INFORMATIONS POUR LA SEQ ID NO: 871:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 379 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(853700..854836)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 871:

```

Gly Leu Ile Phe Arg Lys Asn Pro Glu Met Ser Cys Ile Asp Lys Leu
1          5          10          15
Arg Ile Lys Glu Lys Ala Arg Ser Glu Val Phe Ser Pro Arg Glu Ser
          20          25          30
Thr Met Lys Lys Lys Arg Val Leu Thr Gly Asp Arg Pro Thr Gly Lys
          35          40          45
Leu His Leu Gly His Trp Ile Gly Ser Ile Met Asn Arg Leu Gln Leu
          50          55          60
Gln Asn Asp Ser Arg Tyr Asp Cys Phe Phe Ile Ile Ala Asp Leu His
65          70          75          80
Thr Leu Thr Thr Lys Thr Arg Lys Glu Glu Val Leu Gln Ile Asp Asn
          85          90          95
His Ile Tyr Asp Val Leu Ala Asp Trp Leu Ser Val Gly Ile Asn Pro
          100          105          110
Glu Lys Ser Ala Ile Tyr Leu Gln Ser Ala Ile Pro Glu Ile Tyr Glu
          115          120          125
Leu Asn Leu Ile Phe Ser Met Leu Thr Pro Leu Asn His Ile Met Gly
          130          135          140
Ile Pro Ser Ile Lys Glu Met Ala Ser Asn Ala Ser Leu Asn Glu Glu
          145          150          155          160

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```

Ser Leu Ser His Gly Leu Ile Gly Tyr Pro Val Leu Gln Ser Ala Asp
      165      170      175
Ile Leu Leu Ala Lys Ala His Leu Val Pro Val Gly Lys Asp Asn Glu
      180      185      190
Ala His Val Glu Leu Thr Arg Asp Ile Ala Lys Thr Phe Asn Arg Leu
      195      200      205
Tyr Gly Glu Val Phe Pro Glu Pro Asp Ile Leu Gln Gly Glu Leu Thr
      210      215      220
Ala Leu Val Gly Thr Asn Gly Gln Gly Lys Met Ser Lys Ser Ala Asn
      225      230      235      240
Asn Ala Ile Tyr Leu Ser Asp Asp Ala Lys Thr Val Gln Glu Lys Ile
      245      250      255
Arg Lys Leu Tyr Thr Asp Pro Asn Arg Ile His Ala Thr Thr Pro Gly
      260      265      270
Arg Val Glu Gly Asn Pro Leu Phe Ile Tyr His Asp Leu Phe Asn Pro
      275      280      285
His Lys Glu Glu Val Glu Glu Phe Lys Thr Arg Tyr Arg Gln Gly Cys
      290      295      300
Ile Lys Asp Val Glu Val Lys Ala Arg Leu Ala Glu Glu Ile Asn Leu
      305      310      315      320
Phe Leu Asn Pro Phe Arg Glu Lys Arg Ser Glu Leu Val Ala Gln Pro
      325      330      335
Lys Phe Leu Glu Glu Ala Leu Gln Gln Gly Thr Glu Lys Met Arg Thr
      340      345      350
Val Ala Arg Glu Thr Met Glu Glu Val His Asp His Leu Gly Leu Ser
      355      360      365
Arg Lys Trp Arg Thr Ile Leu Ala Ser Ser Lys
      370      375

```

(2) INFORMATIONS POUR LA SEQ ID NO: 872:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 202 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(854920..855525)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 872:

```

Leu Lys Ser Tyr Lys Lys Leu Gln Leu Thr Phe Phe Leu Thr Leu Arg
1      5      10      15
Tyr Pro Val Met Thr Thr Lys Pro Lys Thr Leu Glu Ile Asp Asn Asn
      20      25      30
Thr Phe Leu Leu Leu Glu Gly Asn Leu Lys Arg Ile Phe Ala Thr Pro
      35      40      45
Ile Gly Tyr Thr Thr Phe Arg Glu Phe Gln Asn Val Val Phe Asn Cys
      50      55      60
Ala Gln Gly Gln Gln Glu Leu Ala Asn Phe Leu Phe Glu Met Leu Ile
      65      70      75      80
Asn Gly Lys Leu Leu Gln Glu Leu Pro Ala Gly Gln Lys Gln Ser Ala
      85      90      95
Gln Ser Leu Ile Val Gln Phe Met Met Pro Ile Arg Val Ala Lys Asp
      100      105      110
Ile His Glu Arg Gly Glu Phe Ile Asn Phe Ile Thr Ser Asp Met Leu

```

```

          115          120          125
Ala Gln Gln Glu Arg Cys Val Phe Leu Asn Arg Leu Ser Arg Val Asp
      130          135          140
Gly Gln Glu Phe Leu Leu Met Thr Asp Val Gln Asn Thr Cys His Leu
145          150          155          160
Ile Arg His Leu Leu Ser Arg Leu Leu Glu Ala Gln Lys Asn Pro Ile
      165          170          175
Gly Glu Lys Asn Leu Gln Glu Ile Gln Glu Asp Leu Asp Ser Leu Arg
      180          185          190
Ala His Phe Glu Glu Leu Thr Lys Ser Val
      195          200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 873:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 - (A) LONGUEUR: 268 acides aminés
 - (B) TYPE: acide aminé
 - (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(855437..856240)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 873:

```

Val Thr Cys Asn Val Met Gly Asn Ile Lys Thr Leu Leu Glu Ile Arg
1          5          10          15
Phe Lys Lys Pro Thr Pro Xaa Lys Met Glu Ser Leu Xaa Lys Lys Arg
      20          25          30
Leu Glu Gly Glu Leu Ser Pro Xaa Xaa Asn Gly Phe Thr Thr Pro Lys
      35          40          45
Leu Cys Ser Gln Glu Glu Ala Arg Phe Arg Gln Leu Leu Glu Glu Tyr
      50          55          60
Ser Phe Ser Lys Glu Ile Ser His Asn Asp Leu Gln Gln Leu Cys His
65          70          75          80
Leu Ser Ala Gln Val Lys Gln Ile His His Gln Ala Val Leu Leu His
      85          90          95
Gly Glu Arg Ile Lys Lys Val Arg Glu Leu Leu Lys Thr Tyr Arg Glu
      100          105          110
Gly Ala Phe Ser Ala Trp Leu Leu Leu Thr Tyr Gly Asn Arg Gln Thr
      115          120          125
Pro Tyr Asn Phe Leu Val Tyr Tyr Glu Leu Phe Ser Ala Leu Pro Asp
      130          135          140
Thr Leu Lys Leu Glu Leu Glu Arg Leu Pro Arg Gln Ala Val Tyr Thr
145          150          155          160
Leu Ala Ser Arg Glu Gly Ser Gln Glu Lys Lys Glu Glu Ile Ile Arg
      165          170          175
Asn Tyr Gln Gly Glu Thr Arg Gly Glu Leu Leu Glu Ile Ile Arg Arg
      180          185          190
Glu Phe Pro Leu Leu Pro Thr Asp Arg Arg Gln Ser Ser Leu Ala Gln
      195          200          205
Gln Ala Phe Ser Phe Phe Ala Lys Gly Thr Lys Leu Leu Gln Arg Cys
      210          215          220
Thr Asp Ile Ser Gln Glu Glu Leu Leu Ser Leu Glu Lys Leu Ile Lys
225          230          235          240
Lys Leu Gln Lys Val Thr Thr Asn Leu Leu Ser Asn Thr Lys Val Ser
      245          250          255

```


(2) INFORMATION POUR LA SEQ ID NO: 874:

(A) LONGUEUR: 317 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 874:

Thr 1	Phe	Leu	Pro	Glu 5	Asp	Thr	Val	Pro	Asn 10	Asn	Ile	Glu	Lys	Arg 15	Tyr
Leu	Glu	Ser	Phe 20	Leu	Thr	Leu	Phe	Ile 25	Ser	Phe	Asn	Leu	Ile	Arg 30	Pro
Cys	Leu	Trp 35	Thr	Asn	Gln	Tyr	Lys 40	Gly	Ile	Lys	Ala	Thr 45	Lys	Lys	Glu
Arg	Gly 50	Phe	Leu	Pro	Leu	Gln 55	Gly	Leu	His	Leu 60	Val	Ile	Asn	Met	Lys
Thr 65	Ile	Ala	Val	Asn	Ser 70	Phe	Lys	Gly	Gly	Thr 75	Ala	Lys	Thr	Ser	Thr 80
Thr	Leu	His	Leu	Gly 85	Ala	Ala	Leu	Ala 90	Gln	Tyr	His	Lys	Ala	Arg 95	Val
Leu	Leu	Ile	Asp 100	Phe	Asp	Ala	Gln	Ala 105	Asn	Leu	Thr	Ala	Gly 110	Leu	Gly
Leu	Asp	Pro 115	Asp	Cys	Tyr	Asp	Ser 120	Leu	Ala	Val	Val	Leu	Gln	Gly	Glu
Lys	Asn 130	Ile	Glu	Glu	Val	Ile 135	Arg	Pro	Ile	Asp 140	Ser	Ser	Gly	Leu	Asp
Leu 145	Ile	Pro	Ala	Asp	Thr 150	Trp	Leu	Glu	Arg	Val 155	Glu	Val	Ser	Gly	Ser 160
Leu	Ala	Ala	Asp 165	Arg	Tyr	Ser	His	Glu	Arg 170	Leu	Lys	Ile	Ile	Leu 175	Ser
Lys	Ile	Glu 180	His	Arg	Tyr	Asp	Tyr 185	Val	Ile	Ile	Asp	Thr	Pro	Pro	Ser
Leu	Cys 195	Trp	Leu	Thr	Glu	Ser	Ala 200	Leu	Ile	Ala	Ala	Gln 205	His	Ala	Leu
Ile	Cys 210	Ala	Thr	Pro	Glu	Phe 215	Tyr	Ser	Val	Lys	Gly 220	Leu	Glu	Arg	Leu
Ala 225	Thr	Phe	Ile	Gln	Gly 230	Ile	Ser	Ser	Arg	His 235	Pro	Leu	Asn	Ile	Leu 240
Gly	Val	Thr	Leu	Ser 245	Phe	Trp	Asn	Tyr	Arg 250	Gly	Lys	Asn	Asn	Ala 255	Ala
Phe	Thr	Glu 260	Leu	Ile	Gln	Lys	Thr 265	Phe	Pro	Gly	Lys	Leu	Leu	Asn 270	Thr
Arg	Ile 275	Arg	Arg	Asp	Ile	Thr	Ile 280	Ser	Glu	Ala	Ala	Ile 285	His	Gly	Lys
Pro	Val 290	Phe	Ser	Thr	Ala	Pro 295	Ser	Ala	Arg	Ala	Ser 300	Glu	Asp	Tyr	Leu
Lys 305	Leu	Thr	Glu	Glu	Leu 310	Leu	Phe	Leu	Leu	Ser 315	Ser	Asp	Met		

(2) INFORMATIONS POUR LA SEQ ID NO: 875:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 663 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(857451..859439)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 875:

Asn	Ala	Thr	Met	Ala	Asn	Thr	Pro	Arg	Lys	Lys	Arg	Arg	Phe	Phe	Ala	1	5	10	15
Ala	Val	Cys	Ser	Lys	Phe	Phe	Ile	Tyr	Gly	Glu	Gly	Met	Ile	His	Val	20	25	30	35
Thr	Cys	Asn	Gln	Glu	Ala	Phe	Glu	Leu	Pro	Glu	Gly	Ala	Ser	Ala	Met	40	45	50	55
Asp	Leu	Ala	Asn	Lys	Met	Lys	Gln	Ser	His	Cys	Phe	Val	Gly	Ala	Leu	60	65	70	75
Ile	Asn	Asp	Gln	Glu	Lys	Asp	Leu	Ser	Thr	Thr	Leu	Gln	Asp	Gly	Asp	80	85	90	95
Thr	Val	Leu	Phe	Leu	Thr	Trp	Asp	Asp	Pro	Lys	Gly	Arg	Glu	Ile	Phe	100	105	110	115
Leu	His	Thr	Ser	Ala	His	Ile	Leu	Ala	Gln	Ala	Val	Leu	Arg	Leu	Trp	120	125	130	135
Pro	Ser	Ala	Gln	Pro	Thr	Ile	Gly	Pro	Val	Ile	Asp	Gln	Gly	Phe	Tyr	140	145	150	155
Tyr	Asp	Phe	Ala	Asn	Leu	Ser	Ile	Ser	Glu	Glu	Asp	Phe	Pro	Ala	Ile	160	165	170	175
Glu	Ala	Met	Ala	Lys	Thr	Ile	Ala	Glu	Glu	Lys	Phe	Pro	Ile	Ser	Arg	180	185	190	195
Gln	Val	Phe	Pro	Asp	Lys	Glu	Ala	Ala	Leu	Ala	Tyr	Phe	Ser	Gln	Asn	200	205	210	215
Pro	Phe	Lys	Ala	Glu	Leu	Ile	Ala	Glu	Leu	Pro	Glu	Glu	Val	Glu	Ile	220	225	230	235
Ser	Ala	Tyr	Thr	Gln	Gly	Glu	Phe	Leu	Asp	Leu	Cys	Arg	Gly	Pro	His	240	245	250	255
Leu	Pro	Ser	Thr	Ala	Pro	Val	Lys	Ala	Phe	Lys	Leu	Leu	Arg	Thr	Ser	260	265	270	275
Ser	Ala	Tyr	Trp	Lys	Gly	Asp	Pro	Ser	Arg	Glu	Ser	Leu	Ile	Arg	Ile	280	285	290	295
Tyr	Gly	Val	Ser	Phe	Pro	Thr	Thr	Lys	Glu	Leu	Lys	Glu	His	Leu	His	300	305	310	315
Gln	Leu	Glu	Glu	Ala	Lys	Lys	Arg	Asp	His	Arg	Val	Leu	Gly	Thr	Lys	320	325	330	335
Leu	Asp	Leu	Phe	Ser	Gln	Gln	Thr	Cys	Ser	Ala	Gly	Met	Pro	Phe	Phe	340	345	350	
His	Pro	Arg	Gly	Met	Val	Val	Trp	Asn	Ala	Leu	Val	Asp	Tyr	Trp	Lys				
Arg	Leu	His	Gln	Arg	Ala	Gly	Tyr	Gln	Gln	Ile	Gln	Thr	Pro	Gln	Leu				
Met	Asn	Arg	Glu	Leu	Trp	Glu	Ile	Ser	Gly	His	Trp	Glu	Asn	Tyr	Lys				
Glu	Asn	Met	Tyr	Thr	Leu	Thr	Val	Asp	Glu	Glu	Asp	Tyr	Ala	Ile	Lys				

```

Pro Met Asn Cys Pro Gly Cys Met Leu Tyr Tyr Lys Thr Gln Leu His
    355                      360                      365
Ser Tyr Arg Glu Phe Pro Leu Arg Ile Ala Glu Ile Gly His Val His
    370                      375                      380
Arg His Glu Leu Ser Gly Ala Leu Ser Gly Leu Met Arg Val Arg Thr
    385                      390                      395                      400
Phe His Gln Asp Asp Ala His Val Phe Leu Thr Pro Glu Gln Val Glu
    405                      410                      415
Glu Glu Thr Leu Asn Ile Leu Asn Leu Val Ser Glu Leu Tyr Gly Thr
    420                      425                      430
Phe Gly Leu Glu Tyr His Leu Glu Leu Ser Thr Arg Pro Glu Gln Gly
    435                      440                      445
Thr Ile Gly Ser Asp Asp Leu Trp Glu Leu Ala Thr Glu Ala Leu Lys
    450                      455                      460
Arg Ala Leu Val Lys Ser Gln Lys Pro Phe Ile Ile Ser Pro Gly Glu
    465                      470                      475                      480
Gly Ala Phe Tyr Gly Pro Lys Ile Asp Ile His Val Lys Asp Ala Ile
    485                      490                      495
Asn Arg Thr Trp Gln Cys Gly Thr Ile Gln Leu Asp Met Phe Leu Pro
    500                      505                      510
Glu Arg Phe Asp Leu Lys Tyr Thr Asn Ala Gln Gly Glu Lys Ser Thr
    515                      520                      525
Pro Ile Met Leu His Arg Ala Leu Phe Gly Ser Ile Glu Arg Phe Leu
    530                      535                      540
Gly Ile Leu Ile Glu His Phe Lys Gly Arg Phe Pro Leu Trp Leu Ser
    545                      550                      555                      560
Pro Glu His Val Arg Ile Ile Thr Val Ala Asp Arg His Glu Ala Arg
    565                      570                      575
Ala Gln Glu Leu Ala Lys His Phe Ser Gln Met Gly Ile Ile Val Ser
    580                      585                      590
Val Asp Ser Ser Asn Glu Ser Val Ser Lys Lys Ile Arg Asn Ala Gln
    595                      600                      605
Asn Met Gln Val Asn Tyr Met Ile Thr Ile Gly Asp Lys Glu Leu Glu
    610                      615                      620
Thr His Leu Leu Ala Val Arg Thr Arg Asp Asn Arg Val Leu Asn Asp
    625                      630                      635                      640
Ile Ala Val Glu Gln Phe Ser His Val Ile Leu Glu Glu Leu Arg Ser
    645                      650                      655
Leu Ser Leu Thr Pro Ser Leu
    660

```

(2) INFORMATIONS POUR LA SEQ ID NO: 876:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 120 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(859587..859946)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 876:

```

Lys Pro Ile Thr Glu Ser Asn Thr Ile Gly Met Ile Ala Gly Arg Gly
1      5      10      15
Arg Arg Arg Asp Ser Arg Leu His Asn Ser Ser Pro Lys Arg Thr Thr

```



```

Val Glu Asn Pro Leu Leu Phe Leu Gln Ala Ile Gly Ala Leu Val Ile
      245                      250                      255
Phe Ser Asn Leu Ile Cys Tyr Asn Leu Phe Ala Lys Leu Leu Arg Ser
      260                      265                      270
Phe Ser Ser Thr Phe Leu Ser Phe Cys Asn Leu Val Met Pro Leu Phe
      275                      280                      285
Ala Ser Phe Phe Gly Trp Leu Leu Leu Gly Glu Ser Phe Pro Pro Gly
      290                      295                      300
Leu Leu Phe Ala Val Gly Phe Met Val Leu Gly Cys Arg Leu Ile Tyr
305                      310                      315                      320
His Glu Glu Phe Arg Gln Gly Tyr Val Leu Thr Ser Glu
      325                      330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 878:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 292 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(860724..861599)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 878:

```

Pro Thr Arg Ala Ala Ser Ala Lys Ser Trp Ser Ser Ser Phe Gln Gln
1      5      10      15
Gln Asn Gln Ala Ile Gln Asn Gln Val Ala Met Ala Pro Glu Ile Gly
      20      25      30
Asn Ala Ile Arg Thr Gln Ala Gly His Gln Ala Lys Ala Thr Glu Leu
      35      40      45
Gln Ala Gln Gln Ser Leu Ile Ser Gly Ile Thr Asn Ile Val Gly Phe
      50      55      60
Ala Val Ser Val Gly Gly Gly Ile Leu Ser Ala Ser Lys Ser Leu Gly
65      70      75      80
Gly Leu Lys Ser Ala Ala Phe Thr Asn Glu Thr Ala Ser Ala Ala Thr
      85      90      95
Ser Ala Thr Ser Ser Leu Ala Lys Thr Ala Thr Ser Ala Leu Asp Asp
      100     105     110
Val Ala Gly Thr Ala Thr Ala Val Gly Ala Lys Ala Thr Ser Gly Ala
      115     120     125
Ala Ser Ala Ala Ser Ser Ala Ala Thr Lys Leu Thr Gln Asn Met Ala
      130     135     140
Glu Ser Ala Ser Lys Thr Leu Ser Gln Thr Ala Ser Lys Ser Ala Gly
145     150     155     160
Gly Leu Phe Gly Gln Ala Leu Asn Thr Pro Ser Trp Ser Glu Lys Val
      165     170     175
Ser Arg Gly Met Asn Val Val Lys Thr Gln Gly Thr Arg Ala Thr Lys
      180     185     190
Phe Ala Gly Arg Ala Leu Ser Ser Ala Met Asn Ile Ser Gln Met Val
      195     200     205
His Gly Leu Thr Ala Gly Ile Asp Gly Ile Val Gly Gly Val Ile Gly
      210     215     220
Ala Gln Val Ala Gln Glu Gln Arg Met Ala Gly Met Ala Glu Ala Arg
225     230     235     240
Ala Glu Glu Leu Lys Ser Leu Asn Ser Val Gln Ala Gln Tyr Ala Ser

```

				245				250						255	
Gln	Ala	Gln	Gln	Leu	Gln	Glu	Gln	Ser	Gln	Gln	Ser	Phe	Asn	Ser	Ala
			260					265					270		
Leu	Gln	Thr	Leu	Gln	Ser	Ile	Ser	Asp	Ser	Ala	Leu	Gln	Thr	Thr	Ala
		275					280					285			
Ser	Met	Phe	Asn												
	290														

(2) INFORMATIONS POUR LA SEQ ID NO: 879:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 158 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(861580..862053)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 879:

Trp	Arg	Ser	Cys	Val	Met	Thr	Thr	Gly	Val	Arg	Gly	Asp	Asn	Ala	Pro
1				5				10						15	
Asp	Pro	Ser	Leu	Leu	Ala	Gln	Leu	Thr	Gln	Asn	Ala	Asn	Ser	Ala	Ser
		20						25					30		
Ala	Ala	Ser	Thr	Gly	Lys	Asn	Gly	Gln	Val	Ala	Gly	Ala	Lys	Gln	Glu
		35					40					45			
Asn	Val	Asp	Ala	Ser	Phe	Glu	Asp	Leu	Leu	Gln	Asp	Ala	Gln	Gly	Thr
	50					55					60				
Gly	Gly	Ser	Lys	Lys	Ala	Thr	Ala	Asn	Gln	Thr	Ser	Lys	Ser	Arg	Lys
65					70					75				80	
Ser	Glu	Lys	Ala	Gln	Ala	Ser	Ser	Gly	Thr	Ser	Thr	Thr	Thr	Ser	Val
				85					90					95	
Ala	Gln	Ala	Ser	Gln	Thr	Ala	Thr	Ala	Gln	Ala	Val	His	Gly	Ala	Arg
			100					105					110		
Asp	Ser	Gly	Phe	Asn	Ser	Asp	Gly	Ser	Ala	Thr	Leu	Pro	Ser	Pro	Thr
		115					120					125			
Gly	Thr	Glu	Val	Asn	Gly	Val	Val	Leu	Arg	Lys	Gly	Met	Gly	Thr	Leu
	130					135					140				
Ala	Leu	Met	Gly	Leu	Ile	Met	Thr	Tyr	Ser	Arg	Ser	Lys	Cys		
145					150					155					

(2) INFORMATIONS POUR LA SEQ ID NO: 880:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 481 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(862098..863540)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 880:

Arg	Gly	Tyr	Met	Ser	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Ser	Asn
1				5				10						15	
Leu	Lys	Asn	Val	Leu	Ser	Gln	Val	Ile	Ala	Ser	Thr	Pro	Gln	Gly	Val
			20					25					30		
Pro	Asn	Ala	Asp	Lys	Leu	Thr	Asp	Asn	Gln	Val	Lys	Gln	Val	Gln	Gln
		35					40					45			
Thr	Arg	Gln	Asn	Arg	Asp	Asp	Leu	Ser	Met	Glu	Ser	Asp	Val	Ala	Val
	50				55					60					
Ala	Gly	Thr	Ala	Gly	Lys	Asp	Arg	Ala	Ala	Ser	Ala	Ser	Gln	Ile	Glu
65				70						75				80	
Gly	Gln	Glu	Leu	Ile	Glu	Gln	Gln	Gly	Leu	Ala	Ala	Gly	Lys	Glu	Thr
			85					90					95		
Ala	Ser	Ala	Asp	Ala	Thr	Ser	Leu	Thr	Gln	Ser	Ala	Ser	Lys	Gly	Ala
			100					105					110		
Ser	Ser	Gln	Cys	Ile	Glu	Asp	Thr	Ser	Lys	Ser	Leu	Glu	Leu	Ser	
		115				120					125				
Ser	Leu	Ser	Ser	Leu	Ser	Ser	Val	Asp	Ala	Thr	His	Leu	Gln	Glu	Ile
	130				135						140				
Gln	Ser	Ile	Val	Ser	Ser	Ala	Met	Gly	Ala	Thr	Asn	Glu	Leu	Ser	Leu
145				150						155					160
Thr	Asn	Leu	Glu	Thr	Pro	Gly	Leu	Pro	Lys	Pro	Ser	Thr	Thr	Pro	Arg
			165					170						175	
Gln	Glu	Val	Met	Glu	Ile	Ser	Leu	Ala	Leu	Ala	Lys	Ala	Ile	Thr	Ala
			180					185					190		
Leu	Gly	Glu	Ser	Thr	Gln	Ala	Ala	Leu	Glu	Asn	Phe	Gln	Ser	Thr	Gln
	195				200							205			
Ser	Gln	Ser	Ala	Asn	Met	Asn	Lys	Met	Ser	Leu	Glu	Ser	Gln	Gly	Leu
	210				215					220					
Lys	Ile	Asp	Lys	Glu	Arg	Glu	Glu	Phe	Lys	Lys	Met	Gln	Glu	Ile	Gln
225				230					235					240	
Gln	Lys	Ser	Gly	Thr	Asn	Ser	Thr	Met	Asp	Thr	Val	Asn	Lys	Val	Met
			245					250						255	
Ile	Gly	Val	Thr	Val	Ala	Ile	Thr	Val	Ile	Ser	Val	Val	Ser	Ala	Leu
			260					265					270		
Phe	Thr	Cys	Gly	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Ala	Ala	Gly	Ala	Thr
		275				280						285			
Ala	Ala	Thr	Ala	Gly	Ala	Thr	Ala	Ala	Ala	Thr	Thr	Ala	Thr	Ser	Val
	290				295						300				
Thr	Thr	Thr	Val	Ala	Thr	Gln	Val	Thr	Met	Gln	Ala	Val	Val	Gln	Val
305				310					315					320	
Val	Lys	Gln	Ala	Ile	Ile	Gln	Ala	Val	Lys	Arg	Ala	Ile	Val	Gln	Ala
			325					330						335	
Ile	Lys	Gln	Gly	Ile	Lys	Gln	Gly	Ile	Lys	Gln	Ala	Ile	Lys	Gln	Ala
		340					345					350			
Val	Lys	Ala	Ser	Val	Lys	Thr	Leu	Ala	Lys	Asn	Val	Gly	Lys	Ile	Phe
		355				360						365			
Ser	Ala	Gly	Lys	Asn	Ala	Val	Ser	Lys	Ser	Phe	Pro	Lys	Leu	Ser	Lys
	370				375						380				
Val	Ile	Asn	Thr	Leu	Gly	Ser	Lys	Trp	Val	Thr	Leu	Gly	Val	Gly	Ala
385				390					395					400	
Leu	Thr	Ala	Val	Pro	Gln	Leu	Val	Ser	Gly	Ile	Thr	Ser	Leu	Gln	Leu
			405					410					415		
Ser	Asp	Met	Gln	Lys	Glu	Leu	Ala	Gln	Ile	Gln	Lys	Glu	Val	Gly	Ala
		420				425						430			
Leu	Thr	Ala	Gln	Ser	Glu	Met	Met	Lys	Ala	Phe	Thr	Leu	Phe	Trp	Gln
		435				440						445			
Gln	Ala	Ser	Lys	Ile	Ala	Ala	Lys	Gln	Thr	Glu	Ser	Pro	Ser	Glu	Thr
	450				455					460					
Gln	Gln	Gln	Ala	Ala	Lys	Thr	Gly	Ala	Gln	Ile	Ala	Lys	Xaa	Cys	Pro

480

Asn 1	Leu	Ile	Leu	Leu 5	Val	Val	Ile	Cys	Tyr 10	Phe	Ile	Phe	Leu	Gly 15	Ile
Ile	Ala	Met	Ser 20	Thr	Pro	Ser	Ser	Asn 25	Asn	Ser	Lys	Lys	Pro 30	Ser	Ala
Ser	Phe	Asn 35	Lys	Lys	Ser	Arg	Ser 40	Arg	Leu	Ala	Glu	Ile 45	Ala	Ala	Gln
Lys	Lys 50	Ala	Lys	Ala	Glu	Asp 55	Leu	Glu	Gln	Lys	Tyr 60	Pro	Val	Pro	Thr


```

Glu Glu Glu Thr Lys Gln Val Leu Met Asp Ile Leu Gln Gly Leu Ser
65          70          75          80
Asn Gly Leu Thr Leu Gln Gln Ile Leu Gly Leu Ser Asp Val Leu Leu
          85          90          95
Glu Glu Ile Tyr Thr Val Ala Tyr Thr Phe Tyr Ser Gln Gly Lys Tyr
          100         105         110
Arg Glu Ala Ile Gly Leu Phe Gln Ile Leu Thr Ala Ser Lys Pro Gln
          115         120         125
Cys Tyr Lys Tyr Ile Leu Gly Leu Ser Ser Cys Tyr His Gln Leu Lys
          130         135         140
Met Tyr Asp Glu Ala Ala Phe Gly Phe Phe Leu Ala Phe Asp Ala Gln
145          150         155         160
Pro Glu Asn Pro Ile Pro Pro Tyr Tyr Ile Ala Asp Ser Leu Met Lys
          165         170         175
Leu Asn Gln Pro Glu Glu Ser Gln Asp Phe Leu Asp Ile Thr Ile Asp
          180         185         190
Met Cys Lys Asn Lys Pro Glu Tyr Lys Val Leu Lys Asp Arg Cys Ser
          195         200         205
Ile Met Lys Gln Ser Leu Asp Ala Val Leu Lys Lys Glu Lys Ser Ala
          210         215         220
Lys Gly Ser Glu Thr Gln Ala Ser Val Ser
225          230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 883:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 437 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 864938..866248

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 883:

```

Ser Arg Ile Arg Leu Leu Asp Ser Val Thr Val Asn Gln Ile Ser Ala
1          5          10          15
Gly Glu Val Ile Glu Asn Ala Ala Ser Val Val Lys Glu Leu Ile Glu
          20          25          30
Asn Ser Leu Asp Ala Gly Ala Asp Glu Ile His Ile Glu Thr Leu Gly
          35          40          45
Gly Gly Arg Gly Gln Ile Val Val Arg Asp Asn Gly Val Gly Met Asp
          50          55          60
Pro Glu Glu Val Pro Val Ala Leu Gln Arg His Ala Thr Ser Lys Ile
65          70          75          80
Ala His Phe Ala Asp Ile Phe Ser Leu Ala Ser Tyr Gly Phe Arg Gly
          85          90          95
Glu Ala Leu Pro Ser Ile Ala Ser Ile Ser Lys Met Glu Ile His Thr
          100         105         110
Ala Arg Ala Gly Gly Leu Gly Ser Lys Thr Leu Ile Glu Lys Gly Glu
          115         120         125
Pro Val Cys Cys Glu Pro Ala Pro Arg Gln Gln Gly Thr Thr Ile Ala
          130         135         140
Val His Ser Leu Phe Tyr Asn Val Pro Met Arg Gln Ser Phe Gln Lys
145          150         155         160
Ser Pro Gln Met Asp Arg Leu Ala Ile Arg Arg Leu Leu Glu Asn Ser

```

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Val Leu Ser Ser Glu Gly Ile Gly Trp Thr Trp Ile Ser Glu Arg Arg
165 170 175
180 185 190
Gln Gln Leu His Val Ala Lys Lys Gln Gly Phe Ile Glu Arg Val Ala
195 200 205
Leu Val Leu Gly Glu Ser Phe Val Gln Glu Ala Phe Phe Ile Asp Lys
210 215 220
Gln Gln Gly Asp Leu Arg Val Leu Gly Phe Leu Gly Ser Pro Asn Gln
225 230 235 240
His Arg Ser Thr Arg Gln Gly Gln Arg Leu Phe Ile Asn Asn Arg Ala
245 250 255
Val Glu Ser Ser Phe Ile Ser Lys Lys Val Ala Glu Ala Tyr Ala Trp
260 265 270
Met Ile Pro Ala Gln Arg Tyr Pro Ile Phe Val Leu Lys Leu Phe Leu
275 280 285
Pro Pro Met Trp Cys Asp Phe Asn Val His Pro Gln Lys Thr Glu Val
290 295 300
Arg Leu Leu Gln Glu Gly Gln Ile Ser Asn Leu Leu Val Glu Ala Ile
305 310 315 320
Ser Glu Ala Leu Leu Arg Arg Ser Ser Ser Leu Glu Glu Ile Val Leu
325 330 335
Lys Val Pro Thr Glu Lys Ile Pro Ile Glu Asn Glu Gly Ile Ser Val
340 345 350
Pro Ser Ile Arg Pro Ala Ile Val Ser Ala Pro Leu Ser Cys Pro Thr
355 360 365
Phe Ser Gln Gln Pro Tyr Leu Lys Thr Glu Met Ala Thr Ile Val Ser
370 375 380
Arg Asp Ser Ala Ser Ser Ser Leu Ser Val Val Glu Lys Val Arg Phe
385 390 395 400
Leu Thr Ser Leu Gly Lys Val Leu Leu Val Glu Asp Ser Glu Gly Val
405 410 415
His Val Val Phe Val Gln Leu Arg Val Asn Ile Cys Phe Met Phe Leu
420 425 430
Tyr Tyr Pro Ser Val
435

```

(2) INFORMATIONS POUR LA SEQ ID NO: 884:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 866303..866605

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 884:

```

Leu Ser Trp Lys Gln Thr Phe Tyr Arg Cys Gly Leu Glu Ala Leu Thr
1 5 10 15
Ala Leu Gly Ile Glu Leu Ser Arg Ile Ser Pro Asp Ser Phe Ala Ile
20 25 30
Glu Ser Ala Pro Pro Phe Ile Gln Glu Glu Glu Leu Lys Glu Trp Ile
35 40 45
Val Ala Leu Ala Gln Glu Gly Ala Leu His Val Gly Glu Ser Phe Glu
50 55 60

```

Gln Leu Val Glu Asn Thr Val Gln Lys Leu Val Phe Ser Arg Asn Ala
 65 70 75 80
 Arg Ala Phe Asp Tyr Ala Trp Leu Asp Ile Leu Trp Lys Leu Gly Lys
 85 90 95
 Pro Glu Lys Ser Val
 100

(2) INFORMATIONS POUR LA SEQ ID NO: 885:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 356 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 866665..867732

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 885:

Met Asn Gln Asn Pro Ile Lys Arg Leu Gln Asp Ser Leu Val Glu Arg
 1 5 10 15
 Ala Leu Asp Ala Phe Leu Ile Glu Lys Asp Glu Asp Ile Ser Tyr Phe
 20 25 30
 Leu Gln Asp Gln Ala Arg Ser Gly Val Leu Leu Ile Thr Arg Asp Glu
 35 40 45
 Ala Val Leu Phe Val Ser Pro Leu Asp Lys Asp Leu Tyr Ala Arg Ile
 50 55 60
 Gln Asp Val Val Leu Val Ser Tyr Ser Lys Ser Val Asp Gln Glu Leu
 65 70 75 80
 Gly Ser Tyr Ile Glu Asn Thr Gly Leu Lys Thr Ile Gly Phe Asp Ser
 85 90 95
 Glu Tyr Thr Pro Tyr Gly Ile Ala Gln Lys Arg Met Asn Ser Gly Tyr
 100 105 110
 Ala Phe Ser Pro Gln Ser Leu Val Ala Glu Lys Leu Arg Cys Val Lys
 115 120 125
 Ser Thr Glu Glu Ile Gln Lys Met Thr Arg Ala Ala Glu Ile Gly Ser
 130 135 140
 Ala Gly Tyr Asp Phe Val Leu Ala Ala Leu Arg Pro Gly Ile Thr Glu
 145 150 155 160
 Lys Glu Leu Val Arg Met Leu His Val Phe Trp Ala Asn Leu Gly Ile
 165 170 175
 Glu Lys Val Ser Phe Pro Pro Ile Ile Ala Phe Gly Glu Asn Ala Ala
 180 185 190
 Phe Pro His Ala Ile Pro Thr Asn Arg Ser Leu Lys Lys Gly Asp Val
 195 200 205
 Val Leu Ile Asp Ile Gly Val Cys Tyr Glu Gly Tyr Cys Ser Asp Met
 210 215 220
 Thr Arg Thr Val Ala Phe Gly Ala Ala Pro Glu Gln Gln Leu Leu Asp
 225 230 235 240
 Gly Tyr Val Ala Val Ala Glu Ala Gln Arg Ala Ala Ile Glu Phe Cys
 245 250 255
 Arg Ala Gly Val Pro Cys Arg Asp Val His Lys Glu Ala Val Arg Ile
 260 265 270
 Leu Arg Ala His Gly Met Glu Lys Ala Phe Ile His Gly Leu Gly His
 275 280 285
 Gly Val Gly Arg Glu Val His Glu Tyr Pro Arg Leu Ser Pro Phe Ser

```

      290              295              300
Asp Ala Thr Leu Gln Leu Asn Met Ala Val Thr Val Glu Pro Gly Val
305              310              315              320
Tyr Phe Pro Gly Val Gly Gly Ile Arg Ile Glu Asp Thr Ile Val Ile
      325              330              335
Gly Val Asn Glu Asn Leu Asn Leu Thr Asn Arg Lys Val Ser Ser Glu
      340              345              350
Ile Ile Ile Ile
      355

```

(2) INFORMATIONS POUR LA SEQ ID NO: 886:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 427 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 867810..869090

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 886:

```

Phe Phe Phe Ser Asn Gln Leu Leu Tyr Thr Ile Leu Phe Cys Phe Ser
1      5      10      15
Val Val Met Arg Gln Leu His Phe Phe Phe Tyr Gln Trp Ile Arg Gly
20      25      30
Ala Ala Leu Ile Gly Ala Ile Ala Gly Val Cys Ser Pro Leu Thr Ala
35      40      45
Glu Glu Lys Gln Pro Ala Cys Ser Gly Ala Trp Ala Leu Gln Asp Phe
50      55      60
Ser Ile Glu Glu Glu Leu Pro Asp Leu Arg Asn Gln Phe Val Phe Leu
65      70      75      80
Gly Cys Asn Lys Arg Pro Asp Ala Arg Ser Gly Lys Phe Phe Leu Glu
85      90      95
Leu Ala Thr Thr Asn Ala Ile Gln Glu Val Ser Leu Gly Glu Lys Val
100      105      110
Phe Leu Arg Gln Gly Pro Asp Glu Glu Thr Leu Val Phe Ser Ala Glu
115      120      125
Pro Thr Pro Leu Trp Leu Glu Cys Arg Pro Ser Ser Asp Gly Arg Ser
130      135      140
Leu Asp Val Val Val Arg Met Lys Gly Ala Leu Gly Gly Ala Val Ser
145      150      155      160
Ser Pro Lys Glu Arg Ala His Phe Ser Leu Ser Met Ala Pro Arg Cys
165      170      175
Ser Gln Thr Trp Glu Ile Gly Gly Met Arg Val Glu Pro Ser Ile Ala
180      185      190
Val Lys Gln Arg Ile Arg Cys Val Gly Gly Asp Lys Phe Leu Leu Met
195      200      205
His Gly Gly Ala Asp Tyr Val Ile Gln Ala Ala Lys Glu Arg Val Asp
210      215      220
Phe Glu Ser Leu Ser Gly Glu Ala Tyr Ser Gln Tyr Leu Ala Val Gly
225      230      235      240
Asp Val Leu Leu Trp Asp Gln Asp Arg Trp Val Pro Tyr Lys Thr Phe
245      250      255
Gln Gly Asp Gly Thr Arg Val Pro Leu Leu Glu Val Lys Arg Leu Asp
260      265      270

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Asp Arg Met Met Val Ile Glu Leu Trp Ser Ile Asp Gly Leu Met Ser
      275                      280          285
Gln Gln Ile Thr Leu Val Lys Gln Val Ser Ser Pro Ile Glu Ile Ala
      290                      295          300
Glu Leu Val Lys Glu Phe Ser Phe Val Gly Met Arg Thr Trp Ser Arg
305                      310          315          320
Pro Ile Ile Thr Ala Gly Lys Asp Arg Leu Val Leu Ser Ala Asp Asp
      325                      330          335
Trp Val Ile His Thr Gly Glu Arg Trp Glu Arg Val Thr Ser Lys Arg
      340                      345          350
Gln Leu Glu Asp Tyr Leu Ser Gly Lys Leu Arg Ser Pro Leu Leu Val
      355                      360          365
Phe Glu Arg Ile Asp Lys Glu Asp Gly Glu Phe Val Phe Lys Gly His
370                      375          380
Val Phe Asn Thr Gln Arg Thr Val Val Glu Thr Ile Ser Leu Pro Leu
385                      390          395          400
Lys Gln Val Leu Glu Thr Val Ala Gln Ser His Leu Gly Gln Glu Ser
      405                      410          415
Gly Thr Lys Asn Ser Arg Ile Gly Gly Gly Ser
      420                      425

```

(2) INFORMATIONS POUR LA SEQ ID NO: 887:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 869094..869357

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 887:

```

Val Lys Asn Ile Leu Gly Tyr Gly Phe Leu Gly Thr Phe Cys Leu Gly
1           5           10           15
Ser Leu Thr Val Pro Ser Phe Ser Ile Thr Ile Thr Glu Lys Leu Ala
      20           25           30
Ser Leu Glu Gly Lys Thr Glu Ser Leu Ala Pro Phe Ser His Ile Ser
      35           40           45
Ser Phe Asn Ala Glu Leu Lys Glu Ala Asn Asp Val Leu Lys Ser Leu
50           55           60
Tyr Glu Glu Ala Leu Ser Leu Arg Ser Arg Gly Glu Thr Ser Gln Ala
65           70           75           80
Val Trp Asp Glu Leu Arg Thr Asp
      85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 888:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 701 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 869270..871372

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 888:

Cys	Ser	Gln	Ile	Phe	Ile	Arg	Arg	Ser	Phe	Val	Ser	Pro	Phe	Ser	Arg	1	5	10	15
Arg	Asp	Phe	Ala	Gly	Gly	Met	Gly	Arg	Val	Ala	Asn	Arg	Leu	Ile	Gly	20	25	30	
Ala	Lys	Gln	Arg	Ile	Arg	Ser	Leu	Glu	Asp	Leu	Trp	Ser	Val	Glu	Val	35	40	45	
Ala	Glu	Arg	Gly	Gly	Asp	Pro	Glu	Asp	Tyr	Ala	Leu	Trp	Asn	His	Pro	50	55	60	
Glu	Thr	Thr	Ile	Tyr	Asn	Leu	Val	Ser	Asp	Tyr	Gly	Asp	Glu	Gln	Ser	65	70	75	80
Ile	Tyr	Val	Ile	Pro	Gln	Asn	Val	Gly	Ala	Met	Arg	Ile	Thr	Ala	Met	85	90	95	
Ser	Lys	Leu	Val	Val	Pro	Lys	Glu	Gly	Phe	Glu	Glu	Cys	Leu	Ser	Leu	100	105	110	
Leu	Leu	Met	Arg	Leu	Gly	Ile	Gly	Ile	Arg	Gln	Val	Ser	Pro	Trp	Ile	115	120	125	
Lys	Glu	Leu	Tyr	Leu	Thr	Asn	Arg	Glu	Glu	Ser	Gly	Val	Leu	Gly	Ile	130	135	140	
Phe	Gly	Ser	Arg	Gln	Glu	Leu	Asp	Ser	Leu	Pro	Met	Thr	Ala	His	Ile	145	150	155	160
Ala	Phe	Val	Leu	Ser	Ser	Lys	Asn	Leu	Asp	Ala	Arg	Ala	Asp	Val	Gln	165	170	175	
Ala	Leu	Arg	Lys	Phe	Ala	Asn	Ser	Asp	Thr	Met	Leu	Ile	Asp	Phe	Ile	180	185	190	
Gly	Gly	Lys	Val	Trp	Leu	Phe	Gly	Ala	Val	Ser	Glu	Ile	Thr	Glu	Leu	195	200	205	
Leu	Lys	Ile	Tyr	Glu	Phe	Leu	Gln	Ser	His	Asn	Ile	Arg	Glu	Glu	His	210	215	220	
Xaa	Ile	Val	Ser	Leu	Ser	Lys	Ile	Glu	Pro	Ser	Glu	Met	Leu	Xaa	Ile	225	230	235	240
Leu	Lys	Ala	Ala	Phe	Arg	Glu	Asp	Leu	Ala	Lys	Glu	Gly	Glu	Asp	Ser	245	250	255	
Ser	Gly	Val	Gly	Leu	Lys	Val	Val	Pro	Leu	Gln	Asn	His	Gly	Arg	Ser	260	265	270	
Leu	Phe	Leu	Ser	Gly	Ala	Leu	Pro	Ile	Val	Gln	Lys	Ala	Ile	Asp	Leu	275	280	285	
Ile	Arg	Glu	Leu	Glu	Glu	Gly	Ile	Glu	Ser	Pro	Thr	Asp	Lys	Thr	Val	290	295	300	
Phe	Trp	Tyr	His	Val	Lys	His	Ser	Asp	Pro	Gln	Glu	Leu	Ala	Ala	Leu	305	310	315	320
Leu	Ser	Gln	Val	His	Asp	Ile	Phe	Ser	Asn	Gly	Ala	Ser	Gly	Ala	Ser	325	330	335	
Ser	Ser	Cys	Asp	Thr	Gly	Val	Val	Ser	Ser	Lys	Ala	Gly	Ser	Ser	Ser	340	345	350	
Asn	Gly	Leu	Gly	Val	His	Ile	Asp	Thr	Ser	Leu	Arg	Ser	Ser	Val	Lys	355	360	365	
Glu	Gly	Ser	Ala	Lys	Tyr	Gly	Ser	Phe	Ile	Ala	Asp	Ser	Lys	Thr	Gly	370	375	380	
Thr	Leu	Ile	Met	Val	Ile	Glu	Lys	Glu	Ala	Leu	Pro	Lys	Ile	Lys	Met	385	390	395	400
Leu	Leu	Lys	Lys	Leu	Asp	Val	Pro	Lys	Lys	Met	Val	Arg	Ile	Glu	Val	405	410	415	
Leu	Leu	Phe	Glu	Arg	Lys	Leu	Ser	Asn	Gln	Arg	Lys	Ser	Gly	Leu	Asn	420	425	430	

Leu Leu Arg Leu Gly Glu Glu Val Cys Lys Gln Gly Thr Gln Ala Val
 435 440 445
 Ser Trp Ala Ser Gly Gly Ile Leu Glu Phe Leu Phe Lys Gly Gly Ala
 450 455 460
 Lys Gly Ile Val Pro Ser Tyr Asp Phe Ala Tyr Gln Phe Leu Met Ala
 465 470 475 480
 Gln Glu Asp Val Arg Ile Asn Ala Ser Pro Ser Val Val Thr Met Asn
 485 490 495
 Gln Thr Pro Ala Arg Ile Ala Ile Val Glu Glu Met Ser Ile Val Val
 500 505 510
 Ser Ser Asp Lys Asp Lys Ala Gln Tyr Asn Arg Ala Gln Tyr Gly Ile
 515 520 525
 Met Ile Lys Ile Leu Pro Val Ile Asn Ile Gly Glu Glu Asp Gly Lys
 530 535 540
 Ser Phe Ile Thr Leu Glu Thr Asp Ile Thr Phe Asp Ser Thr Gly Arg
 545 550 555 560
 Asn His Ala Asp Arg Pro Asp Val Thr Arg Arg Asn Ile Thr Asn Lys
 565 570 575
 Val Arg Ile Gln Asp Gly Glu Thr Val Ile Ile Gly Gly Leu Arg Cys
 580 585 590
 Asn Gln Thr Met Asp Ser Arg Asp Gly Ile Pro Phe Leu Gly Glu Leu
 595 600 605
 Pro Gly Ile Gly Lys Leu Phe Gly Met Asp Ser Ala Ser Asp Ser Gln
 610 615 620
 Thr Glu Met Phe Met Phe Ile Thr Pro Lys Ile Leu Asp Asn Pro Ser
 625 630 635 640
 Glu Thr Glu Glu Lys Leu Glu Cys Ala Phe Leu Ala Ala Arg Pro Gly
 645 650 655
 Glu Asn Asp Asp Phe Leu Arg Ala Leu Val Ala Gly Gln Gln Ala Ala
 660 665 670
 Lys Gln Ala Ile Glu Arg Lys Glu Ser Thr Val Trp Gly Glu Glu Ser
 675 680 685
 Ser Gly Ser Arg Gly Arg Val Glu Tyr Asp Gly Arg Glu
 690 695 700

(2) INFORMATIONS POUR LA SEQ ID NO: 889:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 428 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 871299..872582

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 889:

Lys Glu Lys Ser Leu Pro Tyr Gly Glu Lys Asn Pro Pro Ala Leu Glu
 1 5 10 15
 Glu Gly Trp Ser Met Met Asp Gly Asn Lys Gly Thr Met Gln Asp Leu
 20 25 30
 Leu Asp Arg Leu Pro Tyr Ser Phe Leu Lys Lys Asn Tyr Leu Leu Pro
 35 40 45
 Val Glu Asp Leu Gly Asp Lys Ile Val Phe Ala Arg His Leu Lys Lys
 50 55 60
 Thr Pro Leu Glu Ala Leu Asp Glu Val Arg Leu Ile Thr Gln Lys Pro

65					70					75					80
Leu	Ser	Leu	Val	Ser	Lys	Glu	Glu	Ala	Glu	Ile	Ile	His	Gly	Leu	Gln
				85					90					95	
Lys	Leu	Tyr	Ser	Asp	Lys	Asp	Gly	Lys	Ala	Ser	Glu	Met	Leu	Gln	Ser
			100					105					110		
Met	Gln	Glu	Ala	Val	Val	Pro	Glu	Ser	Glu	Ser	Asp	Thr	Thr	Glu	Leu
		115					120					125			
Leu	Glu	Asn	Gln	Glu	Asn	Ser	Ala	Pro	Val	Val	Arg	Leu	Leu	Asn	Leu
	130				135						140				
Ile	Leu	Lys	Glu	Ala	Ile	Glu	Glu	Arg	Ala	Ser	Asp	Ile	His	Phe	Asp
145				150						155				160	
Pro	Val	Glu	Asp	Leu	Leu	Arg	Ile	Arg	Tyr	Arg	Ile	Asp	Gly	Val	Leu
			165					170					175		
His	Asp	Arg	His	Ala	Pro	Pro	Asn	His	Leu	Arg	Ala	Ala	Leu	Ile	Thr
			180					185					190		
Arg	Ile	Lys	Val	Leu	Thr	Lys	Leu	Asp	Ile	Ala	Glu	His	Arg	Leu	Pro
		195					200					205			
Gln	Asp	Gly	Arg	Ile	Lys	Leu	Gln	Leu	Gly	Gly	Gln	Glu	Ile	Asp	Met
	210				215						220				
Arg	Val	Ser	Thr	Val	Pro	Val	Ile	His	Gly	Glu	Arg	Val	Val	Leu	Arg
225					230					235				240	
Ile	Leu	Asp	Lys	Arg	Asn	Val	Ile	Leu	Asp	Ile	Arg	Gly	Leu	Cys	Met
			245					250					255		
Pro	Pro	Lys	Met	Glu	Thr	Ser	Phe	Arg	Lys	Ala	Ile	Gly	Val	Pro	Glu
			260				265						270		
Gly	Ile	Leu	Leu	Val	Thr	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Thr
	275					280						285			
Leu	Tyr	Ser	Val	Ile	Gln	His	Leu	Ser	Gly	Pro	Phe	Thr	Asn	Ile	Met
	290				295					300					
Thr	Ile	Glu	Asp	Pro	Pro	Glu	Tyr	Lys	Leu	Pro	Gly	Val	Ala	Gln	Ile
305					310					315				320	
Ala	Val	Lys	Pro	Lys	Ile	Gly	Leu	Thr	Phe	Ser	Lys	Gly	Leu	Arg	His
			325					330					335		
Leu	Leu	Arg	Gln	Asp	Pro	Asp	Val	Leu	Met	Val	Gly	Glu	Ile	Arg	Asp
			340				345						350		
Gln	Glu	Thr	Ala	Glu	Ile	Ala	Ile	Gln	Ala	Ala	Leu	Thr	Gly	His	Leu
	355					360						365			
Val	Val	Ser	Thr	Leu	His	Thr	Asn	Asp	Ala	Val	Ser	Ala	Ile	Pro	Arg
	370					375					380				
Leu	Leu	Asp	Met	Gly	Val	Glu	Pro	Tyr	Leu	Leu	Ser	Ala	Thr	Met	Ile
385					390					395				400	
Gly	Leu	Ser	Leu	Asn	Asp	Ser	Ser	Val	Glu	Phe	Val	Arg	Ile	Ala	Lys
			405					410					415		
Asn	Ser	Val	Trp	Pro	Met	Cys	Lys	Asn	Arg	Leu	Tyr				
			420					425							

(2) INFORMATIONS POUR LA SEQ ID NO: 890:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 144 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 872429..872860

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 890:

Cys	Cys	Phe	Cys	Asn	Pro	Ala	Ser	Phe	Arg	His	Gly	Ser	Arg	Ala	Leu
1				5					10					15	
Phe	Ile	Ile	Arg	Asn	Asn	Asp	Arg	Ala	Val	Ala	Gln	Arg	Leu	Val	Arg
			20					25					30		
Arg	Ile	Cys	Thr	His	Cys	Lys	Glu	Phe	Cys	Val	Ala	Asp	Val	Gln	Glu
		35					40					45			
Gln	Ala	Leu	Leu	Arg	Ala	Leu	Gly	Lys	Asp	Pro	Phe	Ala	Pro	Leu	Cys
	50					55					60				
Lys	Gly	Arg	Gly	Cys	Ser	Gln	Cys	Phe	Arg	Ser	Gly	Tyr	Lys	Gly	Arg
65					70					75					80
Gln	Gly	Ile	Tyr	Glu	Phe	Val	Asp	Val	Thr	Thr	Thr	Leu	Arg	Ser	Glu
				85					90					95	
Ile	Ala	Leu	Gly	Arg	Pro	Tyr	His	Ile	Leu	Arg	Gly	Val	Ala	Glu	Arg
			100					105					110		
Glu	Gly	Tyr	Cys	Pro	Leu	Leu	Glu	His	Gly	Val	Glu	Leu	Ala	Leu	Ala
		115					120				125				
Gly	Glu	Thr	Thr	Leu	Ser	Glu	Val	Leu	Arg	Val	Ala	Lys	Arg	Ser	Glu
	130						135				140				

(2) INFORMATIONS POUR LA SEQ ID NO: 891:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 347 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 872875..873915

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 891:

Met	Ala	Arg	Phe	Leu	Cys	Thr	Tyr	Leu	Asp	Gln	Ser	Glu	Lys	Lys	Arg
1				5					10					15	
Arg	Ser	Phe	Val	Glu	Ala	Phe	His	Gln	Arg	Glu	Ala	Arg	Glu	Leu	Leu
			20					25					30		
Ala	Ala	Gln	Gly	Ala	Arg	Ile	Leu	Asp	Ile	Arg	Lys	Val	Arg	Glu	Arg
		35					40					45			
Asn	Tyr	Arg	Val	Thr	Thr	Thr	Glu	Leu	Val	Ile	Phe	Thr	Lys	Gln	Leu
	50					55					60				
Ala	Leu	Leu	Leu	Arg	Ser	Gly	Ile	Ser	Leu	Tyr	Asp	Ala	Leu	Thr	Ser
65					70					75					80
Leu	Arg	Asp	Gln	Tyr	Gln	Gly	His	Ala	Leu	Ala	Gly	Val	Leu	Thr	Ser
			85					90					95		
Leu	Met	Glu	Ala	Leu	Arg	Ser	Gly	Gly	Val	Phe	Ser	Glu	Ala	Leu	Ala
			100					105					110		
Arg	Leu	Pro	His	Ile	Phe	Asp	Ser	Phe	Tyr	Gln	Asn	Ser	Val	Arg	Ser
		115					120					125			
Gly	Glu	Ser	Ile	Gly	Asn	Leu	Glu	Gly	Ala	Leu	Met	Asn	Ile	Ile	Lys
	130					135					140				
Val	Leu	Glu	Glu	Lys	Glu	Lys	Leu	Ser	Lys	Ser	Leu	Ala	Ala	Ala	Leu
145					150					155					160
Ser	Tyr	Pro	Ala	Ile	Leu	Leu	Val	Phe	Ser	Cys	Ala	Val	Val	Val	Phe
			165						170					175	
Phe	Leu	Ile	Gly	Val	Ile	Pro	Thr	Leu	Lys	Glu	Thr	Phe	Glu	Asp	Met

180 185 190
 Glu Met Thr Arg Leu Thr Lys Ala Val Phe Ser Cys Ser Thr Trp Phe
 195 200 205
 Cys Arg Tyr Lys Phe Leu Val Leu Leu Gly Gly Ile Gly Gly Ala Ile
 210 215 220
 Ser Leu Arg Ile Val Trp Lys Lys Arg Ile Gly Lys Arg Thr Leu Glu
 225 230 235 240
 Ala Ile Ile Lys Lys Ile Pro Ile Leu Arg Ser Leu Val Ile Lys Ile
 245 250 255
 Gly Phe Cys Arg Phe Cys Ser Val Thr Ser Ala Val Leu Gln Gly Gly
 260 265 270
 Gly Asn Leu Ile Glu Ala Leu Thr Leu Gly Cys Glu Ala Val Ser Gln
 275 280 285
 Asp Phe Leu Arg Glu Glu Leu Gln Glu Val Ile Gln Ala Val Val Arg
 290 295 300
 Gly Gly Ser Leu Ser Arg Glu Leu Ser His Arg Thr Trp Thr Pro Lys
 305 310 315 320
 Leu Val Ile Gly Met Val Ala Leu Gly Glu Glu Ser Gly Asp Leu Ala
 325 330 335
 Val Val Phe Ala His Val Ala Gln Ile Tyr Arg
 340 345

(2) INFORMATIONS POUR LA SEQ ID NO: 892:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 151 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(873360..873812)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 892:

Asp Ser Ser Arg Leu Lys Asp Pro Pro Arg Thr Thr Ala Trp Ile Thr
 1 5 10 15
 Ser Cys Ser Ser Ser Arg Lys Lys Ser Cys Asp Thr Ala Ser His Pro
 20 25 30
 Asn Val Arg Ala Ser Ile Lys Phe Pro Pro Pro Cys Lys Thr Ala Asp
 35 40 45
 Val Thr Glu Gln Asn Arg Gln Asn Pro Ile Leu Ile Thr Arg Leu Arg
 50 55 60
 Lys Ile Gly Ile Phe Leu Ile Ile Ala Ser Arg Val Leu Phe Pro Ile
 65 70 75 80
 Arg Phe Phe Gln Thr Met Arg Arg Asp Ile Ala Pro Pro Ile Pro Pro
 85 90 95
 Ser Lys Thr Arg Asn Leu Tyr Leu Gln Asn His Val Leu His Glu Lys
 100 105 110
 Thr Ala Phe Val Ser Leu Val Ile Ser Ile Ser Ser Lys Val Ser Phe
 115 120 125
 Asn Val Gly Met Thr Pro Ile Arg Lys Asn Thr Thr Thr Ala Gln Glu
 130 135 140
 Asn Thr Asn Lys Ile Ala Gly
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 893:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 137 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 874028..874438

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 893:

Gln	Ala	Val	Phe	Lys	Arg	Phe	Asn	Tyr	Arg	Arg	Glu	Thr	Val	Lys	Lys
1				5					10					15	
Thr	Lys	Lys	Arg	Lys	Gln	Ser	Ile	Thr	Leu	Val	Glu	Met	Met	Val	Val
			20					25					30		
Ile	Thr	Leu	Ile	Gly	Ile	Ile	Gly	Gly	Ala	Leu	Ala	Phe	Asn	Met	Arg
		35					40					45			
Gly	Ser	Leu	Gln	Lys	Gly	Lys	Ile	Phe	Gln	Thr	Glu	Gln	Asn	Cys	Ala
	50					55					60				
Arg	Val	Tyr	Asp	Val	Leu	Met	Met	Glu	Tyr	Ala	Ser	Gly	Asn	Leu	Ser
65				70					75					80	
Leu	Lys	Glu	Val	Ile	Ala	Asn	Lys	Glu	Ala	Ile	Leu	Glu	Asp	Ser	Ala
			85					90					95		
Trp	Cys	Lys	Glu	Ile	Lys	Lys	Leu	Leu	Lys	Asp	Ala	Trp	Gly	Glu	Asp
			100					105					110		
Leu	Leu	Val	Lys	Met	Asn	Asp	Lys	Gly	Asp	Asp	Ile	Val	Val	Phe	Ser
		115					120					125			
Lys	Lys	Val	Arg	Asn	Glu	Gln	Arg	Gly							
		130					135								

(2) INFORMATIONS POUR LA SEQ ID NO: 894:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 203 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 874778..875386

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 894:

Arg	Arg	Arg	Gln	Ala	Phe	Met	Phe	Gly	Arg	Arg	Tyr	Gly	Gly	Leu	Ile
1				5					10					15	
Pro	Trp	Pro	Glu	Lys	Gly	Ser	Arg	Cys	Thr	Glu	Val	Phe	Met	Phe	Arg
			20					25					30		
Lys	Ile	Lys	Lys	Lys	Arg	Ala	Phe	Leu	Leu	Ser	Glu	Leu	Leu	Ile	Ala
		35					40					45			
Cys	Val	Leu	Ile	Ser	Leu	Leu	Leu	Gly	Ser	Leu	Gly	Tyr	Trp	Thr	Arg
	50					55					60				
Arg	Ile	Trp	Ile	Ser	His	Lys	Glu	Lys	Glu	His	Val	Tyr	Arg	Ile	Phe
65				70					75					80	
Leu	Asn	Glu	Ser	Lys	Thr	Tyr	Arg	Phe	Leu	Arg	Gly	Thr	Phe	Leu	Ser

(2) INFORMATIONS POUR LA SEQ ID NO: 896:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 270 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(877000..877809)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 896:

Phe	Gln	Lys	Pro	Ala	Asp	Tyr	Val	Trp	Thr	Val	Phe	Leu	Leu	Leu	Ala	1	5	10	15
Ala	Arg	Ile	Leu	Ser	Met	Leu	Ser	Ile	Ile	Pro	Phe	Leu	Gly	Ala	Lys	20	25	30	
Leu	Phe	Pro	Ser	Pro	Ile	Lys	Ile	Gly	Ile	Ala	Leu	Ser	Trp	Met	Gly	35	40	45	
Leu	Leu	Leu	Pro	Gln	Val	Ile	Gln	Asp	Ser	Thr	Ile	Val	His	Tyr	Gln	50	55	60	
Asp	Leu	Asp	Ile	Phe	Tyr	Ile	Leu	Leu	Ile	Lys	Glu	Ile	Leu	Ile	Gly	65	70	75	
Val	Leu	Ile	Gly	Phe	Leu	Phe	Ser	Phe	Pro	Phe	Tyr	Ala	Ala	Gln	Ser	85	90	95	
Ala	Gly	Ser	Phe	Ile	Thr	Asn	Gln	Gln	Gly	Ile	Gln	Gly	Leu	Glu	Gly	100	105	110	
Ala	Thr	Ser	Leu	Val	Ser	Ile	Glu	Gln	Thr	Ser	Pro	His	Gly	Ile	Phe	115	120	125	
Tyr	His	Tyr	Phe	Val	Thr	Ile	Val	Phe	Trp	Leu	Ala	Gly	Gly	His	Arg	130	135	140	
Ile	Ile	Leu	Ser	Val	Leu	Gln	Ser	Leu	Glu	Ile	Ile	Pro	Leu	His		145	150	155	
Ala	Val	Phe	Pro	Glu	Ser	Met	Met	Ser	Leu	Arg	Ala	Pro	Met	Trp	Ile	165	170	175	
Ala	Ile	Leu	Lys	Met	Cys	Gln	Leu	Cys	Leu	Ile	Met	Thr	Ile	Gln	Leu	180	185	190	
Ser	Ala	Pro	Ala	Ala	Val	Ala	Met	Leu	Met	Ser	Asp	Leu	Phe	Leu	Gly	195	200	205	
Ile	Ile	Asn	Arg	Met	Ala	Pro	Gln	Val	Gln	Val	Ile	Tyr	Leu	Leu	Ser	210	215	220	
Ala	Leu	Lys	Ala	Phe	Met	Gly	Leu	Leu	Phe	Leu	Thr	Leu	Ala	Trp	Trp	225	230	235	
Phe	Ile	Val	Lys	Gln	Ile	Asp	Tyr	Phe	Thr	Leu	Ala	Trp	Phe	Lys	Glu	245	250	255	
Ile	Pro	Thr	Met	Leu	Phe	Gly	Ala	His	Pro	Pro	Lys	Val	Leu			260	265	270	

(2) INFORMATIONS POUR LA SEQ ID NO: 897:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 92 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(877876..878151)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 897:

```

Met Leu Ala Thr Ser Phe Lys Ser Ile Leu Phe Glu Tyr Ser Tyr Glu
1      5      10      15
Ala Leu Leu Leu Ile Leu Ile Ile Ser Ala Pro Pro Ile Ile Leu Ala
20      25      30
Ser Val Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile
35      40      45
Gln Glu Gln Thr Phe Ala Phe Ala Ile Lys Leu Val Val Ile Phe Gly
50      55      60
Thr Leu Met Ile Thr Gly Gly Trp Leu Cys Ser Met Ile Leu Arg Phe
65      70      75      80
Ala Ala Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
85      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 898:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 225 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(878172..878846)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 898:

```

Ser Glu Thr Tyr Pro Asp Leu Thr Thr Gln Ala Val Ile Leu Leu Phe
1      5      10      15
Leu Ala Leu Ser Pro Phe Leu Val Met Leu Leu Thr Ser Tyr Leu Lys
20      25      30
Ile Ile Ile Thr Leu Val Leu Leu Arg Asn Ala Leu Gly Val Gln Gln
35      40      45
Thr Pro Pro Ser Gln Val Leu Asn Gly Ile Ala Leu Ile Leu Ser Ile
50      55      60
Tyr Val Met Phe Pro Thr Gly Val Ala Met Tyr His Asp Ala Lys Lys
65      70      75      80
Gly Ile Glu Ser Ser Ala Val Pro Arg Asp Leu Phe Ser Ala Glu Gly
85      90      95
Ala Glu Thr Val Phe Val Ala Leu Asn Lys Ser Lys Glu Pro Leu Arg
100      105      110
Ser Phe Leu Ile Lys Asn Thr Pro Lys Pro Gln Ile Gln Ser Phe Tyr
115      120      125
Lys Ile Ser Gln Lys Thr Phe Pro Pro Glu Leu Arg Gln Gln Leu Thr
130      135      140
Pro Ser Asp Phe Met Ile Ile Ile Pro Ala Phe Ile Met Gly Gln Ile
145      150      155      160
Lys Asn Ala Phe Glu Ile Gly Val Leu Ile Tyr Leu Pro Phe Phe Val
165      170      175
Ile Asp Leu Val Thr Ala Asn Val Leu Val Ala Met Gln Met Met Met
180      185      190
Leu Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu Leu Val Val
195      200      205

```

Met Val Asp Gly Trp Thr Leu Leu Leu Glu Gly Leu Met Ile Ser Phe
 210 215 220
 Lys
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 899:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 93 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 878883..879161

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 899:

Gln	Val	Leu	Ser	Phe	Tyr	Arg	Trp	Ser	Ile	Arg	Trp	Thr	Thr	Lys	Arg
1				5					10					15	
Leu	Phe	Ser	Phe	Phe	Trp	Arg	Cys	Trp	Lys	Phe	Leu	Leu	Arg	Ser	Gly
			20					25					30		
Arg	Ala	Arg	Lys	Ala	Arg	Arg	Gly	Ala	Leu	Cys	Cys	Gly	Thr	Ser	Thr
			35				40					45			
Gly	Glu	Ala	Ile	Gly	Ser	Ala	Lys	Asn	Ala	Glu	Lys	Glu	Glu	Asn	Ser
	50					55				60					
Asn	Asn	Gln	Ser	His	Lys	Ile	Gln	Tyr	Leu	Val	Phe	Leu	Ala	Leu	Arg
65					70					75					80
Leu	Ile	Cys	Cys	Arg	Ser	Val	Arg	Arg	Phe	Phe	Met	Phe			
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 900:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 223 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(879105..879773)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 900:

Met	Lys	Phe	Phe	Ser	Leu	Ile	Tyr	Lys	Asp	Gln	Glu	Val	Val	Pro	Asn
1				5					10					15	
Lys	Lys	Val	Leu	Ser	Pro	Asp	Ala	Tyr	Thr	Ala	Val	Leu	Thr	Ala	Gln
			20					25					30		
Glu	Leu	Leu	Glu	Lys	Thr	Gln	Glu	Asp	Cys	Glu	Ala	Tyr	Thr	Gln	Asn
		35				40					45				
Thr	His	Glu	Glu	Cys	Ala	Lys	Leu	Arg	Glu	Glu	Ala	Lys	Asn	Gln	Gly
	50					55				60					
Phe	Gln	Glu	Gly	Ser	Lys	Ala	Trp	Ser	Lys	Gln	Leu	Ala	Phe	Leu	Ile
65					70					75					80
Thr	Glu	Thr	Gln	Ala	Met	Arg	Glu	Gln	Ile	Lys	Ala	Ser	Leu	Val	Pro




```

Ala Leu Arg His Phe Ile His Val Gln Gly Leu Arg Phe Leu Ala Arg
  210                215                220
Ala Leu Ala Lys Glu Asp Ser Ser Phe Leu Trp Tyr Phe Ile Arg Arg
225                230                235                240
Leu Asp Val Gly Arg Gly Tyr Ile Phe Glu Lys Ala Leu Gln Ser Ser
                245                250                255
Ile Asp Ser Pro His Asn Glu Tyr Phe Arg Glu Arg Leu Glu His Cys
                260                265                270
Ile Ser Ile Leu Val Gln
                275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 902:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 314 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(880889..881830)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 902:

```

Phe Ile Leu Ala Leu Phe Phe Cys Ser Ala Cys Asp Ser Arg Ser Met
1           5           10           15
Ile Thr His Gly Leu Ser Gly Arg Asp Ala Asn Glu Ile Val Val Leu
          20           25           30
Leu Val Ser Lys Gly Val Ala Ala Gln Lys Val Pro Gln Ala Ala Ser
          35           40           45
Ser Thr Gly Gly Ser Gly Glu Gln Leu Trp Asp Ile Ser Val Pro Ala
          50           55           60
Ala Gln Ile Thr Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro
65           70           75           80
Arg Met Lys Gly Thr Ser Leu Leu Asp Leu Phe Ser Lys Gln Gly Leu
          85           90           95
Val Pro Ser Glu Met Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser
          100          105          110
Glu Gln Met Ala Thr Thr Ile Arg Lys Met Asp Gly Ile Val Asp Ala
          115          120          125
Ser Val Gln Ile Ser Phe Ser Pro Glu Glu Asp Gln Arg Pro Leu Thr
          130          135          140
Ala Ser Val Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser
145          150          155          160
Ile Met Val Ser Lys Ile Lys Arg Leu Val Ala Ser Ala Val Pro Gly
          165          170          175
Leu Tyr Pro Glu Asn Val Ser Val Val Ser Asp Arg Ala Ser Tyr Ser
          180          185          190
Asp Ile Thr Ile Asn Gly Pro Trp Gly Leu Ser Asp Glu Met Asp Tyr
          195          200          205
Val Ser Val Trp Gly Ile Ile Leu Ala Lys His Ser Leu Thr Lys Phe
          210          215          220
Arg Leu Val Phe Tyr Phe Leu Ile Leu Leu Leu Phe Ile Leu Ser Cys
225          230          235          240
Gly Leu Leu Trp Val Ile Trp Lys Thr His Thr Leu Ile Ser Ala Leu
          245          250          255
Gly Gly Thr Lys Gly Phe Phe Asp Pro Ala Pro Tyr Ser Gln Leu Ser

```

260 265 270
 Phe Thr Gln Asn Lys Pro Ala Pro Lys Glu Thr Pro Gly Ala Ala Glu
 275 280 285
 Gly Ala Glu Ala Gln Thr Ala Ser Glu Gln Pro Pro Lys Glu Asn Ala
 290 295 300
 Glu Lys Gln Glu Glu Asn Asn Glu Asp Ala
 305 310

(2) INFORMATIONS POUR LA SEQ ID NO: 903:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 319 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(881948..882904)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 903:

Lys Met Thr Asp Ser Glu Ser Pro Thr Pro Lys Lys Ser Ile Pro Ala
 1 5 10 15
 Arg Phe Pro Lys Trp Leu Arg Gln Lys Leu Pro Leu Gly Arg Val Phe
 20 25 30
 Ala Gln Thr Asp Asn Thr Ile Lys Asn Lys Gly Leu Pro Thr Val Cys
 35 40 45
 Glu Glu Ala Ser Cys Pro Asn Arg Thr His Cys Trp Ser Arg His Thr
 50 55 60
 Ala Thr Tyr Leu Ala Leu Gly Asp Ala Cys Thr Arg Arg Cys Gly Phe
 65 70 75 80
 Cys Asp Ile Asp Phe Thr Arg Asn Pro Leu Pro Pro Asp Pro Glu Glu
 85 90 95
 Gly Ala Lys Ile Ala Glu Ser Ala Lys Ala Leu Gly Leu Lys His Ile
 100 105 110
 Val Ile Thr Met Val Ser Arg Asp Leu Glu Asp Gly Gly Ala Ser
 115 120 125
 Ala Leu Val His Ile Ile Glu Thr Leu His Thr Glu Leu Pro Thr Ala
 130 135 140
 Thr Ile Glu Val Leu Ala Ser Asp Phe Glu Gly Asn Ile Ala Ala Leu
 145 150 155 160
 His His Leu Leu Asp Thr His Ile Ala Ile Tyr Asn His Asn Val Glu
 165 170 175
 Thr Val Glu Arg Leu Thr Pro Phe Val Arg His Lys Ala Thr Tyr Arg
 180 185 190
 Arg Ser Leu Met Met Leu Glu Asn Ala Ala Lys Tyr Leu Pro Asn Leu
 195 200 205
 Met Thr Lys Ser Gly Ile Met Val Gly Leu Gly Glu Gln Glu Ser Glu
 210 215 220
 Val Lys Gln Thr Leu Lys Asp Leu Ala Asp His Gly Val Lys Ile Val
 225 230 235 240
 Thr Ile Gly Gln Tyr Leu Arg Pro Ser Arg Arg His Ile Pro Val Lys
 245 250 255
 Ser Tyr Val Ser Pro Glu Thr Phe Asp Tyr Tyr Arg Ser Val Gly Glu
 260 265 270
 Ser Leu Gly Leu Phe Ile Tyr Ala Gly Pro Phe Val Arg Ser Ser Phe
 275 280 285

```

Asn Ala Asp Ser Val Phe Glu Ala Met Arg Gln Gly Lys Pro Gln Pro
 290                295                300
Leu Arg Tyr Phe Arg Thr Lys Ile Ser His Ile Thr Cys Ser Phe
305                310                315

```

(2) INFORMATIONS POUR LA SEQ ID NO: 904:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(882901..883794)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 904:

```

Thr Ser Lys Lys Ser Leu Lys Lys Trp Pro Leu Leu Ala Glu Gly Val
 1          5          10          15
Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val
 20          25          30
Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Pro Asp
 35          40          45
Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe
 50          55          60
Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val
 65          70          75          80
Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val
 85          90          95
Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala
100          105          110
Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met
115          120          125
Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys
130          135          140
Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg
145          150          155          160
Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser
165          170          175
Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr
180          185          190
Ala Ala Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe
195          200          205
Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala
210          215          220
Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val
225          230          235          240
Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val
245          250          255
Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His
260          265          270
Pro Thr Leu Ala Glu Val Trp Ala Glu Ser Ala Leu Leu Ala Val Asp
275          280          285
Thr Pro Leu His Met Pro Pro Ala Lys Lys
290          295

```

(2) INFORMATIONS POUR LA SEQ ID NO: 905:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 212 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(883661..884296)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 905:

```

Met Asn Glu Ala Phe Asp Cys Val Val Ile Gly Ala Gly Pro Gly Gly
1          5          10          15
Tyr Val Ala Ala Ile Thr Ala Ala Gln Ala Gly Leu Lys Thr Ala Leu
          20          25          30
Ile Glu Lys Arg Glu Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
          35          40          45
Pro Ser Lys Ala Leu Leu Ala Gly Ala Glu Val Val Thr Gln Ile Arg
          50          55          60
His Ala Asp Gln Phe Gly Ile His Val Glu Gly Phe Ser Ile Asn Tyr
65          70          75          80
Pro Ala Met Val Gln Arg Lys Asp Ser Val Val Arg Ser Ile Arg Asp
          85          90          95
Gly Leu Asn Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Phe Ser Gly
          100          105          110
Xaa Gly Ser Leu Ile Ser Ser Thr Glu Val Lys Ile Leu Gly Glu Asn
          115          120          125
Pro Ser Val Ile Lys Ala His Ser Ile Ile Leu Ala Thr Gly Ser Glu
          130          135          140
Pro Arg Ala Phe Pro Gly Ile Pro Phe Ser Ala Glu Ser Pro Arg Ile
145          150          155          160
Leu Cys Ser Thr Gly Val Leu Asn Leu Lys Glu Ile Pro Gln Lys Met
          165          170          175
Ala Ile Ile Gly Gly Arg Cys Asp Arg Leu Arg Ile Arg Phe Leu Ile
          180          185          190
Pro Tyr Val Arg Leu Arg Ser Phe Cys Asp Arg Ser Lys Leu Ser Asn
          195          200          205
Pro Cys Phe Glu
          210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 906:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 163 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(884508..884996)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 906:

```

Arg Xaa Asp Leu Met Pro Phe Ala Lys Glu Ala Asp Leu Gln Arg Thr
1      5      10      15
Cys Trp Lys Cys Glu Gly Ser Val Ser Ala Cys Met Pro Gln Cys Pro
      20      25      30
Tyr Cys Ser Ala Phe Leu Gln Asp Pro Pro Val Thr Ser Lys Gly Phe
      35      40      45
Ser Ser Cys His Ile Thr Phe Pro Ser Glu Ala Ser Lys Lys Asn Gly
      50      55      60
Asp Ser Asp Leu Phe Ala Val Ser Ser Glu Asp Trp Glu Ala Val Leu
65      70      75      80
Asn Ser Gln Asn Thr Phe Glu Glu Pro Val Gln Glu Pro Ala Pro Ser
      85      90      95
Gln Trp Asp Trp Leu Gln Tyr Trp Pro Thr Ala Ala Leu Phe Leu Gly
      100     105     110
Cys Gly Phe Leu Thr Phe Ser Leu Met Ile Leu Leu Phe Ser Thr Asp
      115     120     125
Ser Gly Leu Val Leu Ser Trp Pro Lys Asn Arg Ser Tyr Ile Tyr Ala
      130     135     140
Leu Val Gly Ile Leu Leu Ala Tyr Arg Gly Tyr Arg Ser Leu Pro Glu
145      150      155      160
His Ser Lys

```

(2) INFORMATIONS POUR LA SEQ ID NO: 907:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(885166..888777)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 907:

```

Gln Arg Leu Ile Leu Met Ile Leu Asn Ser Leu Ser Met Phe Arg His
1      5      10      15
Gln Ala Thr Arg Phe Leu Gln Asp Asn Arg Asp Ser Ile Ala Val Ser
      20      25      30
Phe Ser Lys Asn Thr Tyr Lys Ile Thr Ile Pro Asp Glu Asp Ser Pro
      35      40      45
Asp Gly Glu Trp Ile Ser Thr Leu Ser Phe Asn Asp Glu Glu Arg Leu
      50      55      60
Ser Phe Ala Ala Cys Ser Cys Pro Asp Gly Asp Cys Cys Glu His Leu
65      70      75      80
Leu Thr Ala Thr Leu Ala Ala Tyr Asp Pro Thr Glu Gly Ala Leu Leu
      85      90      95
His Val Lys Phe Glu Ser Ser Phe Trp Trp Gly Leu Phe Tyr Gln Leu
      100     105     110
Phe Leu Ser Lys Ala Pro Leu His Ala Pro Gly Asp Lys Val Tyr Thr
      115     120     125
Ile Gln Ser Gln Gln Leu Ser Val Ser Leu Gln Cys Leu Ser Ala Glu
      130     135     140
Ala Leu Thr Tyr Trp Leu Pro Ile Val His Thr Ser Pro Glu Pro Gln
145      150      155      160
Thr Ile Ser Lys Glu Thr Phe Ser Gln Ser Ala Leu Tyr Arg Ile Ala

```

165 170 175
 Arg Glu Leu Phe Met Phe Ser Gln Lys Gly Ala Ser Leu Val Ile Gln
 180 185 190
 Glu Asn Pro Gln Gly Phe Pro Ser Leu Phe Ser Leu Gln Trp Glu Gly
 195 200 205
 Ile Ala Leu Ser Ile Glu Val Leu Asp Val Asp Thr Leu Lys Ala Leu
 210 215 220
 Phe Pro Leu Leu Glu Phe Ser Gln Thr Ser Leu Tyr Ser Gly Glu Pro
 225 230 235 240
 Tyr Leu Leu His Asn Val His Val Val Pro Glu Gln Ala Arg Ile Tyr
 245 250 255
 Phe Thr Lys Glu Tyr Pro Pro Leu Pro Lys Ser Ile Lys Glu Tyr Gln
 260 265 270
 Glu Thr Val Leu Gly Pro Ile Lys Tyr Phe Ala Glu Ala Lys Lys Cys
 275 280 285
 Thr Ser Ile Pro Lys Thr Leu Ser Leu Pro Ile His Ile Ile Pro Ala
 290 295 300
 Leu Asp Arg Ser Phe Arg Glu His Leu Leu Ser Gln Leu Cys Tyr Glu
 305 310 315 320
 Thr Glu Glu Arg Pro Ile His Tyr Ala Ile His Phe Leu Arg Asp Ala
 325 330 335
 Ser Leu Ser Phe Ser Ala Tyr Leu Glu Thr Pro Gly Asp Leu Ser Glu
 340 345 350
 Gly His Ile Ile Tyr Pro Glu Phe Cys Tyr Ile Pro Asn Lys Gly Leu
 355 360 365
 Leu Ala Val Ser Gly Leu Leu Ser Pro Glu Ser Ser Phe Thr Ile Arg
 370 375 380
 Ser Asp His Ile Glu Asn Phe Leu Asp Glu Tyr Gly Pro Phe Ile Lys
 385 390 395 400
 Glu Pro Gly Phe Glu Thr Phe Ser Asn Gln Ser Pro Val Gly Ser Leu
 405 410 415
 Ser Tyr Asn Val Thr Glu Gln Gly Val Leu Leu Phe His Tyr Asp Thr
 420 425 430
 Gly Asn Ala Ala Asp Ile Glu Leu Arg Phe Gly Lys Trp Thr Tyr Tyr
 435 440 445
 Ser Arg Gln Gly Phe Phe Leu Asn Ser Arg Leu Asp Leu Ala Leu Gln
 450 455 460
 Asp Gly Leu Thr Ile Glu Ala Pro Gln Val Ala Asp Phe Ile Leu Thr
 465 470 475 480
 His Glu Val Ala Leu Lys Ser Ile Pro Asn Phe Phe Ala Ala Gln Pro
 485 490 495
 Pro Leu Lys Ser Ile Arg Phe Glu Val His Lys Glu Lys Lys Gly Ser
 500 505 510
 Gly Ile Tyr Leu Gln Pro Ile Phe Glu Gly Leu Glu His Glu Ser Cys
 515 520 525
 Arg Leu Phe Gly Gln Phe Leu Tyr Arg Glu Asn Val Gly Phe Ser Leu
 530 535 540
 Leu Pro Ala Ala Leu Gln Met Leu Cys Gln Ile Pro Thr Glu Ile Pro
 545 550 555 560
 Ala Asp Gln Val Ala Glu Phe Leu Leu Gln Phe Ser Lys Asp Asp Arg
 565 570 575
 Met Val Phe Pro Asp Pro Gln Leu Ala Leu Pro Glu Arg Val Glu Leu
 580 585 590
 Asn Ile Leu Ala Ile His Arg Pro His Pro Ser Ser Pro Leu His Leu
 595 600 605
 Lys Ile Glu Ile Lys Thr Asn Ile Gly Ser Ile Pro Leu Gly Thr Val
 610 615 620
 Leu Gln Ala Leu Lys Gly Lys Lys Asp Phe Leu Phe Ser Lys Ala Gly
 625 630 635 640

Phe Leu Asn Leu Asp Asn Cys Leu Phe Val Phe Leu Lys Gln Phe Leu
 645 650 655
 Ser Ser Gln Arg Tyr Asp Ile Gln Glu Asn Thr Leu Ile Thr Met Val
 660 665 670
 Thr Asp Ile Phe Lys Leu Asp Ala Leu Ala Pro Met Ile Thr Asp Pro
 675 680 685
 Asn Ile Gln Ala Ser Glu Glu Asp Leu Ala Tyr Phe Ser Gln Leu Lys
 690 695 700
 Ser Ala Cys Leu Pro Pro Ile Pro Val Asn Leu Phe Ser Thr Asp His
 705 710 715 720
 Lys Leu Arg Pro Tyr Gln Asn Ser Gly Leu Leu Trp Leu Trp Phe Leu
 725 730 735
 Tyr Asn His Arg Leu Ser Gly Leu Leu Cys Asp Glu Met Gly Leu Gly
 740 745 750
 Lys Thr His Gln Ala Thr Ala Leu Leu Asp Ile Val Ala Gln Thr Ala
 755 760 765
 Lys Asn Pro Lys Phe Leu Val Val Cys Pro Thr Ser Val Leu Pro His
 770 775 780
 Trp Glu His Val Leu Ala Ser His Leu Pro Gln Ala Ser Leu Phe Ser
 785 790 795 800
 Phe His Gly Pro His Lys Pro Lys Thr Leu Pro Asp Cys Asp Ile Leu
 805 810 815
 Ile Thr Ser Tyr Gly Thr Leu Arg Gln Asn Tyr Ala Leu Phe Tyr Lys
 820 825 830
 Val Ser Phe Thr Val Ala Val Phe Asp Glu Ile His Thr Ala Lys Asn
 835 840 845
 Lys Ser Ser Gln Ile His Lys Ile Leu Cys Arg Leu Asp Ala Gln Met
 850 855 860
 Lys Leu Gly Leu Thr Gly Thr Pro Val Glu Asn Asn Leu Ile Glu Phe
 865 870 875 880
 Lys Gly Leu Leu Asp Ile Ile Leu Pro Asn Tyr Leu Pro Ser Asp Ala
 885 890 895
 Leu Phe Lys Arg Leu Phe Thr His Lys Asn Ala Ser Glu Thr Asp Glu
 900 905 910
 Asp Ile Ile Ser Ser Lys Asp Leu Leu Lys Leu Thr Arg Pro Phe
 915 920 925
 Ile Leu Arg Arg Thr Lys Lys Leu Val Leu Pro Glu Leu Pro Glu Lys
 930 935 940
 Val Glu Ser Leu Ile Pro Cys Arg Leu Ser Pro Glu Gln Ser Gln Leu
 945 950 955 960
 Tyr Ser Ser Thr Leu Glu Lys Glu Lys Cys Gln Ile Gln Gln Leu Glu
 965 970 975
 Lys Glu Glu Asp Pro Ala Ser Val Asn Tyr Leu His Val Phe Ala Leu
 980 985 990
 Leu Asn Gln Leu Lys Gln Ile Cys Asp His Pro Ala Val Tyr Phe Lys
 995 1000 1005
 Asp Pro Glu Ser Tyr Lys Asn His Ser Ser Gly Lys Trp Ala Ala Phe
 1010 1015 1020
 Val Lys Leu Leu Asn Asp Ser Leu Ala Ser Gly Tyr Lys Val Val Val
 1025 1030 1035 1040
 Phe Ser Gln Tyr Ile Gln Met Ile Arg Ile Ile Ala Leu Tyr Leu Glu
 1045 1050 1055
 Glu His Ala Ile Glu Tyr Ala Leu Val Gln Gly Lys Ser Gln Asn Arg
 1060 1065 1070
 Lys Glu Glu Ile Asp Arg Phe Ser Asn Asp Pro Asn Cys Arg Val Phe
 1075 1080 1085
 Ile Gly Ser Leu Leu Ala Ala Gly Thr Gly Ile Asn Leu Thr Ala Gly
 1090 1095 1100
 Asn Val Val Ile Met Tyr Asp Arg Trp Trp Asn Pro Ala Lys Glu Asn

```

1105          1110          1115          1120
Gln Ala Leu Asp Arg Val His Arg Ile Gly Gln Lys Asn Thr Val Phe
          1125          1130          1135
Ile Tyr Lys Leu Val Thr Glu Asp Thr Leu Glu Glu His Ile His Tyr
          1140          1145          1150
Leu Ile Glu Lys Lys Met Arg Leu Leu Asn Gln Val Thr Thr Thr Gln
          1155          1160          1165
Asp Ser Asn Ile Leu His Val Leu Asn Arg Glu Asp Leu Ile Thr Ile
          1170          1175          1180
Leu Ser Tyr Lys Asp Glu His Met Leu Ser Glu Glu Val Gln Glu Asp
1185          1190          1195          1200
Ser Gly Asp Ser

```

(2) INFORMATIONS POUR LA SEQ ID NO: 908:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 403 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(888940..890148)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 908:

```

Ser His Lys Gly Leu Ser Ile Trp Ser Ile Gly Gly Ser Ile Phe Ala
1          5          10          15
Met Phe Phe Gly Ala Gly Asn Val Val Phe Pro Leu Ala Leu Gly His
          20          25          30
His Phe Tyr Tyr His Ile Ser Tyr Ala Cys Leu Gly Met Ile Leu Thr
          35          40          45
Ala Val Leu Thr Pro Leu Leu Gly Leu Phe Ala Met Met Leu Tyr Ser
          50          55          60
Gly Asn Tyr Arg Ser Phe Phe Ala Ser Ile Gly Arg Met Pro Gly Met
65          70          75          80
Val Leu Met Val Ala Ile Leu Cys Ile Ile Gly Pro Phe Gly Gly Ile
          85          90          95
Pro Arg Thr Ile Ala Val Ser Tyr Asp Thr Leu Ala Ser Leu Gly Asp
          100          105          110
Lys His Pro Thr Leu Leu Pro Ser Leu Pro Trp Phe Ser Val Phe Phe
          115          120          125
Cys Val Leu Val Tyr Leu Phe Val Cys Lys Leu Ser Lys Leu Ile Gln
          130          135          140
Trp Leu Gly Ser Val Phe Phe Pro Val Met Leu Gly Thr Leu Ala Trp
145          150          155          160
Leu Ile Ile Lys Gly Leu Leu Leu Pro Ala His Ala Leu Pro Ser Glu
          165          170          175
Ser Val Thr Phe Ser Lys Gln Gln Ala Phe Val Thr Gly Leu Ser Glu
          180          185          190
Gly Phe Asn Thr Met Asp Leu Leu Gly Ala Phe Phe Phe Cys Ser Ile
          195          200          205
Val Leu Val Ser Ile Gln Gln Leu Met Val Gln Gln Lys His Glu Ser
          210          215          220
Ser Glu Glu Lys Pro Leu Glu Phe His His Ile Gly Lys Thr Glu Lys
225          230          235          240

```



```

Tyr Lys Leu Ala Met Ser Phe Leu Leu Ala Ala Ala Leu Leu Ser Leu
      245                      250                      255
Val Tyr Leu Gly Phe Ala Phe Cys Ala Ala Arg His Ala Gly Ala Leu
      260                      265                      270
Ile Asp Val Gln Arg Gly Gln Ile Leu Gly Arg Ile Ser Ala Leu Val
      275                      280                      285
Val Gly Pro Asn Ser Phe Leu Thr Gly Leu Ser Val Phe Leu Ala Cys
      290                      295                      300
Leu Thr Thr Ala Ile Ala Val Thr Gly Ile Phe Ala Asp Phe Ile Ala
305                      310                      315                      320
Arg Val Val Ser Ser Gln Lys Met Ser Tyr Ser Asn Ala Leu Ile Val
      325                      330                      335
Thr Leu Val Pro Thr Tyr Leu Val Ser Ile Leu Ser Phe Glu Asn Ile
      340                      345                      350
Ser Lys Ile Leu Ile Pro Ile Leu Glu Met Ser Tyr Pro Ala Leu Ile
      355                      360                      365
Ala Leu Thr Cys Gly Val Ile Ala Lys Lys Leu Trp Asp Phe Arg His
      370                      375                      380
Val Lys Thr Leu Phe Tyr Leu Val Phe Ala Leu Thr Ile Leu Tyr Lys
385                      390                      395                      400
Leu Ser Val

```

(2) INFORMATIONS POUR LA SEQ ID NO: 909:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 280 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(890325..891164)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 909:

```

Ala Ile Ser Thr Pro Ala Leu Ala Cys Ser Leu Leu His Ile Asp Asp
1      5      10      15
Leu Ala Glu Cys Leu Thr Thr Asp Tyr Gly Glu Glu Glu Ala Ile Arg
      20      25      30
Leu Ala Lys Ile Phe Leu Glu Glu Ala Pro Cys Ser Ile Arg Val Asn
      35      40      45
Thr Arg Arg Ile Ser Val Asp Lys Leu Gln Lys Val Leu Pro Phe Pro
50      55      60
Cys Gln Arg Gly Ala Ala Pro Ser Ser Leu Arg Phe Glu Lys Arg Tyr
65      70      75      80
Pro Leu Gln His Thr Arg Ala Phe Arg Arg Gly Leu Phe Glu Ile Gln
      85      90      95
Asp Glu Ser Ser Gln Ile Ile Thr Asn Ala Ile Leu Ile Lys Asp Ser
100      105      110
Asp Thr Val Leu Asp Phe Cys Ala Gly Ala Gly Lys Ser Leu Ile
115      120      125
Phe Ala Gln Arg Ala Arg His Val Thr Leu His Asp Ser Arg Pro Gln
130      135      140
Ala Leu Glu Glu Ala Arg His Arg Ser Pro Arg Ser Gly Ile Lys Asn
145      150      155      160
Phe Thr Ile Pro Ser Gln Pro Leu Lys Lys His Ser Phe Ser Leu Val

```

(2) INFORMATION POUR LA SEQ ID NO: 910:

(A) LONGUEUR: 116 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(891116..891463)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 910:

(2) INFORMATION POUR LA SEQ ID NO: 911:

(A) LONGUEUR: 437 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 911:

Met	Arg	Thr	Phe	Phe	Leu	Leu	Cys	Arg	Phe	Phe	Ile	Cys	Leu	Ala	Pro
1			5						10					15	
Phe	Phe	Leu	Ser	Phe	Pro	Leu	Tyr	Ala	Asp	Pro	His	Thr	Val	Leu	Thr
		20						25				30			
Lys	Gly	Ile	Ala	Ala	Ala	Val	Val	His	Ala	Asp	Ser	Gly	Ala	Ile	Leu
		35					40					45			
Lys	Glu	Lys	Asn	Leu	Asp	His	Lys	Ile	Phe	Pro	Ala	Ser	Met	Thr	Lys
	50					55				60					
Ile	Ala	Thr	Ala	Leu	Leu	Ile	Leu	Arg	Gln	Tyr	Pro	Asp	Val	Leu	Thr
65					70					75					80
Arg	Phe	Ile	Thr	Thr	Arg	Arg	Glu	Pro	Leu	Thr	Ser	Ile	Thr	Pro	Gln
			85						90					95	
Ala	Lys	Gln	Gln	Ser	Gly	Tyr	Arg	Ser	Pro	Pro	His	Trp	Leu	Glu	Thr
			100					105					110		
Asp	Gly	Met	Thr	Ile	Gln	Leu	Lys	Val	Lys	Glu	Glu	Val	Ser	Gly	Trp
		115					120					125			
Asp	Leu	Phe	His	Ala	Leu	Leu	Ile	Ser	Ser	Ala	Asn	Asp	Ala	Ala	Asn
	130					135					140				
Val	Leu	Ala	Asp	Ala	Cys	Cys	Gln	Ser	Val	Ser	Ala	Phe	Met	Arg	Gln
145					150					155					160
Leu	Asn	Glu	Phe	Leu	Arg	Glu	Leu	Gly	Cys	Gln	Asn	Thr	His	Phe	Asn
			165						170					175	
Ser	Pro	His	Gly	Leu	His	His	Pro	Asp	His	Tyr	Thr	Thr	Ala	Arg	Asp
			180					185					190		
Leu	Ser	Leu	Ile	Met	Lys	Glu	Ala	Leu	Lys	Glu	Pro	Leu	Phe	Arg	Gln
		195					200					205			
Val	Ile	His	Thr	Ala	Ser	Tyr	Thr	Met	Glu	Ala	Thr	Asn	Leu	Ser	Pro
	210					215					220				
Glu	Arg	Val	Leu	Ser	Ser	Thr	Asn	Lys	Leu	Leu	Ser	Ser	Ser	Ser	Thr
225					230					235					240
Tyr	Phe	Tyr	Pro	Pro	Cys	Leu	Gly	Gly	Lys	Thr	Gly	Thr	Thr	Lys	Ser
			245						250					255	
Ala	Gly	Lys	Asn	Ile	Ile	Phe	Ala	Ala	Glu	Lys	Asn	Asn	Arg	Ser	Ile
			260					265					270		
Ile	Val	Val	Ala	Ala	Gly	Tyr	Phe	Gly	Pro	Ala	Ala	Gln	Leu	Tyr	Gln
		275					280					285			
Asp	Ala	Ile	Ala	Leu	Cys	Glu	Asp	Leu	Phe	Asn	Glu	Gln	Leu	Leu	Arg
	290					295					300				
Cys	Phe	Leu	Ile	Pro	Pro	Ala	Ser	His	Tyr	Pro	Val	Pro	Thr	Arg	Phe
305					310					315					320
Gly	Thr	Val	Thr	Ala	Pro	Val	Ala	Gln	Gly	Ile	Tyr	Tyr	Asp	Phe	Tyr
			325						330					335	
Pro	Ser	Glu	Gly	Asp	Pro	Leu	Leu	Thr	Leu	Ser	Leu	Glu	Pro	Asn	Lys
			340					345					350		
Ile	Ser	Phe	Pro	Ile											

435

(2) INFORMATIONS POUR LA SEQ ID NO: 912:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 151 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 893356..893808

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 912:

Gln Ile Thr Leu Glu Lys Gly Glu Thr Ala Val Ser Leu Asp Phe Leu
 1 5 10 15
 Glu Asp Phe Phe Arg Arg Ser Ile Thr Asn His Asn Thr Ala Phe Pro
 20 25 30
 Glu Gly Phe Leu Asp Ile Ser Asp Val Leu Ala Arg Ser Ala Leu Asp
 35 40 45
 Phe Lys Ala Glu Glu Leu Ala Asp Ser Ala Val Asn Asp Phe Ile Val
 50 55 60
 Ser Glu Ser Ser Asp Lys Leu Thr Leu Phe Asn Thr Asn Phe Ala Val
 65 70 75 80
 Trp Leu Val Pro Thr Leu Val Asp Gly Glu Ala Ile Thr Arg Gly Tyr
 85 90 95
 Ile Ala Leu Asn Gln Gly Glu Glu Phe Ser Pro Glu Leu Thr Phe Glu
 100 105 110
 Ala Ser Gly Lys Tyr Asn Asn Ser Ser Leu Ile Leu Glu Ala Leu Arg
 115 120 125
 Arg Tyr Leu Cys Asp Ile Gln Asp Thr Glu Lys Glu Leu Arg Ala Leu
 130 135 140
 Arg Pro Pro Ser Ile Asp Gly
 145 150

(2) INFORMATIONS POUR LA SEQ ID NO: 913:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 89 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(893643..893909)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 913:

Gln Asn Thr Arg Trp Met Phe Leu Ile Met Arg Glu Leu Thr Thr Gln
 1 5 10 15
 Met Leu Ser Leu Ser Leu Tyr Thr Gln Asn Leu Thr Thr His Ser Leu
 20 25 30
 Ile Tyr Pro Ser Ile Glu Gly Gly Arg Lys Ala Arg Asn Ser Phe Ser
 35 40 45

```

Val Ser Trp Ile Ser His Lys Tyr Leu Arg Asn Ala Ser Lys Ile Lys
  50                      55                      60
Leu Glu Leu Leu Tyr Phe Pro Asp Ala Ser Lys Val Asn Ser Gly Glu
  65                      70                      75                      80
Asn Ser Ser Pro Trp Phe Lys Ala Met
                        85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 914:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 146 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(893821..894258)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 914:

```

Met Thr Phe Ser Glu Gly Glu Gln Val Phe Pro Ala Thr Leu Gln Asp
  1                      5                      10                      15
Leu Tyr Pro Met Leu Asp Phe Val Lys Arg Ala Gly Val His Cys Asn
                20                      25                      30
Cys Thr Gln Lys Lys Leu Ser Lys Leu Glu Leu Ala Cys Glu Glu Leu
        35                      40                      45
Leu Leu Asn Ile Ile Thr His Ala Tyr Lys Gly Leu Pro Ser Thr Gly
  50                      55                      60
Trp Ile Arg Ile Leu Cys Thr Glu Thr Pro Asp Ala Leu Leu Val Arg
  65                      70                      75                      80
Ile Thr Asp His Gly Pro Ala Phe Asn Pro Ile Thr Ala Ser Pro Asp
                85                      90                      95
Ile Met Arg Leu Asp Leu Pro Ile Glu Gln Arg Arg Ile Gly Gly Leu
        100                      105                      110
Gly Ile Phe Leu Ala Lys Tyr Ser Val Asp Val Phe Asp Tyr Glu Arg
        115                      120                      125
Val Asn Asp Thr Asn Val Val Thr Leu Thr Leu Tyr Thr Lys Pro His
  130                      135                      140
Asn Ser
145

```

(2) INFORMATIONS POUR LA SEQ ID NO: 915:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 177 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(894248..894778)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 915:

```

Ser Ala Cys Gly Tyr Thr Val Leu Ser Pro His Tyr Val Glu Lys Lys

```

```

1           5           10           15
Phe Ser Leu Ser Glu Gly Ile Tyr Val Cys Pro Ile Glu Gly Asp Ser
20           25           30
Leu Gly Asp Leu Val Ser Ser Leu Ser Tyr Glu Leu Glu Lys Arg Gly
35           40           45
Leu His Thr Arg Ser Gln Gly Thr Ser Ser Gly Tyr Val Leu Lys Val
50           55           60
Ser Leu Phe Asn Glu Thr Tyr Glu Asn Ile Gly Phe Ala Tyr Thr Pro
65           70           75           80
Gln Lys Pro Asp Glu Lys Pro Val Lys His Phe Ile Val Ser Asn Glu
85           90           95
Gly Arg Leu Ala Leu Ser Ala Lys Val Gln Leu Ile Lys Asn Arg Thr
100          105          110
Gln Glu Ile Leu Val Glu Lys Cys Leu Arg Lys Ser Val Thr Phe Asp
115          120          125
Phe Gln Pro Asp Leu Gly Thr Ala Asn Ala His Gln Leu Ala Leu Gly
130          135          140
Gln Phe Glu Met His Asn Glu Ala Ile Lys Ser Ala Ser Arg Ile Leu
145          150          155          160
Tyr Ser Gln Leu Ala Glu Thr Ile Val Gln Gln Val Tyr Tyr Asp Leu
165          170          175
Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 916:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 281 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(895050..895892)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 916:

```

Thr Lys Ala Ile Arg Asp Leu Thr Asn Ser Leu Phe Leu Phe Tyr Asp
1           5           10           15
Asp Ala Leu Leu Leu Leu Ser Leu Arg Leu Ala Met Lys Val Ile Leu
20           25           30
Arg Ala Leu Cys Leu Phe Leu Val Leu Pro Cys Gly Cys Tyr Ala Arg
35           40           45
Val Pro Ser Phe Glu Pro Phe Arg Gly Ala Ile Ala Pro Asn Arg Tyr
50           55           60
Ile Pro Lys His Ser Pro Glu Leu Tyr Phe Glu Met Gly Asp Lys Tyr
65           70           75           80
Phe Gln Ala Lys Lys Phe Lys Gln Ala Leu Leu Cys Phe Gly Met Ile
85           90           95
Thr His His Phe Pro Glu His Ala Leu His Pro Lys Ala Gln Phe Leu
100          105          110
Val Gly Leu Cys Tyr Leu Glu Met Gly His Pro Asp Leu Ala Asp Lys
115          120          125
Ala Leu Thr Gln Tyr Gln Glu Leu Ala Asp Thr Glu Tyr Ser Glu Gln
130          135          140
Leu Phe Ala Ile Lys Tyr Ser Ile Ala Gln Ser Phe Ala Asn Gly Lys
145          150          155          160

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Arg Lys Asn Ile Val Pro Leu Glu Gly Phe Pro Lys Leu Leu Lys Ala
      165                      170                      175
Asp Thr Asp Ala Leu Arg Ile Phe Glu Glu Ile Val Thr Ala Ser Ser
      180                      185                      190
Asp Ala Asp Leu Lys Ala Ser Ala Leu Tyr Ala Lys Gly Ala Leu Leu
      195                      200                      205
Phe Asp Arg Lys Glu Tyr Ser Glu Ala Ile Lys Thr Leu Lys Lys Val
      210                      215                      220
Ser Leu Gln Phe Pro Ser His Ser Leu Ser Pro Glu Ser Phe Thr Leu
225                      230                      235                      240
Ile Ala Lys Ile His Cys Leu Gln Ala Leu Gln Glu Pro Tyr Asn Glu
      245                      250                      255
Gln Tyr Leu Gln Asp Ala Arg Met Lys Gln Gln Leu Tyr Val Asn Asn
      260                      265                      270
Thr Leu Ile Ile Leu Ala Ile Gln Lys
      275                      280

```

(2) INFORMATIONS POUR LA SEQ ID NO: 917:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 293 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 895951..896829

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 917:

```

Lys Gly Trp Val Met Lys Lys Val Val Phe Ile Ala Ala Ile Phe Ser
1      5      10      15
Ser Ile Val Phe Trp Asp Lys Ile Pro Tyr Ser His Arg Ile Lys Gln
      20      25      30
Phe Ala Met Asp Tyr Gly Ile Glu Leu Val Glu Lys Ser Ser Gln Leu
      35      40      45
Val Arg Lys Ile Ser Gly Asn Glu Arg Leu Cys Val Phe Glu Arg Arg
      50      55      60
Val Ser Glu Glu Gln Val Leu Ala Met Phe Ala Lys Asp Lys Ala Ser
65      70      75      80
Ala Glu Leu Leu Phe Val Pro His Val Leu Met Arg Val Arg Phe Ser
      85      90      95
Gly Glu Glu Asp Lys Arg Ala Gly Ser His Glu Gly Ala Met Leu Trp
      100     105     110
Ser Leu Ser Asn Gly Glu Met Val Leu Asn Thr Gly Ser Trp Thr Tyr
      115     120     125
Ser Lys Gly Phe Arg Glu Cys Leu Met Leu Lys Ala Gly Lys Gln Asp
      130     135     140
Val Gln Leu Met Gln Val Leu Ala Gly Met Gly Gly Ser Ala Ser Arg
145     150     155     160
Glu Val Leu Ser Gln Ala Leu Ser Met Arg Asn Val Arg Ala Asp Arg
      165     170     175
Val Ile Arg Ala Cys Gln Lys Lys Lys Leu Ile Phe Thr His Asp Asn
      180     185     190
Leu Ile Tyr Ser His Phe Gln Gln Pro Gln Pro Ile Lys Gly Cys Met
      195     200     205
Thr Val Phe Asn Ser Ser Pro Val Trp Leu Ala Lys Pro Lys Gly Ser

```

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      210      215      220
Thr Val Cys Ser Val Val Tyr Pro Glu Asp Arg Ile Gln Asn Leu Val
225      230      235      240
Glu Met Ile Phe Gly Asp Asn Phe Phe Ile Leu Ser Ser Glu Gln Ile
      245      250      255
His Val Pro Val Tyr Lys Val Ser Ile Ala Ala Ser Asp Ser Ser Val
      260      265      270
Arg Val Glu Tyr Ile Asn Ala Ile Thr Gly Lys Pro Phe Asp Phe Ala
      275      280      285
Pro Thr Tyr Cys Lys
      290

```

(2) INFORMATIONS POUR LA SEQ ID NO: 918:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 1240 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(897064..900783)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 918:

```

Arg Ala Val Leu Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser
1      5      10      15
Ile Leu Asp Ala Thr Cys Ser Ile Lys Lys Phe Val Ala Lys Ala Val
      20      25      30
Glu Tyr Gln Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Phe
      35      40      45
Gly Ala Val Glu Phe Tyr Lys Thr Cys Lys Gln Asn Ala Ile Lys Pro
      50      55      60
Ile Ile Gly Cys Glu Leu Tyr Val Ala Pro Ser Arg Phe Asp Lys
      65      70      75      80
Lys Lys Glu Arg Lys Ser Arg Val Ala Asn His Leu Ile Leu Leu Cys
      85      90      95
Lys Asp Glu Glu Gly Tyr Arg Asn Leu Cys Leu Leu Ser Ser Leu Ala
      100      105      110
Tyr Thr Glu Gly Phe Tyr Tyr Val Pro Arg Ile Asp Arg Asp Leu Leu
      115      120      125
Ser Gln His Ser Lys Gly Leu Ile Cys Leu Ser Ala Cys Leu Ser Gly
      130      135      140
Ser Val Ala Gln Ala Ala Leu Glu Ser Glu Glu Asp Leu Glu Lys Asp
      145      150      155      160
Leu Leu Trp Tyr Gln Asp Leu Phe Gln Glu Asp Phe Phe Ser Glu Val
      165      170      175
Gln Leu His Lys Ser Ser Glu Glu Lys Val Ala Leu Phe Glu Glu Ala
      180      185      190
Trp Leu Lys Gln Asn Tyr Tyr Gln Phe Ile Glu Lys Gln Leu Lys Val
      195      200      205
Asn Glu Ala Val Leu Ala Thr Ser Lys Arg Leu Gly Ile Pro Ser Val
      210      215      220
Ala Thr Asn Asp Ile His Tyr Leu Asn Pro Asp Asp Trp Leu Ala His
      225      230      235      240
Glu Val Leu Leu Asn Val Gln Ser Arg Glu Pro Ile Arg Thr Ala Lys
      245      250      255

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Gln	Asn	Thr	Tyr	Ile	Pro	Asn	Pro	Lys	Arg	Lys	Thr	Tyr	Pro	Ser	Arg		
			260					265					270				
Glu	Phe	Tyr	Phe	Lys	Ser	Pro	Gln	Glu	Met	Ala	Glu	Leu	Phe	Ala	Ala		
		275					280					285					
His	Pro	Glu	Thr	Ile	Thr	Asn	Thr	Cys	Ile	Val	Ala	Glu	Arg	Cys	His		
	290					295				300							
Leu	Glu	Leu	Asp	Phe	Glu	Thr	Lys	His	Tyr	Pro	Ile	Tyr	Val	Pro	Glu		
305					310					315					320		
Ala	Leu	Gln	Lys	Lys	Gly	Ser	Tyr	Thr	Glu	Glu	Glu	Arg	Tyr	Lys	Ala		
			325						330					335			
Ser	Ser	Ala	Phe	Leu	Glu	Glu	Leu	Cys	Glu	Gln	Gly	Leu	Thr	Ser	Lys		
		340						345					350				
Tyr	Thr	Pro	Glu	Leu	Leu	Gly	His	Ile	Ala	Lys	Lys	Phe	Pro	Gly	Glu		
	355						360					365					
Asp	Pro	Leu	Thr	Leu	Val	Lys	Glu	Arg	Leu	Lys	Leu	Glu	Ser	Ser	Ile		
	370					375					380						
Ile	Ile	Ser	Lys	Gly	Met	Cys	Asp	Tyr	Leu	Leu	Ile	Val	Trp	Asp	Ile		
385					390					395					400		
Ile	Asn	Trp	Ala	Lys	Asp	His	Gly	Ile	Pro	Val	Gly	Pro	Gly	Arg	Gly		
			405						410					415			
Ser	Gly	Ala	Gly	Ser	Val	Met	Leu	Phe	Leu	Leu	Gly	Ile	Thr	Glu	Ile		
		420						425					430				
Glu	Pro	Ile	Arg	Phe	Asp	Leu	Phe	Phe	Glu	Arg	Phe	Ile	Asn	Pro	Glu		
	435						440					445					
Arg	Ile	Ser	Tyr	Pro	Asp	Ile	Asp	Ile	Asp	Ile	Cys	Met	Ile	Gly	Arg		
	450					455					460						
Glu	Arg	Val	Ile	Asn	Tyr	Ala	Ile	Glu	Arg	His	Gly	Lys	Asp	Asn	Val		
465				470						475					480		
Ala	Gln	Ile	Ile	Thr	Phe	Gly	Thr	Met	Lys	Ala	Lys	Met	Xaa	Ile	Lys		
			485					490						495			
Asp	Val	Gly	Arg	Thr	Leu	Asp	Thr	Pro	Leu	Ala	Lys	Val	Asn	Phe	Ile		
	500						505						510				
Ala	Lys	His	Ile	Pro	Asp	Leu	Asn	Ala	Thr	Ile	Thr	Ser	Ala	Leu	Glu		
	515						520					525					
Ala	Asp	Pro	Glu	Leu	Lys	Gln	Leu	Tyr	Val	Asp	Asp	Ala	Glu	Ala	Ala		
	530					535					540						
Glu	Val	Ile	Asp	Met	Ala	Lys	Lys	Leu	Glu	Gly	Ser	Ile	Arg	Asn	Thr		
545				550						555					560		
Gly	Val	His	Ala	Ala	Gly	Val	Ile	Ile	Cys	Gly	Asp	Pro	Leu	Thr	Asn		
			565						570					575			
His	Ile	Pro	Ile	Cys	Val	Pro	Lys	Asp	Ser	Ser	Met	Ile	Ser	Thr	Gln		
	580							585					590				
Tyr	Ser	Met	Lys	Pro	Val	Glu	Ser	Val	Gly	Met	Leu	Lys	Val	Asp	Phe		
	595						600					605					
Leu	Gly	Leu	Lys	Thr	Leu	Thr	Gly	Ile	His	Ile	Ala	Thr	Gln	Ala	Ile		
	610					615					620						
Tyr	Lys	Lys	Thr	Gly	Ile	Leu	Leu	Arg	Ala	Ala	Thr	Ile	Pro	Leu	Asp		
625				630						635					640		
Asp	Gln	Asn	Thr	Phe	Ser	Leu	Leu	His	Gln	Gly	Lys	Thr	Met	Gly	Ile		
			645						650					655			
Phe	Gln	Met	Glu	Ser	Arg	Gly	Met	Gln	Asp	Leu	Ala	Lys	Asn	Leu	Arg		
		660						665					670				
Pro	Asp	Ala	Phe	Glu	Glu	Ile	Ile	Ala	Ile	Gly	Ala	Leu	Tyr	Arg	Pro		
	675						680					685					
Gly	Pro	Met	Asp	Met	Ile	Pro	Ser	Phe	Ile	Asn	Arg	Lys	His	Gly	Lys		
	690					695					700						
Glu	Asn	Ile	Glu	Xaa	Asp	His	Pro	Leu	Met	Glu	Pro	Ile	Leu	Lys	Glu		
705				710						715					720		
Thr	Phe	Gly	Ile	Met	Val	Tyr	Gln	Glu	Gln	Val	Met	Gln	Ile	Ala	Gly		

725 730 735
 Ser Leu Ala Lys Tyr Ser Leu Gly Glu Gly Asp Val Leu Arg Arg Ala
 740 745 750
 Met Gly Lys Lys Asp His Glu Gln Met Val Lys Glu Arg Glu Lys Phe
 755 760 765
 Cys Ser Arg Ala Ala Ala Asn Gly Ile Asp Pro Ser Ile Ala Thr Thr
 770 775 780
 Ile Phe Asp Lys Met Glu Lys Phe Ala Ser Tyr Gly Phe Asn Lys Ser
 785 790 795 800
 His Ala Ala Ala Tyr Gly Leu Ile Thr Tyr Thr Thr Ala Tyr Leu Lys
 805 810 815
 Ala Asn Tyr Pro Lys Glu Trp Leu Ala Ala Leu Leu Thr Cys Asp Tyr
 820 825 830
 Asp Asp Ile Glu Lys Val Gly Lys Leu Ile Gln Glu Ala His Ser Met
 835 840 845
 Asn Ile Leu Val Leu Pro Pro Asp Ile Asn Glu Ser Gly Gln Asp Phe
 850 855 860
 Glu Ala Thr Gln Glu Gly Ile Arg Phe Ser Leu Gly Ala Val Lys Gly
 865 870 875 880
 Val Gly Met Ser Ile Val Asp Ser Ile Val Glu Glu Arg Glu Lys Asn
 885 890 895
 Gly Pro Tyr Lys Ser Leu Gln Asp Phe Val Gln Arg Ala Asp Phe Lys
 900 905 910
 Lys Val Thr Lys Lys Gln Leu Glu Asn Leu Val Asp Ala Gly Thr Phe
 915 920 925
 Asp Cys Phe Glu Pro Asn Lys Asp Leu Ala Leu Ala Ile Leu Asn Asp
 930 935 940
 Leu Tyr Asp Thr Phe Phe Arg Glu Lys Lys Glu Ala Ala Thr Gly Val
 945 950 955 960
 Leu Thr Phe Phe Ser Leu Asp Ser Met Xaa Arg Asp Pro Val Lys Ile
 965 970 975
 Thr Val Xaa Pro Glu Asn Val Ile Gln Arg Ser Pro Lys Glu Leu Leu
 980 985 990
 Lys Arg Glu Lys Glu Leu Leu Xaa Val Tyr Leu Thr Ala His Pro Met
 995 1000 1005
 Asp Ala Val Glu His Met Leu Pro Phe Leu Ser Val Val Pro Ala Arg
 1010 1015 1020
 Asp Phe Glu Gly Leu Pro His Gly Thr Ile Ile Arg Thr Val Phe Leu
 1025 1030 1035 1040
 Ile Asp Lys Val Thr Thr Lys Ile Ser Ser Ala Glu Gln Lys Lys Phe
 1045 1050 1055
 Ala Leu Leu Gln Val Ser Asp Glu Val Asp Ser Tyr Glu Leu Pro Ile
 1060 1065 1070
 Trp Ala Asp Met Tyr Ala Glu Tyr His Asp Leu Leu Glu Glu Asp Arg
 1075 1080 1085
 Leu Ile Tyr Ala Ile Leu Ala Ile Asp Arg Arg Ser Asp Ser Leu Arg
 1090 1095 1100
 Leu Ser Cys Arg Trp Met Arg Asp Leu Ser Thr Val Asn Asp Ser Val
 1105 1110 1115 1120
 Ile Ala Glu Cys Asp Glu Val Tyr Asp Arg Leu Lys Ser Gln Lys Val
 1125 1130 1135
 Tyr Ser Ser Thr Lys Lys Ser Thr Gly Ala Gln Ser Ser Ala Met Ile
 1140 1145 1150
 Lys Lys Val Glu Thr Arg Glu Ile Ser Pro Val Thr Ile Ser Leu Asp
 1155 1160 1165
 Leu Asn Lys Leu Arg His Ser His Leu Phe Ile Leu Lys Gly Leu Ile
 1170 1175 1180
 Arg Lys Tyr Ser Gly Ser Gln Ala Leu Ser Leu Val Phe Thr Lys Asp
 1185 1190 1195 1200

```

Asn Gln Arg Phe Ala Ser Ile Ser Pro Asp Ala Asp Phe Phe Val Thr
      1205                      1210                      1215
Asp Asp Ile Ser Ser Leu Leu Gln Glu Ile Glu Ala Thr Asn Ile Pro
      1220                      1225                      1230
Ala Arg Val Leu Ala Thr Thr Val
      1235                      1240

```

(2) INFORMATIONS POUR LA SEQ ID NO: 919:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 414 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(900791..902032)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 919:

```

Leu Phe Phe Tyr Phe Thr Arg Lys Ser Xaa Xaa Phe Ala Met Pro Thr
1      5      10      15
Leu Ile Ala Asp Leu Gly Phe Asp Lys Ala Gln Leu Gly Ile Ile Gly
      20      25      30
Ser Thr Leu Tyr Ile Thr Tyr Gly Ile Ser Lys Phe Val Ser Gly Val
      35      40      45
Met Ser Asp Gln Ser Asn Pro Arg Tyr Phe Met Ala Ile Gly Leu Ile
      50      55      60
Ile Thr Gly Ile Ser Asn Ile Phe Phe Gly Leu Ser Ser Thr Ile Pro
      65      70      75      80
Leu Phe Val Leu Phe Trp Gly Ile Asn Gly Trp Phe Gln Gly Trp Gly
      85      90      95
Trp Pro Pro Cys Ala Arg Leu Leu Thr His Trp Tyr Ser Lys Ser Glu
      100      105      110
Arg Gly Thr Trp Trp Ser Val Trp Ser Thr Ser His Asn Ile Gly Gly
      115      120      125
Ala Leu Ile Pro Val Leu Thr Gly Val Ala Ile Asp Tyr Thr Gly Trp
      130      135      140
Arg Gly Val Met Phe Ile Pro Gly Ile Ile Cys Ile Ile Met Gly Phe
      145      150      155      160
Ile Leu Ile Asp Arg Leu Arg Asp Thr Pro Gln Ser Leu Gly Leu Pro
      165      170      175
Ala Ile Glu Lys Phe Arg Lys Glu Glu Asp Ala His Pro His Glu Glu
      180      185      190
Thr Thr Ala Asp Ile Leu Glu Glu Glu Ala Glu Arg Glu Leu Ser Thr
      195      200      205
Lys Glu Ile Leu Phe Thr Tyr Val Leu Ser Asn Lys Trp Leu Trp Phe
      210      215      220
Leu Ser Phe Ala Ser Phe Phe Ile Tyr Val Val Arg Met Ala Val Asn
      225      230      235      240
Asp Trp Ser Ala Leu Tyr Leu Ile Glu Thr Lys Asp Tyr Ser Thr Val
      245      250      255
Lys Ala Asn Leu Cys Val Ser Leu Phe Glu Ile Gly Gly Leu Phe Gly
      260      265      270
Met Leu Leu Ala Gly Trp Leu Ser Asp Thr Ile Ser Lys Gly Lys Arg
      275      280      285
Gly Pro Met Asn Val Val Phe Ser Leu Gly Leu Leu Val Ser Ile Leu

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290	295	300
Gly Leu Trp Gly Thr Arg Asp Tyr Phe Val Trp Trp Ile Asp Gly Thr		
305	310	315
Phe Leu Phe Ile Ile Gly Phe Phe Leu Phe Gly Pro Gln Met Met Ile		
	325	330
Gly Leu Ala Ala Ala Glu Leu Ser His Lys Lys Ala Ala Gly Thr Ala		
	340	345
Ser Gly Phe Thr Gly Trp Phe Ala Tyr Phe Gly Ala Ala Phe Ala Gly		
	355	360
Tyr Pro Leu Gly Lys Val Ala Gln Asp Trp Gly Trp His Gly Phe Phe		
	370	375
Val Ala Leu Leu Ala Cys Ala Leu Ile Ala Leu Ile Leu Phe Leu Pro		
385	390	395
Thr Trp Asn Ala Ser Glu Gln Ser Leu Arg Lys His Ser His		
	405	410

(2) INFORMATIONS POUR LA SEQ ID NO: 920:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 400 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 902677..903876

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 920:

Trp Lys Arg Val Glu His Ala Ala His Arg Ile Cys Asn Leu Tyr Gly		
1	5	10
Phe Asp Glu Ile Arg Thr Pro Val Phe Glu Lys Thr Glu Thr Phe Leu		
	20	25
Arg Val Gly Glu His Ser Asp Ile Val Lys Lys Glu Val Tyr Thr Xaa		
	35	40
Leu Asp Lys Lys Gly Arg Ser Leu Thr Leu Arg Pro Glu Gly Thr Ala		
	50	55
Ala Val Val Arg Ala Leu Leu Asp His Ser Ala Asp Met Arg Lys Asp		
65	70	75
Asn Lys Phe Tyr Tyr Ile Leu Pro Met Phe Arg Tyr Glu Arg Xaa Gln		
	85	90
Ser Gly Arg Tyr Arg Gln His His Gln Phe Gly Leu Glu Ala Ile Gly		
	100	105
Val Arg His Pro Leu Arg Asp Ala Glu Val Leu Ser Leu Leu Trp Asp		
	115	120
Phe Tyr Ala Ala Val Gly Leu Gln His Met Gln Ile His Val Asn Phe		
	130	135
Leu Gly Gly Gln Lys Thr Arg Ala Arg Tyr Asp Glu Ala Leu Arg Glu		
145	150	155
Phe Phe Arg Lys Asp Leu Asp Arg Leu Ser Pro Leu Ser Gln Glu Arg		
	165	170
Tyr His Ala Asn Leu Leu Arg Ile Leu Asp Ser Lys Glu Pro Glu Asp		
	180	185
Gln Glu Phe Ile Glu Lys Ala Pro Ser Ile Leu Asp Tyr Ile Asp Asp		
	195	200
Arg Asp Leu Ser Tyr Phe Asp Ala Val Leu Ala Gln Leu Lys Ala Leu		
	210	215
		220

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Gly Ile Pro Phe Ala Ile Asn Pro Arg Leu Val Arg Gly Leu Asp Tyr
225                230                235                240
Tyr Thr Asp Leu Val Phe Glu Ala Val Thr Val Val Gly Glu Arg Ser
                245                250                255
Tyr Ala Leu Gly Gly Gly Gly Arg Tyr Asp Glu Leu Val Ala Gln Ser
                260                265                270
Gly Gly Pro Ser Met Pro Ala Phe Gly Phe Gly Val Gly Leu Glu Arg
                275                280                285
Val Ile Gln Thr Leu Leu Glu Gln Gly Asn Ser Leu Ser Thr Ser Thr
                290                295                300
Arg Arg Leu Arg Leu Ile Pro Met Asp Glu Gln Ala Asp Ala Phe Cys
305                310                315                320
Phe Ser Trp Ala Asn Arg Leu Arg Asn Leu Gly Ile Ala Thr Glu Val
                325                330                335
Asp Trp Ser His Lys Lys Pro Lys Leu Ser Leu Lys Asp Ala Ala Asp
                340                345                350
Gln Gln Val Ser Phe Val Cys Leu Leu Gly Glu Gln Glu Leu Ala Thr
                355                360                365
Lys Gln Phe Ile Val Lys Asp Met Ser Leu His Gln Ser Phe Ser Gly
                370                375                380
Ala Gln Gln Asp Val Glu Gln Arg Leu Val Tyr Glu Val Gln Asn Ala
385                390                395                400

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(2) INFORMATIONS POUR LA SEQ ID NO: 921:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 87 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(903471..903731)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 921:

```

Ser Ala Ala Ser Leu Arg Asp Asn Leu Gly Phe Leu Trp Leu Gln Ser
1                5                10                15
Thr Ser Val Ala Met Pro Arg Leu Arg Lys Arg Phe Ala His Glu Lys
                20                25                30
Gln Asn Ala Ser Ala Cys Ser Ser Ile Gly Ile Asn Arg Asn Arg Arg
                35                40                45
Val Glu Val Asp Lys Glu Phe Pro Cys Ser Asn Ser Val Trp Ile Thr
                50                55                60
Leu Ser Asn Pro Thr Pro Lys Pro Lys Ala Gly Ile Glu Gly Pro Pro
65                70                75                80
Asp Cys Ala Thr Asn Ser Ser
                85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 922:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 582 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 903860..905605

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 922:

```

Met Lys Tyr Arg Thr His Lys Cys Asn Glu Leu Ser Leu Asp His Val
1      5      10      15
Gly Glu His Val Arg Leu Ser Gly Trp Val His Arg Tyr Arg Asn His
20      25      30
Gly Gly Val Val Phe Ile Asp Leu Arg Asp Arg Phe Gly Ile Thr Gln
35      40      45
Ile Val Cys Arg Gln Glu Glu Asn Pro Glu Leu His Gln Leu Met Asp
50      55      60
Gln Val Arg Ser Glu Trp Val Leu Cys Val Glu Gly Leu Val Cys Ala
65      70      75      80
Arg Leu Glu Gly Met Glu Asn Pro Asn Leu Val Thr Gly Ser Ile Glu
85      90      95
Val Glu Val Ser Ser Leu Glu Val Leu Ser Arg Ala Gln Asn Leu Pro
100     105     110
Phe Ser Ile Ser Asp Glu His Ile Asn Val Asn Glu Glu Leu Arg Leu
115     120     125
Thr Tyr Arg Tyr Leu Asp Met Arg Arg Gly Asp Ile Leu Asp Arg Leu
130     135     140
Met Cys Arg His Lys Val Met Leu Ala Cys Arg Gln Tyr Leu Asp Glu
145     150     155     160
Gln Gly Phe Thr Glu Val Val Thr Pro Ile Leu Gly Lys Ser Thr Pro
165     170     175
Glu Gly Ala Arg Asp Tyr Leu Val Pro Ser Arg Ile Tyr Pro Gly Asn
180     185     190
Phe Tyr Ala Leu Pro Gln Ser Pro Gln Leu Phe Lys Gln Ile Leu Met
195     200     205
Val Gly Gly Leu Asp Arg Tyr Phe Gln Ile Ala Thr Cys Phe Arg Asp
210     215     220
Glu Asp Leu Arg Ala Asp Arg Gln Pro Glu Phe Thr Gln Ile Asp Met
225     230     235     240
Glu Met Ser Phe Gly Gly Pro Glu Asp Leu Phe Pro Val Val Glu Glu
245     250     255
Leu Val Thr Arg Leu Phe Ala Val Lys Gly Ile Glu Leu Lys Ala Pro
260     265     270
Phe Leu Arg Met Thr Tyr Gln Glu Ala Lys Asp Ser Tyr Gly Thr Asp
275     280     285
Lys Pro Asp Leu Arg Phe Ala Leu Arg Leu Lys Asn Cys Cys Glu Tyr
290     295     300
Ala Arg Lys Phe Thr Phe Ser Ile Phe Leu Asp Gln Leu Ala His Gly
305     310     315     320
Gly Thr Val Lys Gly Phe Cys Val Pro Gly Gly Ala Asp Met Ser Arg
325     330     335
Lys Gln Leu Asp Ile Tyr Thr Asp Phe Val Lys Arg Tyr Gly Ser Met
340     345     350
Gly Leu Val Trp Ile Lys Lys Gln Asp Gly Gly Val Ser Ser Asn Val
355     360     365
Ala Lys Phe Ala Ser Glu Asp Val Phe Gln Glu Met Phe Glu Ala Phe
370     375     380
Glu Ala Lys Asp Gln Asp Ile Leu Leu Leu Ile Ala Ala Pro Glu Ala
385     390     395     400
Val Ala Asn Gln Ala Leu Asp His Leu Arg Arg Leu Ile Ala Lys Glu
405     410     415

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Arg Gln Leu Tyr Asp Ser Thr Gln Tyr Asn Phe Val Trp Ile Thr Asp
      420      425      430
Phe Pro Leu Phe Ala Lys Glu Glu Gly Glu Leu Cys Pro Glu His His
      435      440      445
Pro Phe Thr Ala Pro Leu Asp Glu Asp Ile Ser Leu Leu Asp Ser Asp
      450      455      460
Pro Phe Ala Val Arg Ser Ser Ser Tyr Asp Leu Val Leu Asn Gly Tyr
465      470      475      480
Glu Ile Ala Ser Gly Ser Gln Arg Ile His Asn Pro Asp Leu Gln Asn
      485      490      495
Lys Ile Phe Ala Leu Leu Lys Leu Ser Gln Glu Ser Val Lys Glu Lys
      500      505      510
Phe Gly Phe Phe Ile Asp Ala Leu Ser Phe Gly Thr Pro Pro His Leu
      515      520      525
Gly Ile Ala Leu Gly Leu Asp Arg Ile Met Met Val Leu Thr Gly Ala
      530      535      540
Glu Thr Ile Arg Glu Val Ile Ala Phe Pro Lys Thr Gln Lys Ala Gly
545      550      555      560
Asp Leu Met Met Ser Ala Pro Ser Glu Ile Leu Pro Ile Gln Leu Lys
      565      570      575
Glu Leu Gly Leu Lys Leu
      580

```

(2) INFORMATIONS POUR LA SEQ ID NO: 923:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 243 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 905746..906474

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 923:

```

Met Lys Asn Ile Leu Ser Trp Met Leu Met Phe Ala Val Ala Leu Pro
1      5      10      15
Ile Val Gly Cys Asp Asn Gly Gly Gly Ser Gln Thr Ser Ala Thr Glu
      20      25      30
Lys Ser Met Val Glu Asp Ser Ala Leu Thr Asp Asn Gln Lys Leu Ser
      35      40      45
Arg Thr Phe Gly His Leu Leu Ala Arg Gln Leu Ser Arg Thr Glu Asp
50      55      60
Phe Ser Leu Asp Leu Val Glu Val Ile Lys Gly Met Gln Ser Glu Ile
65      70      75      80
Asp Gly Gln Ser Ala Pro Leu Thr Asp Thr Glu Tyr Glu Lys Gln Met
      85      90      95
Ala Glu Val Gln Lys Ala Ser Phe Glu Ala Lys Cys Ser Glu Asn Leu
      100      105      110
Ala Ser Ala Glu Glu Phe Leu Lys Glu Asn Lys Glu Lys Ala Gly Val
      115      120      125
Ile Glu Leu Glu Pro Asn Lys Leu Gln Tyr Arg Val Val Lys Glu Gly
130      135      140
Thr Gly Arg Ala Leu Ser Gly Lys Pro Thr Ala Leu Leu His Tyr Thr
145      150      155      160
Gly Ser Phe Ile Asp Gly Lys Asp Phe Asp Ser Ser Glu Lys Asn Lys

```

```

                165                170                175
Ala Ala Ile Leu Leu Pro Leu Thr Lys Val Ile Pro Gly Phe Ser Gln
                180                185                190
Gly Met Gln Gly Met Lys Glu Gly Glu Val Arg Val Leu Tyr Ile His
                195                200                205
Pro Asp Leu Ala Tyr Gly Thr Ala Gly Gln Leu Pro Pro Asn Ser Leu
                210                215                220
Leu Ile Phe Glu Val Xaa Leu Ile Glu Ala Asn Asp Asp Asn Val Ser
225                230                235                240
Val Thr Glu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 924:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 119 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 906589..906945

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 924:

```

Pro Leu Gly Phe Ser Leu Ala Asp Lys Phe Val Lys Arg Ala Gly Met
1          5          10          15
Asp Tyr Trp Glu Arg Leu Ser Leu Ser Val Val Asp Ser Leu Glu Glu
20          25          30
Ala Leu Leu Gly Val Pro Lys Glu Arg Ile Phe Cys Leu Thr Thr Lys
35          40          45
Gly Ser Ser Tyr Tyr Gly Glu Arg Glu Leu Pro Leu Asp Gly Thr Tyr
50          55          60
Ile Phe Gly Ala Glu Ser Lys Gly Leu Ser Gln Thr Val Leu Asp Ala
65          70          75          80
Tyr Ser Ser Gln Cys Leu Tyr Ile Pro Met Ile Glu Gly Thr Arg Ser
85          90          95
Leu Asn Leu Ala Thr Ser Val Gly Ile Val Met Tyr Glu Val Ala Arg
100         105         110
Gln Asn Tyr Lys Thr Leu Phe
115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 925:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 102 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(907001..907306)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 925:


```

Met Val Gln Val Val Ser Gln Glu Asn Phe Ala Asp Ser Ile Ala Ser
1          5          10          15
Gly Leu Val Leu Ile Asp Phe Phe Ala Glu Trp Xaa Gly Pro Cys Lys
          20          25          30
Met Leu Thr Pro Val Leu Glu Ala Leu Ala Ala Glu Leu Pro His Val
          35          40          45
Thr Ile Leu Lys Val Asp Ile Asp Ser Ser Pro Arg Pro Ala Glu Gln
          50          55          60
Tyr Ser Val Ser Ser Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Lys
65          70          75          80
Glu Val Glu Arg Ser Val Gly Leu Lys Asp Lys Asp Ser Leu Ile Lys
          85          90          95
Leu Ile Ser Lys His Gln
          100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 926:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 214 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 908101..908742

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 926:

```

Gln Arg Thr Cys Phe Xaa Xaa Glu Gln Ser Leu Arg Leu Ser Pro Val
1          5          10          15
Val Phe Val Arg Asp Lys Ile Ile Phe Lys Ser Thr Glu Asp Ala Ile
          20          25          30
Gln Leu Leu Glu Ala Asp Lys Lys Ile Trp Arg Glu Thr Glu Ile Gln
          35          40          45
Ile Ser Ser Gly Lys Pro Glu Val Asn Glu Gln Thr Lys Arg Ile Tyr
          50          55          60
Ile Cys Pro Phe Thr Gly Lys Val Phe Ala Asp Asn Val Tyr Ala Asn
65          70          75          80
Pro Gln Asp Ala Ile Tyr Asp Trp Leu Ser Ser Cys Pro Gln Asn Arg
          85          90          95
Glu Arg Gln Ser Gly Val Ala Val Lys Arg Phe Leu Val Ser Asp Asp
          100          105          110
Pro Glu Val Ile Arg Ala Tyr Ile Val Pro Pro Lys Glu Pro Ile Ile
          115          120          125
Lys Thr Val Tyr Ala Ser Ala Val Thr Gly Lys Leu Phe His Ser Leu
          130          135          140
Pro Thr Leu Leu Glu Asp Phe Lys Thr Ser Tyr Leu Arg Pro Met Thr
145          150          155          160
Leu Glu Glu Val Gln Asn Gln Asn Lys Phe Gln Leu Glu Ser Ser Phe
          165          170          175
Leu Thr Leu Leu Gln Asn Ala Leu Glu Glu Glu Lys Ile Ala Glu Phe
          180          185          190
Val Glu Ser Leu Ala Asp Asp Thr Ala Phe His Lys Tyr Ile Ser Gln
          195          200          205
Trp Val Asp Thr Glu Glu
          210

```

(2) INFORMATION POUR LA SEQ ID NO: 927:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 158 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 908721..909194

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 927:

```

Pro Met Gly Arg Tyr Arg Arg Val Thr His Ser Cys Glu Glu Thr Ile
1          5          10          15
Asp Leu Ala Thr Arg Val Gly Arg Asp Leu Thr Pro Gly Met Val Val
          20          25          30
Leu Leu Ser Gly Asp Tyr Gly Ser Gly Lys Thr Glu Phe Val Arg Gly
          35          40          45
Ile Val Gln Gly Phe Leu Gly Glu Ala Ala Val Asp Gln Val Ala Ser
          50          55          60
Pro Ser Phe Ala Leu Leu His Val Tyr Glu Ala Gly Gly Arg Arg Val
65          70          75          80
Cys His Tyr Asp Leu Tyr Arg Leu Glu Thr Met Asp Ile Arg Asn Gly
          85          90          95
Ala Asp Leu Phe Gln Asp Ala Glu Glu Glu Asp Leu Ile Cys Val Glu
          100          105          110
Trp Pro Glu Ala Val Asn Leu Leu Pro Gln Phe Arg Lys Ser Val Cys
          115          120          125
Val Gln Met Arg Ser Leu Thr Asp Ala Gln Arg Glu Val Ser Ile Gly
          130          135          140
Val Thr Asp Gly Cys Asp Leu Ser Phe Phe Met Glu Asn Asp
145          150          155

```

(2) INFORMATION POUR LA SEQ ID NO: 928:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 129 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 909198..909584

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 928:

```

Arg Val Val Leu Leu Lys Asp Val Glu Phe Val Cys Leu Asp Cys Glu
1          5          10          15
Thr Thr Gly Leu Asp Val Lys Lys Asp Arg Val Ile Glu Phe Ala Ala
          20          25          30
Ile Arg Phe Thr Phe Asp Glu Ile Ile Asp Ser Val Glu Phe Leu Ile
          35          40          45
His Pro Glu Arg Ala Val Ser Ala Glu Ser Gln Lys Ile His Lys Ile
          50          55          60

```

Ser Asp Ala Met Leu Arg Asp Lys Pro Lys Phe Gly Glu Val Phe Ser
 65 70 75 80
 Arg Ile Lys Gly Phe Phe Lys Glu Arg Asp His Ile Val Gly His His
 85 90 95
 Val Gly Phe Asp Leu Gln Val Leu Ser Gln Glu Ser Glu Arg Leu Gly
 100 105 110
 Glu Thr Leu Leu Pro Lys His His Tyr Val Ile Asp Thr Leu Arg Leu
 115 120 125
 Ala

(2) INFORMATIONS POUR LA SEQ ID NO: 929:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 123 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 909583..909951

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 929:

Leu Lys Glu Tyr Gly Asp Ser Pro Asn Asn Ser Leu Glu Ala Leu Ala
 1 5 10 15
 Arg His Phe Asn Val Pro His Gln Gly Asn His Arg Ala Met Lys Asp
 20 25 30
 Val Glu Met Asn Val Lys Val Phe Lys His Leu Thr Lys Arg Phe Arg
 35 40 45
 Thr Leu Ser Gln Val Thr His Ile Leu Ser Lys Pro Ile Lys Met Lys
 50 55 60
 Tyr Met Pro Leu Gly Lys Tyr Lys Gly Trp Leu Phe Thr Asp Ile Pro
 65 70 75 80
 Leu Glu Tyr Leu Leu Trp Ala Ser Lys Met Asp Phe Asp Gln Asp Leu
 85 90 95
 Leu Phe Ser Ile Arg Ser Glu Ile Lys Ser Arg Lys Lys Gly Thr Gly
 100 105 110
 Phe Ala Gln Ala Asn Asn Pro Phe Leu Gly Leu
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 930:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 163 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 910081..910569

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 930:

Lys Gly Asp Val Arg Lys Asp Asn Lys Glu Asp Lys Arg Lys Lys Val

```

1              5              10              15
Ser Ala Ser Cys Ile Thr Asp His Ile Tyr Lys Ile Phe Pro Asn Asp
20              25              30
Leu Asn Thr Asn Asn Thr Xaa Phe Gly Gly Leu Leu Met Ser Leu Leu
35              40              45
Asp Arg Leu Ala Leu Val Val Ala Glu Arg His Cys Glu Ser Ile Cys
50              55              60
Val Thr Ala Phe Val Asp Ala Met Arg Phe Tyr Ala Pro Ala Tyr Met
65              70              75              80
Gly Glu Asn Leu Ile Cys Cys Ala Ser Val Asn Arg Ser Trp Arg Thr
85              90              95
Ser Leu Glu Val Gly Val Lys Val Trp Ala Glu Asn Ile Tyr Lys Gln
100             105             110
Glu His Arg His Ile Thr Ser Ala Tyr Phe Thr Phe Val Ala Val Asp
115             120             125
Lys Asn Asn Ser Pro Val Glu Val Pro Glu Leu Ile Pro Glu Ser Gln
130             135             140
Glu Glu Ile Arg Arg Phe Arg Glu Ala Asp Gln Arg Arg Ala Leu Arg
145             150             155             160
Leu Lys Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 931:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 110 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 910615..910944

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 931:

```

Ala Ser Lys Gly Val Pro Leu Val Phe Lys Pro Val Ser Tyr Ile Ile
1              5              10              15
Leu Ser Trp Val Leu Val Cys Leu Ala Gln Pro Asp Val Ser Val Val
20              25              30
Ala Ser Val Val Ser Cys Ile Cys Gly Tyr Ser Leu Leu Trp Ala Gly
35              40              45
Leu Phe Ala Leu Val Glu Gln Leu Ser Trp Lys Lys Val Trp Cys Ile
50              55              60
Ala Phe Ile Trp Thr Trp Thr Val Glu Gly Ala His Phe Ser Trp Met
65              70              75              80
Leu Glu Asp Leu Tyr Val Gly Thr Ser Ile Tyr Phe Val Trp Gly Ile
85              90              95
Leu Leu Ser Tyr Leu Ala Thr Leu Phe Ala Ser Phe Ser Cys
100             105             110

```

(2) INFORMATIONS POUR LA SEQ ID NO: 932:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 438 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 910948..912261

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 932:

Val	Val	Trp	Cys	Cys	Arg	Lys	Gln	Tyr	Arg	Gly	Ala	Leu	Val	Trp	Leu	1	5	10	15
Pro	Gly	Val	Trp	Val	Ala	Ile	Glu	Ala	Ile	Arg	Tyr	Tyr	Gly	Leu	Leu	20	25	30	
Ser	Gly	Val	Ser	Phe	Asp	Phe	Ile	Gly	Trp	Pro	Leu	Thr	Ala	Thr	Ala	35	40	45	
Tyr	Gly	Arg	Gln	Phe	Gly	Ser	Phe	Phe	Gly	Trp	Ala	Gly	Gln	Ser	Phe	50	55	60	
Leu	Val	Ile	Ala	Ala	Asn	Ile	Cys	Cys	Phe	Ala	Ala	Cys	Leu	Leu	Lys	65	70	75	80
His	Ser	Phe	Ser	Lys	Gly	Leu	Trp	Leu	Thr	Leu	Cys	Ala	Phe	Pro	Tyr	85	90	95	
Leu	Leu	Gly	Gly	Ala	His	Tyr	Glu	Tyr	Leu	Lys	Lys	His	Phe	Ser	Asp	100	105	110	
Ser	Glu	Val	Leu	Arg	Val	Ala	Ile	Val	Gln	Pro	Gly	Tyr	Ser	Pro	His	115	120	125	
Met	His	Ala	Gly	Arg	Met	Ala	Ser	Ala	Ile	Trp	Arg	Gly	Leu	Val	Ser	130	135	140	
Leu	Cys	Gln	Thr	Ile	Gln	Thr	Pro	Val	Asp	Val	Ile	Val	Phe	Pro	Glu	145	150	155	160
Val	Ser	Val	Pro	Phe	Gly	Leu	His	Arg	Gln	Ala	Tyr	Thr	Leu	His	Glu	165	170	175	
Asn	Gln	Pro	Val	Leu	Glu	Ser	Leu	Leu	Pro	Asn	Lys	Ser	Trp	Gly	Glu	180	185	190	
Phe	Phe	Thr	Asn	Leu	Asp	Trp	Ile	Gln	Ala	Ile	Ala	Glu	Arg	Tyr	Gln	195	200	205	
Cys	Thr	Val	Ile	Met	Gly	Met	Glu	Arg	Trp	Glu	Asn	Lys	Gly	Gly	Ile	210	215	220	
Leu	His	Leu	Tyr	Asn	Ala	Glu	Cys	Val	Ser	Arg	Glu	Gly	Glu	Ile		225	230	235	240
Thr	Ser	Tyr	Asp	Lys	Arg	Ile	Leu	Val	Pro	Gly	Gly	Glu	Tyr	Ile	Pro	245	250	255	
Gly	Gly	Lys	Ile	Gly	Phe	Ser	Leu	Cys	Gln	Thr	Phe	Phe	Pro	Glu	Phe	260	265	270	
Ala	Leu	Pro	Phe	Gln	Arg	Leu	Pro	Gly	Glu	Phe	Ser	Gly	Val	Val	Asn	275	280	285	
Ile	Thr	Glu	Arg	Ile	Lys	Ala	Gly	Ile	Ser	Ile	Cys	Tyr	Glu	Glu	Thr	290	295	300	
Phe	Gly	Tyr	Ala	Ile	Arg	Pro	Tyr	Lys	Arg	Gln	Gln	Ala	Asp	Ile	Leu	305	310	315	320
Val	Asn	Leu	Thr	Asn	Asp	Gly	Trp	Tyr	Pro	Arg	Ser	Arg	Leu	Pro	Leu	325	330	335	
Val	His	Phe	Tyr	His	Gly	Met	Leu	Arg	Asn	Gln	Glu	Leu	Gly	Ile	Pro	340	345	350	
Cys	Ile	Arg	Ala	Cys	His	Thr	Gly	Val	Ser	Ala	Ala	Val	Asp	Ser	Leu	355	360	365	
Gly	Arg	Ile	Val	Gly	Ile	Leu	Pro	Trp	Glu	Ser	Arg	Thr	Cys	Pro	Val	370	375	380	
Ser	Thr	Gly	Val	Leu	Gln	Val	Ser	Val	Pro	Leu	Tyr	Ser	Tyr	His	Thr	385	390	395	400
Val	Tyr	Ala	Arg	Leu	Gly	Asp	Ala	Pro	Leu	Leu	Leu	Ile	Ala	Val	Cys				

Ser Val Ile Gly Ala Ile Ala Tyr Phe Tyr Arg Lys Lys Lys Glu Thr
 405 410 415
 420 425 430
 Pro Pro Gln Thr Phe Phe
 435

(2) INFORMATIONS POUR LA SEQ ID NO: 933:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 77 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 912399..912629

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 933:

Gly Met Leu Phe Arg Gly Gly Ser Ala Phe Trp Lys Ser Cys Asp Ala
 1 5 10 15
 Tyr Xaa Arg Ala Arg Arg Gly Lys Tyr Arg Arg Ile Phe Ser Arg His
 20 25 30
 Ala Ala Ser Glu Gln Tyr Ile Pro Ala Arg Leu Ala Asn Val Cys Gly
 35 40 45
 Thr Gly Arg Ser Thr Thr Leu Ser Leu Asp Gly Ser Val Ile Ser Thr
 50 55 60
 Val Glu His Leu Leu Ala Ser Leu Leu Leu Arg Ser Gly
 65 70 75

(2) INFORMATIONS POUR LA SEQ ID NO: 934:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 208 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 912595..913218

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 934:

Asn Thr Cys Trp His Arg Ser Tyr Phe Gly Val Asp Asn Val Arg Ile
 1 5 10 15
 Tyr Cys Ser Glu Asp Glu Ile Pro Ile Gly Asp Gly Ser Ala Gln Val
 20 25 30
 Phe Met Asp Leu Ile Asp Gln Ala Gly Ile Gln Glu Gln Gln Thr
 35 40 45
 Val Gln Ile Ala Arg Leu Ala His Pro Val Tyr Tyr Gln Tyr Gln Asp
 50 55 60
 Thr Ile Leu Ala Ala Phe Pro Ser Asp Glu Phe Lys Ile Ser Tyr Thr
 65 70 75 80
 Leu His Tyr Ser His Asn Ser Thr Ile Gly Thr Gln Tyr Arg Ser Leu
 85 90 95

Val	Ile	Ser	Glu	Glu	Ser	Phe	Arg	Lys	Glu	Ile	Ala	Pro	Cys	Arg	Thr
			100					105					110		
Phe	Ala	Leu	Tyr	Ser	Glu	Leu	Cys	Phe	Leu	Met	Glu	Lys	Gly	Leu	Ile
		115					120					125			
Gly	Gly	Gly	Cys	Val	Gly	Asn	Ala	Val	Leu	Ser	Lys	Xaa	Asp	Gly	Val
	130					135					140				
Ile	Ser	Leu	Gly	Lys	Leu	Arg	Phe	Pro	Asp	Glu	Pro	Val	Arg	His	Lys
145					150					155					160
Ile	Leu	Asp	Leu	Ile	Gly	Asp	Leu	Ser	Leu	Val	Gly	Thr	Pro	Phe	Leu
			165					170						175	
Ala	His	Val	Ile	Ala	Val	Gly	Ser	Gly	His	Ser	Ser	Asn	Ile	Ala	Leu
		180						185					190		
Gly	Asn	Arg	Ile	Leu	Glu	Ala	Leu	Gln	His	Glu	Gln	Glu	Leu	Val	Lys
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 935:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 158 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 913203..913676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 935:

Thr	Gly	Val	Ser	Gln	Met	Asn	Glu	Lys	Pro	Val	Leu	Gly	Ile	Gln	Asp
1				5					10					15	
Ile	Gln	Asn	Leu	Leu	Pro	His	Arg	Tyr	Pro	Phe	Leu	Leu	Val	Asp	Lys
		20						25					30		
Ile	Leu	Ser	Tyr	Asp	Leu	Asn	Thr	Arg	Ser	Val	Val	Ala	Gln	Lys	Asn
		35					40					45			
Val	Thr	Ile	Asn	Glu	Pro	Phe	Phe	Ala	Gly	His	Phe	Pro	Gly	Ala	Pro
	50					55					60				
Ile	Met	Pro	Gly	Val	Leu	Ile	Leu	Glu	Ala	Leu	Ala	Gln	Ala	Ala	Gly
65					70				75					80	
Val	Leu	Leu	Gly	Ile	Ile	Leu	Glu	Asn	Asp	Arg	Asp	Lys	Lys	Ile	Ala
			85					90					95		
Leu	Phe	Leu	Gly	Ile	Gln	Lys	Ala	Lys	Phe	Arg	Gln	Pro	Val	Lys	Pro
		100						105					110		
Gly	Asp	Val	Leu	Thr	Leu	Lys	Ala	Glu	Phe	Ser	Leu	Ile	Ser	Ala	Lys
		115					120					125			
Gly	Gly	Lys	Ala	Phe	Ala	Gln	Ala	Phe	Val	Gly	Ser	Gln	Val	Val	Ala
	130					135					140				
Glu	Gly	Glu	Leu	Ser	Phe	Val	Leu	Val	Lys	Lys	Glu	Ser	Ile		
145					150					155					

(2) INFORMATIONS POUR LA SEQ ID NO: 936:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 265 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 913691..914485

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 936:

```

Met Thr Asn Ile His Pro Thr Ala Ile Val Glu Asp Gly Ala Arg Ile
1      5      10      15
Gly Asn Asn Val Thr Ile Glu Pro Tyr Ala Ile Val Lys Lys Ser Val
      20      25      30
Thr Leu Trp Asn Asp Val Val Val Lys Ser Tyr Ala Tyr Ile Asp Gly
      35      40      45
Phe Thr Thr Ile Gly Arg Xaa Thr Thr Val Trp Pro Ser Ala Met Ile
      50      55      60
Gly Asn Lys Pro Gln Asp Leu Lys Phe Lys Gly Glu Lys Thr Phe Val
      65      70      75      80
Glu Ile Gly Glu His Cys Glu Ile Arg Glu Phe Ala Met Ile Thr Ser
      85      90      95
Ser Thr Phe Glu Gly Thr Thr Val Ser Ile Gly Asn Asn Cys Leu Ile
      100      105      110
Met Pro Trp Ala His Ile Ala His Asn Cys Ser Val Gly Asn Asn Val
      115      120      125
Val Phe Ser Thr His Val Gln Leu Ala Gly His Val Gln Val Gly Asp
      130      135      140
Cys Val Thr Ile Gly Ser Met Val Gly Val His Gln Phe Val Arg Ile
      145      150      155      160
Gly Ser Tyr Ser Met Val Gly Ala Met Ser Gly Ile Arg Arg Asp Ile
      165      170      175
Pro Pro Phe Thr Ile Gly Thr Gly Asn Pro Tyr Ala Leu Gly Gly Ile
      180      185      190
Asn Lys Val Gly Leu Gln Arg Arg Gln Val Ser Phe Glu Thr Arg Leu
      195      200      205
Ala Leu Ile Lys Thr Phe Lys Arg Val Phe Arg Ser Asp Glu Ser Phe
      210      215      220
Gln Ala Ser Leu Glu Ser Val Leu Glu Asp Phe Gly Glu Val Pro Glu
      225      230      235      240
Val Arg His Phe Val Glu Phe Cys Arg Gln Pro Ser Lys Arg Gly Ile
      245      250      255
Glu Arg Gly Val Asp Cys Glu Asp Leu
      260      265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 937:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 207 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 914516..915136

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 937:

```

Leu Ser Leu Ser Leu Arg Val Val Tyr Leu Gly Thr Pro Gln Phe Ala
1      5      10      15

```


Ala	Thr	Val	Leu	Lys	Thr	Leu	Leu	Asp	Ala	His	Thr	His	Ile	Val	Gly
			20					25					30		
Val	Val	Thr	Arg	Ala	Asp	Lys	Pro	Gln	Lys	Arg	Ser	Ser	Lys	Leu	Ile
		35					40					45			
Ser	Ser	Pro	Val	Lys	Gln	Leu	Ala	Leu	Ser	Lys	Asn	Ile	Pro	Leu	Leu
		50				55					60				
Gln	Pro	Ile	Lys	Thr	Thr	Asp	Pro	Ala	Phe	Leu	Ala	Gln	Leu	Arg	Glu
65					70					75					80
Trp	Gln	Ala	Asp	Val	Phe	Ile	Val	Val	Ala	Tyr	Gly	Val	Ile	Leu	Lys
				85					90					95	
Gln	Glu	Leu	Leu	Asp	Ile	Pro	Thr	Tyr	Gly	Cys	Tyr	Asn	Leu	His	Ala
			100					105					110		
Gly	Leu	Leu	Pro	Ala	Tyr	Arg	Gly	Ala	Ala	Pro	Ile	Gln	Arg	Cys	Ile
			115				120					125			
Met	Asp	Gly	Gly	Val	Leu	Ser	Gly	Asn	Thr	Val	Ile	Arg	Met	Asp	Ala
	130					135					140				
Gly	Met	Asp	Thr	Gly	Asp	Ile	Ala	Asn	Val	Asn	Tyr	Val	Ala	Ile	Gly
145					150					155					160
Glu	Asp	Met	Thr	Ala	Gly	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Ala	Ser	Gly
				165					170					175	
Gly	Glu	Leu	Leu	Leu	Lys	Thr	Leu	Gln	Glu	Ile	Glu	Ala	Gly	Thr	Val
			180					185					190		
Arg	His	Val	Pro	Gln	Asn	Glu	Ala	Met	Leu	Arg	Trp	Leu	Leu	Asn	
		195					200					205			

(2) INFORMATIONS POUR LA SEQ ID NO: 938:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 108 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 915144..915467

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 938:

Gly	Arg	Gly	Arg	Asp	Ser	Leu	Gly	Cys	Ser	Ser	Phe	Ser	Ser	Ile	Arg
1				5					10					15	
Ala	Tyr	Pro	Gly	Ser	Leu	Ala	Cys	Ser	Gly	Arg	Leu	Asp	Ser	Leu	Ser
			20					25					30		
Ile	Pro	Arg	Glu	Arg	Gly	Xaa	Arg	Leu	Gly	Val	Leu	Ser	Ala	Arg	Met
		35				40						45			
Glu	Ser	Phe	Ser	Gly	Asn	Tyr	Gly	Asp	Pro	Gly	Glu	Val	Leu	Gly	Val
	50				55						60				
Ser	Gly	Glu	Asp	Leu	Leu	Ile	Ala	Cys	Arg	Gln	Gly	Ala	Leu	Arg	Leu
65					70					75					80
Arg	Met	Val	Gln	Pro	Glu	Gly	Lys	Ala	Ser	Met	Lys	Ala	Lys	Asp	Phe
			85					90						95	
Phe	Asn	Gly	Gln	Ser	Arg	Leu	Val	Ser	Lys	Leu	Phe				
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 939:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 335 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 915629..916633

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 939:

```

Val Asn Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn
1      5      10      15
Ala Leu Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val
20      25      30
Val Asn Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser
35      40      45
Ala Ala Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly
50      55      60
Ser Ser Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp
65      70      75      80
Ala Arg Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro
85      90      95
Gly Thr Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala
100     105     110
Ser Gln Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys
115     120     125
Val Ser His Lys Arg Arg Ala Ala Val Cys Ser Phe Ile Gly
130     135     140
Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe
145     150     155     160
Val Asn Lys Ile Trp Arg Asn Arg Phe Phe Leu Pro Lys Leu Lys Gln
165     170     175
Ile Trp Asp Leu Leu Leu Ala Ile Leu Trp Arg Leu Thr Met Gln Arg
180     185     190
Leu Trp Trp Val Leu Asp Ser Leu Ser Val Arg Lys Glu Gln Ile Ala
195     200     205
Lys Pro Pro Ala Leu Val Leu Arg Glu Lys Ser Arg His Ser Asn Cys
210     215     220
Arg Glu Arg Lys Met Leu Ala Arg Gly Glu Ser Leu Glu Arg Lys Pro
225     230     235     240
Arg Arg Ser Arg Ala Ser Ser Met His Ser Ser Leu Cys Thr Arg Ser
245     250     255
Phe Trp Asn Ala Leu Pro Thr Phe Ser Asn Trp Cys Arg Cys Leu Leu
260     265     270
Gln Trp Val Phe Val Gln Leu Trp Leu Arg Asp Val Arg Ser Leu Pro
275     280     285
Gln Leu Leu Asp Cys Gly Leu Ser Ala Thr Glu Tyr Xaa Gly Phe Phe
290     295     300
Lys Phe Leu Lys Lys Lys Ala Val Ser Lys Lys Lys Gln Pro Phe Leu
305     310     315     320
Ser Thr Lys Cys Leu Ala Phe Leu Ile Val Lys Ile Val Phe Leu
325     330     335

```

(2) INFORMATIONS POUR LA SEQ ID NO: 940:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 163 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 916051..916539

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 940:

```

Leu His Arg Arg Asn Tyr Leu Pro Arg Asp Ile Arg Ser Tyr Pro Ser
1          5          10          15
Asp Ser Val Cys Gln Gln Asn Leu Ala Gln Pro Phe Leu Ser Ser Gln
          20          25          30
Thr Lys Ala Asn Met Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn
          35          40          45
His Ala Ala Phe Val Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg
          50          55          60
Ala Asp Cys Glu Ala Pro Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser
65          70          75          80
Leu Glu Leu Ser Gly Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly
          85          90          95
Glu Lys Ala Lys Thr Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met
          100          105          110
His Glu Lys Phe Leu Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro
          115          120          125
Leu Pro Ile Thr Met Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr
          130          135          140
Phe Thr Thr Ala Val Ile Gly Leu Trp Thr Phe Cys Asn Arg Val Xaa
145          150          155          160
Gly Ile Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 941:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 221 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 916965..917627

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 941:

```

Met Arg Ser Gln Leu Ser Leu Ile Gly Lys Lys Glu Gly Met Met His
1          5          10          15
Val Phe Asp Lys Asn Gly Asn Leu Val Ala Cys Ser Val Ile Ser Val
          20          25          30
Asp Ala Asn Val Val Ala Gln Leu Lys Thr Ala Ser Ser Asp Gly Tyr
          35          40          45
Asn Ala Val Gln Ile Gly Ala Asp Val Val Gln Ala Pro Glu Lys Thr
          50          55          60
Ile Glu Lys Arg Phe Ser Lys Ala Leu Leu Gly His Phe Lys Lys Ser
65          70          75          80
Gly Gly Arg Ala Cys Arg Val Leu Lys Glu Val Val Val Ser Glu Glu

```

(2) INFORMATION POUR LA SEQ ID NO: 942:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 917639..918304

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 942:

Met	Val	Leu	Leu	Ser	Lys	Phe	Asp	Phe	Ser	Gly	Lys	Glu	Leu	Gly	Lys
1				5					10					15	
Phe	Glu	Leu	Pro	Asp	Ala	Phe	Phe	Thr	Glu	Gly	Arg	Glu	Gln	Ser	Val
			20					25					30		
Lys	Asp	Tyr	Leu	Val	Ala	Ile	Gln	Ala	Asn	Lys	Arg	Gln	Trp	Ser	Ala
		35					40					45			
Cys	Thr	Arg	Gly	Arg	Ser	Glu	Val	Ser	His	Ser	Thr	Lys	Lys	Pro	Phe
	50					55					60				
Arg	Gln	Lys	Gly	Thr	Gly	Asn	Ala	Arg	Gln	Gly	Cys	Leu	Ala	Ala	Pro
65					70					75					80
Gln	Phe	Arg	Gly	Gly	Gly	Ile	Val	Phe	Gly	Pro	Lys	Pro	Lys	Phe	Asp
				85					90					95	
Gln	His	Ile	Arg	Ile	Asn	Lys	Lys	Glu	Arg	Arg	Ala	Ala	Ile	Arg	Leu
			100					105					110		
Leu	Leu	Ala	Gln	Lys	Ile	Gln	Thr	Gly	Lys	Leu	Ile	Val	Ala	Glu	Asn
		115					120					125			
Ser	Val	Phe	Val	Ser	Ser	Leu	Asp	Ala	Pro	Lys	Thr	Lys	Glu	Ala	Leu
	130					135					140				
Arg	Phe	Leu	Lys	Glu	Cys	Asn	Val	Glu	Cys	Arg	Gly	Val	Leu	Phe	Val
145					150					155					160
Asp	Ser	Leu	Ala	His	Val	Gly	Ser	Asn	Glu	Asn	Leu	Arg	Leu	Ser	Val
				165					170					175	
Arg	Asn	Leu	Ser	Ala	Val	Arg	Gly	Phe	Thr	Tyr	Gly	Glu	Asn	Ile	Ser
			180					185					190		
Gly	Tyr	Asp	Ile	Ala	Ala	Ala	Arg	Asn	Ile	Val	Val	Ser	Glu	Lys	Ala
		195					200					205			

Leu Glu Leu Leu Val Glu Ser Leu Val Ser Thr Thr Lys Asp
 210 215 220

(2) INFORMATIONS POUR LA SEQ ID NO: 943:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 93 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 918377..918655

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 943:

Met	Leu	Glu	Gly	Leu	Ser	Leu	Gly	Asp	Gly	Glu	Gly	Lys	Lys	Lys	Gly
1				5					10					15	
Ser	Phe	Cys	Lys	Asp	Pro	Lys	Tyr	Thr	Phe	Ile	Val	Ala	Gly	Asp	Ala
			20					25					30		
Thr	Lys	Pro	Met	Ile	Ala	Glu	Ala	Ile	Glu	Ala	Ile	Tyr	Ser	Ala	Lys
			35				40					45			
Gly	Val	Lys	Val	Lys	Lys	Val	Asn	Thr	Met	Cys	Val	Lys	Pro	Gln	Pro
	50				55					60					
Thr	Arg	Ile	Phe	Arg	Gly	Arg	Arg	Lys	Gly	Arg	Thr	Ala	Gly	Phe	Lys
65				70					75						80
Lys	Ala	Ile	Val	Thr	Phe	Val	Asp	Gly	His	Ser	Ile	Gly			
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 944:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 284 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 918682..919533

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 944:

Met	Phe	Lys	Lys	Phe	Lys	Pro	Val	Thr	Pro	Gly	Thr	Arg	Gln	Leu	Ile
1				5					10					15	
Leu	Pro	Ser	Phe	Asp	Glu	Leu	Thr	Thr	Gln	Gly	Glu	Leu	Lys	Gly	Ser
			20					25					30		
Ser	Ser	Arg	Arg	Ser	Val	Arg	Pro	Asn	Lys	Lys	Leu	Ser	Phe	Phe	Lys
		35				40					45				
Lys	Ser	Ser	Gly	Gly	Arg	Asp	Asn	Leu	Gly	His	Ile	Ser	Cys	Arg	His
	50				55					60					
Arg	Gly	Gly	Gly	Val	Arg	Arg	His	Tyr	Arg	Val	Ile	Asp	Phe	Lys	Arg
65				70					75						80
Asn	Lys	Asp	Gly	Ile	Glu	Ala	Lys	Val	Ala	Ser	Val	Glu	Tyr	Asp	Pro
				85					90					95	
Asn	Arg	Ser	Ala	Tyr	Ile	Ala	Leu	Leu	Asn	Tyr	Val	Asp	Gly	Glu	Lys

(2) INFORMATION POUR LA SEQ ID NO: 945:

(A) LONGUEUR: 96 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 919542..919829

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 945:

(2) INFORMATION POUR LA SEQ ID NO: 946:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 919738..920157

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 946:

Trp	Leu	Asp	Thr	Ser	Trp	Glu	Ser	Ser	Leu	Gln	Gln	Glu	Cys	Leu	Arg
1				5					10					15	
Ala	Ile	Pro	Leu	Lys	Lys	Gly	Ile	Ile	Arg	Arg	Gln	Val	Met	Phe	Lys
			20					25					30		
Ala	Thr	Ala	Arg	Tyr	Ile	Arg	Val	Gln	Pro	Arg	Lys	Ala	Arg	Leu	Ala
		35				40						45			
Ala	Gly	Leu	Met	Arg	Asn	Arg	Ser	Val	Val	Glu	Ala	Gln	Gln	Gln	Leu
	50				55					60					
Ser	Phe	Ser	Gln	Met	Lys	Ala	Gly	Arg	Cys	Leu	Lys	Lys	Val	Leu	Asp
65					70				75						80
Ser	Ala	Ile	Ala	Asn	Ala	Glu	Ser	Asn	Glu	Asn	Ile	Lys	Arg	Glu	Asn
				85				90						95	
Leu	Cys	Val	Leu	Glu	Val	Arg	Val	Asp	Ala	Gly	Pro	Met	Phe	Lys	Arg
			100					105					110		
Met	Lys	Ser	Lys	Ser	Arg	Gly	Gly	Arg	Ala	Pro	Ile	Leu	Lys	Arg	Thr
		115				120						125			
Ser	His	Leu	Thr	Val	Ile	Val	Gly	Glu	Arg	Gly	Gln				
	130					135					140				

(2) INFORMATIONS POUR LA SEQ ID NO: 947:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 219 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 920184..920840

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 947:

Met	Ser	Ser	Arg	Val	Xaa	Thr	Ala	Val	Thr	Lys	Lys	Trp	Arg	Ser	Leu
1				5					10					15	
Trp	Tyr	Gly	Asn	Asn	Gln	Glu	Phe	Ala	Lys	Phe	Leu	Ile	Glu	Asp	Val
			20					25					30		
Lys	Ile	Arg	Glu	Phe	Leu	Lys	Lys	Lys	Pro	Ser	Cys	Gln	Gly	Ala	Ala
		35					40					45			
Gly	Phe	Val	Val	Lys	Arg	Met	Ser	Gly	Lys	Ile	Glu	Val	Thr	Ile	His
	50					55					60				
Thr	Ala	Arg	Pro	Gly	Leu	Val	Ile	Gly	Lys	Lys	Gly	Ala	Glu	Val	Asp
65					70				75						80
Ser	Leu	Lys	Ala	Glu	Leu	Lys	Lys	Leu	Thr	Gly	Lys	Asp	Val	Trp	Val
				85				90						95	
Glu	Ile	Ala	Glu	Val	Lys	Arg	Pro	Glu	Leu	Asn	Ala	Gln	Leu	Val	Ala
			100					105					110		
Asp	Gly	Ile	Ala	Lys	Gln	Ile	Glu	Arg	Arg	Val	Ser	Phe	Arg	Arg	Ala
		115				120						125			
Met	Lys	Lys	Ala	Leu	Gln	Ser	Val	Met	Asp	Ala	Gly	Ala	Leu	Gly	Val

```

      130      135      140
Lys Val Gln Val Ser Gly Arg Leu Ala Gly Ala Glu Ile Ala Arg Ser
145      150      155      160
Glu Trp Tyr Lys Asn Gly Arg Val Pro Leu His Thr Leu Arg Ala Asp
      165      170      175
Ile Asp Tyr Ala Thr Ala Ser Ala Glu Thr Thr Tyr Gly Ile Ile Gly
      180      185      190
Ile Lys Val Trp Ile Asn Leu Gly Glu Lys Lys Ala Val Pro Ala Ala
      195      200      205
Asn His Ala Gly Ala Ala Ser Thr Ala Ala Ala
      210      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 948:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 143 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 920866..921294

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 948:

```

Met Asn Gln Tyr Ala Lys Ala Ala Gly Lys Arg Thr Lys Phe Arg Lys
1      5      10      15
Gln Gln Lys Gly Gln Phe Ala Gly Leu Ser Lys Gly Ala Thr Phe Val
      20      25      30
Asp Phe Gly Glu Phe Gly Met Gln Thr Leu Glu Arg Gly Trp Ile Thr
      35      40      45
Ser Arg Gln Ile Glu Ala Cys Arg Val Ala Ile Asn Arg Tyr Leu Lys
      50      55      60
Arg Lys Gly Lys Val Trp Ile Arg Val Phe Pro Asp Lys Ser Val Thr
      65      70      75      80
Lys Lys Pro Ala Glu Thr Arg Met Gly Lys Gly Lys Gly Ala Pro Asp
      85      90      95
His Trp Val Ala Val Val Arg Pro Gly Arg Ile Leu Phe Glu Val Ala
      100      105      110
Asn Val Ser Lys Glu Asp Ala Gln Asp Ala Leu Arg Arg Ala Ala Ala
      115      120      125
Lys Leu Gly Ile Arg Thr Arg Phe Val Lys Arg Val Glu Arg Val
      130      135      140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 949:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 72 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921299..921514

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 949:

```

Met Gly Ala Lys Lys Asn Leu Leu Ala Glu Leu Arg Glu Lys Ser Ser
1           5           10           15
Glu Glu Leu Asp Glu Phe Ile Arg Asp Asn Lys Lys Ala Leu Phe Ala
          20           25           30
Leu Arg Ala Glu Ala Ala Leu Gln Asn Lys Val Val Lys Thr His Gln
          35           40           45
Phe Ser Leu Tyr Lys Lys Ser Ile Ala Arg Ala Leu Ile Ile Lys Gln
          50           55           60
Glu Lys Lys Asp Arg Val His Gly
65           70

```

(2) INFORMATIONS POUR LA SEQ ID NO: 950:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 83 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921510..921758

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 950:

```

Met Ala Ser Asp Val Arg Gly Arg Arg Lys Thr Lys Ile Gly Val Val
1           5           10           15
Val Ser Ser Lys Met Glu Lys Thr Val Val Val Arg Val Glu Arg Val
          20           25           30
Tyr Ser His Pro Gln Tyr Ala Lys Val Val Arg Asp Ser Ser Lys Tyr
          35           40           45
Tyr Ala His Asn Glu Leu Asp Val Lys Glu Gly Asp Thr Val Arg Ile
          50           55           60
Gln Glu Thr Arg Pro Leu Ser Lys Thr Lys Arg Trp Arg Val Val Gly
65           70           75           80
Arg Val Asn

```

(2) INFORMATIONS POUR LA SEQ ID NO: 951:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 122 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 921778..922143

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 951:

```

Met Ile Gln Gln Glu Ser Gln Leu Lys Val Ala Asp Asn Thr Gly Ala
1           5           10           15
Lys Lys Val Lys Cys Phe Lys Val Leu Gly Gly Ser Arg Arg Arg Tyr

```

(2) INFORMATION POUR LA SEQ ID NO: 952:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(B) TYPE: acide amine
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 922159..922491

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 952:

(2) INFORMATION POUR LA SEQ ID NO: 953:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 155 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 922571..923035

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 953:

```

Met Gln Ile Pro Val Leu Lys Lys Ile Val Ile Ser Met Gly Leu Ala
1      5      10      15
Glu Ala Ala Lys Asp Lys Asn Leu Phe Gln Ala His Leu Glu Glu Leu
20      25      30
Ala Val Ile Ser Gly Gln Lys Pro Leu Val Thr Arg Ala Lys Asn Ser
35      40      45
Ile Ala Gly Phe Lys Leu Arg Glu Gly Gln Gly Ile Gly Ala Lys Val
50      55      60
Thr Leu Arg Gly Ile Arg Met Tyr Asp Phe Met Asp Arg Phe Cys Asn
65      70      75      80
Ile Val Ser Pro Arg Ile Arg Asp Phe Arg Gly Phe Ser Cys Lys Gly
85      90      95
Asp Gly Arg Gly Cys Tyr Ser Leu Gly Leu Asp Asp Gln Gln Ile Phe
100     105     110
Pro Glu Val Asp Leu Asp Arg Val Lys Arg Ser Gln Gly Met Asn Ile
115     120     125
Thr Trp Val Thr Thr Ala Gln Thr Asp Ala Glu Cys Leu Thr Leu Leu
130     135     140
Glu Cys Met Gly Leu Arg Phe Lys Lys Ala Gln
145     150     155

```

(2) INFORMATIONS POUR LA SEQ ID NO: 954:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 98 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 923160..923453

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 954:

```

Ser Asn Ile Arg Ile Leu Lys Gln His Gly Phe Val Ala His Phe Leu
1      5      10      15
Val Lys Glu Glu Asn Arg Lys Arg Leu Met Arg Val Phe Leu Arg Tyr
20      25      30
Gly Glu Asp Arg Arg Pro Val Ile His Ala Leu Lys Arg Val Ser Lys
35      40      45
Pro Ser Arg Arg Val Tyr Val Ser Ala Ala Lys Ile Pro Tyr Val Phe
50      55      60
Gly Asn Met Gly Ile Ala Val Leu Ser Thr Pro Gln Gly Val Leu Glu
65      70      75      80
Gly Ser Val Ala Arg Ala Lys Asn Val Gly Gly Glu Leu Leu Cys Leu
85      90      95
Val Trp

```

(2) INFORMATIONS POUR LA SEQ ID NO: 955:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 923484..924032

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 955:

```

Met Ser Arg Lys Ala Arg Asp Pro Ile Val Leu Pro Gln Gly Val Glu
1      5      10
Val Ser Ile Gln Asn Asp Glu Ile Ser Val Lys Gly Pro Lys Gly Ser
      20      25      30
Leu Thr Gln Val Leu Ala Lys Glu Val Glu Ile Ala Val Lys Gly Asn
      35      40      45
Glu Val Phe Val Ala Pro Ala Ala His Val Val Asp Arg Pro Gly Arg
      50      55      60
Met Gln Gly Leu Tyr Trp Ala Leu Ile Ala Asn Met Val Lys Gly Val
65      70      75      80
His Thr Gly Phe Glu Lys Arg Leu Glu Met Ile Gly Val Gly Phe Arg
      85      90      95
Ala Ala Val Gln Gly Ser Leu Leu Asp Leu Ser Ile Gly Val Ser His
      100      105      110
Pro Thr Lys Met Pro Ile Pro Thr Gly Leu Glu Val Ser Val Glu Lys
      115      120      125
Asn Thr Leu Ile Ser Ile Lys Gly Ile Asn Lys Gln Leu Val Gly Glu
      130      135      140
Phe Ala Ala Cys Val Arg Ala Lys Arg Pro Pro Glu Pro Tyr Lys Gly
145      150      155      160
Lys Gly Ile Arg Tyr Glu Asn Glu Tyr Val Arg Arg Lys Ala Gly Lys
      165      170      175
Ala Ala Lys Thr Gly Lys Lys
      180

```

(2) INFORMATIONS POUR LA SEQ ID NO: 956:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 123 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924057..924425

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 956:

```

Met Glu Ser Ser Leu Tyr Lys Lys Thr Ser Gly Lys Ala Arg Arg Ala
1      5      10
Leu Arg Val Arg Lys Ala Leu Lys Gly Cys Ser Leu Lys Pro Arg Leu
      20      25      30
Ser Val Val Lys Thr Asn Lys His Val Tyr Val Gln Leu Ile Asp Asp
      35      40      45
Val Glu Gly Lys Thr Leu Ala Phe Ile Ser Thr Leu Ala Lys Val Ala
      50      55      60
Lys Thr Ser Gly Leu Thr Arg Lys Asn Gln Asp Asn Ala Lys Ala Leu
65      70      75      80
Gly Ile Lys Ile Ala Glu Leu Gly Lys Gly Leu Gln Val Asp Arg Val
      85      90      95

```

Val Phe Asp Arg Gly Ala His Lys Tyr His Gly Val Val Ala Met Val
 100 105 110
 Pro Asp Gly Ala Arg Glu Gly Gly Leu Gln Phe
 115 120

(2) INFORMATIONS POUR LA SEQ ID NO: 957:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 165 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924443..924937

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 957:

Xaa Thr Leu Ser Arg Asn Ser His Lys Glu Asp Gln Leu Glu Glu Lys
 1 5 10 15
 Val Leu Val Val Asn Arg Cys Cys Lys Val Val Lys Gly Gly Arg Lys
 20 25 30
 Phe Ser Phe Ser Ala Leu Ile Leu Val Gly Asp Arg Lys Gly Arg Leu
 35 40 45
 Gly Phe Gly Phe Ala Lys Ala Asn Glu Leu Thr Asp Ala Ile Arg Lys
 50 55 60
 Gly Gly Asp Ala Ala Arg Lys Asn Leu Val Ser Ile Asn Ser Leu Glu
 65 70 75 80
 Gly Gly Ser Ile Pro His Glu Val Leu Val Asn His Asp Gly Ala Glu
 85 90 95
 Leu Leu Leu Lys Pro Ala Lys Pro Gly Thr Gly Ile Val Ala Gly Ser
 100 105 110
 Arg Ile Arg Leu Ile Leu Glu Met Ala Gly Val Lys Asp Ile Val Ala
 115 120 125
 Lys Ser Leu Gly Ser Asn Asn Pro Met Asn Gln Val Lys Ala Ala Phe
 130 135 140
 Xaa Ala Leu Leu Thr Leu Ser Cys Lys Asp Asp Ile Met Lys Arg Arg
 145 150 155 160
 Ala Val Ile Asn Asp
 165

(2) INFORMATIONS POUR LA SEQ ID NO: 958:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 144 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 924933..925364

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 958:

Met Ile Lys Leu Glu Cys Leu Gln Asp Pro Ser Pro Arg Lys Arg Arg

```

1          5          10          15
Thr Lys Leu Leu Gly Arg Gly Pro Ser Thr Gly His Gly Lys Thr Ser
20          25          30
Gly Arg Gly His Lys Gly Asp Gly Ser Arg Ser Gly Tyr Lys Arg Arg
35          40          45
Phe Gly Tyr Glu Gly Gly Gly Val Pro Leu Tyr Arg Arg Val Pro Thr
50          55          60
Arg Gly Phe Ser His Lys Arg Phe Asp Lys Cys Val Glu Glu Ile Thr
65          70          75          80
Thr Gln Arg Leu Asn Glu Ile Phe Asp Asn Gly Ala Glu Val Ser Leu
85          90          95
Glu Ala Leu Lys Glu Arg Lys Val Ile His Arg Glu Thr Ser Arg Val
100          105          110
Lys Val Ile Leu Lys Gly Ala Leu Asp Lys Lys Leu Val Trp Lys Asp
115          120          125
Ala Ala Ile Val Leu Ser Glu Gly Val Lys Ser Leu Ile Glu Ala Val
130          135          140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 959:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 457 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 925390..926760

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 959:

```

Met Ala Thr Leu Arg Gln Val Phe Ser Ile Ser Glu Leu Arg Gln Lys
1          5          10          15
Ile Phe Phe Thr Phe Ser Leu Leu Ala Leu Cys Lys Ile Gly Val Phe
20          25          30
Ile Pro Val Pro Gly Ile Asn Gly Asp Arg Ala Val Ala Tyr Phe Asn
35          40          45
Gln Leu Leu Gly Ser Ser Gln Asn Leu Phe Gln Leu Ala Asp Ile Phe
50          55          60
Ser Gly Gly Ala Phe Ala Gln Met Thr Val Ile Ala Leu Gly Val Val
65          70          75          80
Pro Tyr Ile Ser Ala Ser Ile Ile Val Gln Leu Leu Val Val Phe Met
85          90          95
Pro Thr Leu Gln Arg Glu Met Arg Glu Ser Pro Asp Gln Gly Lys Arg
100          105          110
Lys Leu Gly Arg Met Thr Arg Leu Phe Thr Leu Val Leu Ala Cys Val
115          120          125
Gln Ser Leu Leu Phe Ala Lys Phe Ala Leu Arg Met Asn Leu Val Val
130          135          140
Pro Gly Ile Val Leu Pro Ala Met Leu Ser Leu Lys Leu Phe Gly Val
145          150          155          160
Pro Trp Val Phe Tyr Leu Thr Thr Val Val Val Met Thr Thr Gly Thr
165          170          175
Leu Leu Leu Met Trp Val Gly Glu Gln Ile Ser Asp Lys Gly Ile Gly
180          185          190
Asn Gly Ile Ser Leu Ile Ile Thr Leu Gly Ile Leu Ala Ser Phe Pro
195          200          205

```

```

Ser Val Leu Gly Ser Ile Phe Asn Lys Leu Asn Leu Gly Ser Gln Asp
 210                215                220
Pro Ser Glu Phe Gly Ile Val Ser Leu Leu Ile Leu Cys Ala Val Phe
225                230                235                240
Val Phe Val Leu Ile Ala Thr Val Leu Ile Ile Glu Gly Val Arg Lys
                245                250                255
Ile Pro Val Gln His Ala Arg Arg Ile Ile Gly Arg Arg Glu Val Val
                260                265                270
Gly Gly Gly Ser Tyr Leu Pro Leu Lys Val Asn Tyr Ala Gly Val Ile
                275                280                285
Pro Val Ile Phe Ala Ser Ser Leu Leu Met Phe Pro Ala Thr Ile Gly
                290                295                300
Gln Phe Leu Ser Ser Glu Ser Ser Trp Leu Lys Arg Ile Ala Thr Met
305                310                315                320
Leu Ser Pro Gly Ser Val Ala Tyr Ser Ile Phe Tyr Val Leu Leu Ile
                325                330                335
Ile Phe Phe Thr Tyr Phe Trp Thr Ala Thr Gln Phe Arg Pro Glu Gln
                340                345                350
Ile Ala Ser Glu Met Lys Lys Asn Gly Ala Phe Ile Pro Gly Ile Arg
                355                360                365
Gln Gly Lys Pro Thr Gln Thr Tyr Leu Glu Tyr Thr Met Asn Arg Val
                370                375                380
Thr Leu Leu Gly Ala Val Phe Leu Ala Val Val Ala Ile Leu Pro Ser
385                390                395                400
Val Leu Gly Arg Ile Leu Arg Val Asp Ala Asn Val Ser Tyr Phe Leu
                405                410                415
Gly Gly Thr Ala Met Leu Ile Val Val Gly Val Ile Leu Asp Thr Met
                420                425                430
Lys Gln Ile Asp Ala Phe Leu Leu Val Arg Arg Tyr Asp Gly Val Leu
                435                440                445
Lys Lys Asp Arg Pro Lys Gly Arg Pro
 450                455

```

(2) INFORMATIONS POUR LA SEQ ID NO: 960:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 926819..927184

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 960:

```

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 1                5                10                15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Leu Ser Lys Glu
                20                25                30
Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu
                35                40                45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln Ser Asp Tyr
 50                55                60
Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
 65                70                75                80
Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu

```

				85					90					95					
Pro	Val	Arg	Gly	Gln	Arg	Thr	Lys	Thr	Asn	Ser	Arg	Thr	Arg	Lys	Gly				
				100					105					110					
Lys	Arg	Lys	Thr	Ile	Ala	Gly	Lys	Lys	Lys										
				115					120										

(2) INFORMATIONS POUR LA SEQ ID NO: 961:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 132 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 927209..927604

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 961:

Leu	Val	Lys	Asn	Gln	Ala	Gln	Lys	Arg	Gly	Val	Lys	Arg	Lys	Gln	Val				
1				5					10					15					
Lys	Asn	Ile	Pro	Ser	Gly	Val	Val	His	Val	Lys	Ala	Thr	Phe	Asn	Asn				
			20					25					30						
Thr	Ile	Val	Thr	Ile	Thr	Asp	Pro	Ala	Gly	Asn	Val	Ile	Ser	Trp	Ala				
			35				40					45							
Ser	Ala	Gly	Lys	Val	Gly	Tyr	Ser	Gly	Ser	Arg	Lys	Ser	Ser	Ala	Phe				
	50					55				60									
Ala	Ala	Thr	Val	Ala	Ala	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Met	Ser	Ser				
65					70					75					80				
Gly	Leu	Lys	Glu	Val	Glu	Val	Gly	Leu	Lys	Gly	Thr	Gly	Ala	Gly	Arg				
				85					90						95				
Glu	Ser	Ala	Val	Arg	Ala	Leu	Ile	Ser	Ser	Gly	Leu	Ile	Val	Ser	Val				
			100					105					110						
Ile	Arg	Asp	Glu	Thr	Pro	Val	Pro	His	Asn	Gly	Cys	Arg	Pro	Arg	Lys				
		115					120					125							
Arg	Arg	Arg	Val																
			130																

(2) INFORMATIONS POUR LA SEQ ID NO: 962:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 176 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 927628..928155

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 962:

Met	Ser	Asp	Ser	Ser	His	Asn	Leu	Leu	Tyr	Asn	Lys	Phe	Glu	Leu	Pro				
1				5					10					15					
Glu	Ser	Val	Lys	Met	Ser	Pro	Val	Glu	Gly	Ala	Val	Gly	Gly	Ile	Asp				
			20					25					30						


```

Lys Val Ala Arg Phe Val Ala Asp Pro Leu Glu Lys Gly Met Gly His
   35               40               45
Thr Leu Gly Ser Ala Leu Arg Arg Ala Leu Leu Ile Gly Leu Glu Ala
   50               55               60
Pro Ala Ile Val Ser Phe Ser Met Thr Gly Val Leu His Glu Tyr Met
   65               70               75               80
Ala Val Glu Gly Ile Ile Glu Asp Val Thr Asn Ile Val Leu Asn Leu
               85               90               95
Lys Gly Ser Leu Leu Lys Lys Tyr Pro Leu Gln Asp Cys Glu Gly Gly
               100               105               110
Arg Cys Ser Gln Lys Leu Arg Ala Thr Ile Ser Val Asp Ala Ser Asp
               115               120               125
Leu Ala Ala Ala Gly Gly Gln Lys Glu Val Thr Leu Gly Asp Leu Leu
               130               135               140
Gln Glu Gly Thr Phe Glu Ala Val Asn Pro Glu His Val Ile Phe Thr
   145               150               155               160
Val Thr Arg Pro Met Gln Leu Glu Val Met Leu Pro Ser Cys Phe Trp
               165               170               175

```

(2) INFORMATIONS POUR LA SEQ ID NO: 963:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 220 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 928100..928759

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 963:

```

Phe Leu Arg Ser Arg Val Gln Cys Asn Leu Arg Leu Cys Cys Arg Val
1               5               10               15
Ala Phe Gly Arg Gly Tyr Ser Pro Ser Glu Arg Ile Val Leu Glu Glu
               20               25               30
Arg Gly Met Asn Glu Ile Val Leu Asp Ala Ala Phe Ser Pro Val Val
               35               40               45
Leu Val Asn Tyr Phe Val Glu Asp Thr Arg Val Gly Gln Asp Thr Asp
   50               55               60
Phe Asp Arg Leu Val Leu Gln Val Glu Thr Asp Gly Arg Val Ala Pro
   65               70               75               80
Lys Glu Ala Val Ala Phe Ala Thr Gln Ile Leu Ser Lys His Phe Ser
               85               90               95
Val Phe Glu Lys Met Asp Glu Lys Arg Ile Val Phe Glu Glu Ala Ile
               100               105               110
Ser Val Glu Lys Glu Asn Lys Asp Asp Ile Leu His Lys Leu Val Leu
               115               120               125
Gly Ile Asn Glu Ile Glu Leu Ser Val Arg Ser Thr Asn Cys Leu Ser
               130               135               140
Asn Ala Asn Ile Glu Thr Ile Gly Glu Leu Val Ile Met Pro Glu Pro
   145               150               155               160
Arg Leu Leu Gln Phe Arg Asn Phe Gly Lys Lys Ser Leu Cys Glu Ile
               165               170               175
Lys Asn Lys Leu Lys Glu Met Lys Leu Glu Leu Gly Met Asp Leu Ser
               180               185               190
Gln Phe Gly Val Gly Leu Asp Asn Val Lys Glu Lys Met Lys Trp Tyr

```


Asn Glu Ile Gly Tyr Ala Thr Arg Ile Val Asp Leu Leu Glu Tyr Val
325 330 335
Gln Glu Asn Ser Lys
340

(2) INFORMATION POUR LA SEQ ID NO: 965:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 145 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 930222..930656

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 965:

[illegible]

(2) INFORMATION POUR LA SEQ ID NO: 966:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 157 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 930608..931078

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 966:

Arg	Arg	Gly	Ser	Cys	Arg	Leu	Tyr	Cys	Cys	Thr	Pro	Ala	Ser	Thr	Pro
1				5					10					15	
Val	Ala	Pro	Met	Ser	Lys	Lys	Glu	Arg	Arg	Lys	Glu	Phe	Lys	Asn	Glu

(2) INFORMATION POUR LA SEQ ID NO: 967:

(A) LONGUEUR: 100 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: 931367..931666

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 967:

(2) INFORMATION POUR LA SEQ ID NO: 968:

(A) LONGUEUR: 137 acides aminés

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 931549..931959

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 968:

```

Tyr Cys Gly Met Gly Glu Tyr Leu Ser Asp Val Val Trp Cys Leu Phe
1      5      10      15
Lys Asn Glu Arg Ser Leu Leu Arg Asn Lys Lys Gln Met Gln Ile Gln
20      25      30
Ser Ala Ser Lys Glu Gln Ser Leu Ala Glu Trp Glu Gln Gln Val Cys
35      40      45
Glu Leu Lys Ser Gln Leu Ala Ser Gln Glu Asn Ala Asn Gln Gln Glu
50      55      60
Ile Ser Lys Leu Gln Ala Glu Asn His Trp Leu Gln Asn Arg Leu Ala
65      70      75      80
Glu Lys Leu Gln Gln Ala Arg His Gln Asn Asp Val Ile Asp Glu Leu
85      90      95
Lys Arg Asp Leu Val Glu Ser Val Gln Gln Met Glu Val Ser Glu Gly
100     105     110
Arg Arg Leu Cys Tyr Glu His Lys Ile Arg Val Leu Glu Glu Gln Ile
115     120     125
Asp Arg Phe Leu Ala Lys Glu Glu Val
130     135

```

(2) INFORMATIONS POUR LA SEQ ID NO: 969:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 170 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 932070..932579

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 969:

```

Met Ala Asp Leu Ile Met Gly Ile Asp Pro Gly Thr Leu Val Cys Gly
1      5      10      15
Tyr Ala Leu Ile Lys Val Glu Asn Arg Tyr His Ile His Pro His Ser
20      25      30
Phe Gly Lys Val Lys Leu Ser Gln Lys Leu Ala Leu Ala His Arg Tyr
35      40      45
Lys Gln Leu Phe Thr Glu Ile Ser Thr Ile Leu Gln Gln Glu Ser Pro
50      55      60
Lys Ala Val Val Leu Glu Thr Gln Tyr Val His Lys Asn Pro Gln Ser
65      70      75      80
Thr Ile Lys Leu Gly Met Ala Arg Gly Val Leu Leu Leu Ala Ala Ser
85      90      95
Leu Gln Asp Val Pro Val Phe Glu Tyr Ala Pro Asn Thr Ala Lys Lys
100     105     110
Ala Ala Val Gly Lys Gly Asn Ala Ser Lys Lys Gln Val Gln Leu Met
115     120     125
Val Ser Lys Leu Leu Arg Val Pro Asp Leu Leu Ala Glu Asp Asn Glu
130     135     140
Asp Ile Ala Asp Ala Phe Ala Leu Ala Met Cys His Ala His Leu Ala
145     150     155     160
Pro Tyr Gln Asp Leu Lys Lys Thr Leu Val

```

165

170

(2) INFORMATIONS POUR LA SEQ ID NO: 970:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 200 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 932602..933201

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 970:

Met	Tyr	Glu	Tyr	Ile	Lys	Gly	Thr	Leu	Thr	His	Ile	Asp	Gly	Ser	Tyr
1				5				10						15	
Val	Val	Ile	Glu	Ser	Phe	Gly	Ile	Gly	Tyr	Ala	Ile	Met	Leu	Ser	Glu
		20						25					30		
Arg	Phe	Leu	Val	Asp	Leu	Arg	Ala	Phe	Met	His	Gln	Glu	Val	Leu	Ile
		35					40					45			
Tyr	Val	His	Ser	Val	Ile	Arg	Glu	Thr	Glu	His	Val	Leu	Tyr	Gly	Phe
	50					55				60					
Ser	Ser	Arg	Ala	Glu	Arg	Glu	Cys	Phe	Arg	Leu	Leu	Ile	Ser	Phe	Ser
65				70					75					80	
Gly	Ile	Gly	Pro	Lys	Thr	Gly	Leu	Ser	Ile	Leu	Asn	Met	Phe	Pro	Leu
				85				90					95		
Gln	Glu	Leu	Cys	Ser	Ile	Ala	Arg	Leu	Glu	Asn	Val	Lys	Ala	Ile	Ala
		100						105					110		
Ser	Val	Pro	Gly	Ile	Gly	Lys	Lys	Thr	Ala	Glu	Lys	Leu	Met	Val	Asp
		115					120					125			
Leu	Lys	Gln	Lys	Leu	Pro	Thr	Leu	Met	Pro	Leu	Tyr	Leu	Glu	Glu	Pro
	130					135					140				
Val	Val	Pro	Ser	Ser	Thr	Ala	Asn	Ser	Ser	Phe	Lys	Glu	Gly	Ile	Gly
145					150					155				160	
Ala	Leu	Met	Asn	Leu	Gly	Phe	Ser	Arg	Leu	Ala	Ala	Asp	Arg	Met	Met
			165					170					175		
Thr	Glu	Ala	Val	Lys	Glu	Leu	Ser	Glu	Glu	Ala	Ser	Val	Ala	Glu	Leu
		180					185					190			
Leu	Pro	Ile	Ala	Leu	Arg	Lys	Ser								
		195					200								

(2) INFORMATIONS POUR LA SEQ ID NO: 971:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 86 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 933364..933621

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 971:

```

Met Glu Gln Thr Leu Ser Ile Ile Lys Pro Asp Ser Val Gly Lys Ala
1           5           10           15
His Ile Gly Glu Ile Ile Ala Ile Phe Glu Lys Ser Gly Leu Arg Ile
20           25           30
Ala Ala Met Lys Met Val His Leu Ser Val Lys Glu Ala Glu Gly Phe
35           40           45
Tyr Val Val His Lys Glu Arg Pro Phe Phe Gln Glu Leu Val Asp Phe
50           55           60
Met Ile Ser Gly Pro Val Val Val Met Val Leu Gln Gly Glu Asn Leu
65           70           75           80
Ser Pro Val Thr Glu Ser
85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 972:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 933522..933785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 972:

```

Arg Glu Thr Phe Phe Pro Arg Thr Gly Arg Leu Tyr Asp Leu Trp Ser
1           5           10           15
Cys Cys Ser Asn Gly Thr Ala Arg Gly Lys Pro Val Ala Arg Asn Arg
20           25           30
Glu Leu Met Gly Ala Thr Asn Pro Lys Glu Ala Ala Glu Gly Ser Ile
35           40           45
Arg Ala Leu Phe Gly Glu Ser Ile Gly Val Asn Ala Val His Gly Ser
50           55           60
Asp Ser Leu Glu Asn Ala Ala Ile Glu Val Ser Tyr Phe Phe Ala Lys
65           70           75           80
Thr Glu Val Val Asn Ser Val Ala
85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 973:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 233 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(933848..934546)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 973:

```

Met Leu Ile Asn Cys Val Phe Val His Cys Glu Gly Leu Pro Ile Phe
1           5           10           15
Lys Gln Leu Gln Leu Glu Glu Ala Leu Leu Arg Thr Ser Ser Gln Asn

```

```

                20                25                30
Phe Cys Leu Val Asn Thr His Leu Pro Glu Ala Val Val Leu Gly Ile
                35                40                45
Ser Arg Lys Pro Glu Arg Asp Leu His Val Glu His Leu Lys Glu Asp
                50                55                60
Gly Ile Pro Ile Ile Arg Arg Tyr Ser Gly Gly Gly Thr Val Phe Leu
65                70                75                80
Asp Ala Asp Ser Leu Met Val Ser Trp Ile Ile Asn Ser Pro Thr Pro
                85                90                95
Ser Pro Ser Ser Lys Asp Leu Leu Gln Trp Thr Gln Asp Ile Tyr Ala
                100                105                110
Pro Ile Phe Pro Thr Gly Phe Lys Ile Thr Glu Asn Asp Tyr Thr Phe
                115                120                125
Leu Asp Lys Lys Ile Gly Gly Asn Ala Gln Tyr Ile Gln Lys Tyr Arg
130                135                140
Trp Val His His Thr Thr Phe Phe Trp Asn Met Asn Pro Lys Lys Leu
145                150                155                160
Ala Arg Tyr Leu Pro Thr Pro Glu Ile Gln Pro Ser Tyr Arg Gln Asn
                165                170                175
Arg Ser His Asp Glu Phe Leu Thr Thr Ile Tyr Glu Leu Phe Asp Ser
                180                185                190
Arg Glu Asp Phe Leu Ser Gln Leu Lys Gln Ser Ala Ala Ser Lys Met
                195                200                205
Val Trp Glu Gln Gly Ser Ile Gln Thr Leu Thr Pro Met Leu Ser Leu
210                215                220
Pro His Arg Lys Ala Thr Gln Ile Leu
225                230

```

(2) INFORMATIONS POUR LA SEQ ID NO: 974:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 610 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(934539..936368)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 974:

```

Met Trp Thr Phe Pro Val Asp Tyr Asp Val Ile Val Ile Gly Ala Gly
1                5                10                15
His Ala Gly Cys Glu Ala Ala Tyr Cys Ala Ala Lys Met Gly Ala Ser
                20                25                30
Val Leu Leu Leu Thr Ser Asn Leu Asp Thr Ile Ala Lys Leu Ser Cys
35                40                45
Asn Pro Ala Val Gly Gly Ile Gly Lys Gly His Ile Val Arg Glu Ile
50                55                60
Asp Ala Leu Gly Gly Ile Met Ala Glu Ile Thr Asp Leu Ser Gly Ile
65                70                75                80
Gln Phe Arg Ile Leu Asn Gln Thr Lys Gly Pro Ala Val Arg Ala Pro
                85                90                95
Arg Ala Gln Val Asp Lys Gln Leu Tyr His Ile His Met Lys Arg Leu
                100                105                110
Leu Glu Gln Val Pro Gly Leu His Ile Met Gln Gly Thr Ala Glu Ala
115                120                125

```


Leu	Leu	Asp	Asn	Gly	Glu	Lys	Val	Leu	Gly	Val	Ser	Thr	Lys	Glu	Gly
130						135					140				
Trp	Ala	Tyr	Leu	Gly	Lys	Thr	Val	Val	Leu	Ser	Ser	Gly	Thr	Phe	Met
145					150					155					160
Arg	Gly	Leu	Ile	His	Ile	Gly	Thr	Gln	Asn	Phe	Ser	Gly	Gly	Arg	Leu
				165					170					175	
Gly	Asp	Ala	Ala	Ser	Leu	Gly	Leu	Ser	Glu	Asp	Leu	Lys	Arg	Leu	Gly
			180					185					190		
Phe	Pro	Leu	Gly	Arg	Leu	Lys	Thr	Gly	Thr	Pro	Ala	Arg	Leu	Leu	Ala
		195					200					205			
Ser	Ser	Ile	Asp	Phe	Ser	Val	Met	Glu	Glu	Gln	Pro	Gly	Asp	His	Asn
	210					215					220				
Val	Cys	Phe	Val	His	Arg	Asn	Glu	Met	Phe	Val	Pro	Thr	Leu	Pro	Gln
225					230					235					240
Val	Ser	Cys	His	Ile	Thr	His	Thr	Thr	Asp	Gln	Thr	Lys	Asp	Leu	Ile
				245					250					255	
Thr	Lys	Asn	Leu	His	Arg	Ser	Ala	Leu	Tyr	Gly	Gly	Arg	Ile	Glu	Gly
			260					265					270		
Val	Gly	Pro	Arg	Tyr	Cys	Pro	Ser	Ile	Glu	Asp	Lys	Ile	Val	Lys	Phe
		275					280					285			
Ala	Asp	Lys	Asp	Arg	His	His	Ile	Phe	Ile	Glu	Pro	Glu	Gly	Leu	Asn
	290					295					300				
Thr	Gln	Glu	Val	Tyr	Val	Asn	Gly	Leu	Ser	Thr	Ser	Met	Pro	Phe	Asp
305					310					315					320
Val	Gln	Tyr	Asp	Ile	Ile	Arg	Ser	Val	Ser	Gly	Leu	Glu	Asn	Ala	Ile
				325					330					335	
Ile	Thr	Arg	Pro	Ala	Tyr	Ala	Ile	Glu	Tyr	Asp	Tyr	Val	His	Gly	Asn
			340					345					350		
Val	Ile	Phe	Pro	Ser	Leu	Glu	Ser	Lys	Leu	Ile	Glu	Gly	Leu	Phe	Leu
		355					360					365			
Cys	Gly	Gln	Ile	Asn	Gly	Thr	Thr	Gly	Tyr	Glu	Glu	Ala	Ala	Ala	Gln
	370					375					380				
Gly	Leu	Ile	Ala	Gly	Val	Asn	Ala	Val	Asn	Lys	Val	Leu	Arg	Arg	Pro
385					390					395					400
Pro	Phe	Val	Pro	Ser	Arg	Gln	Glu	Ser	Tyr	Ile	Gly	Val	Met	Leu	Asp
				405					410					415	
Asp	Leu	Thr	Thr	Gln	Val	Leu	Asp	Glu	Pro	Tyr	Arg	Met	Phe	Thr	Ser
			420					425					430		
Arg	Ala	Glu	His	Arg	Leu	Leu	Leu	Arg	Gln	Asp	Asn	Ala	Gly	Met	Arg
		435					440					445			
Leu	Ser	His	Tyr	Gly	His	Ser	Leu	Gly	Leu	Leu	Ser	Ser	Glu	Arg	Tyr
	450					455					460				
Ala	Met	Phe	Gln	Glu	Gln	Lys	Ala	Cys	Ile	Glu	Gln	Glu	Lys	Glu	Arg
465					470					475					480
Leu	Ser	Lys	Thr	Phe	Arg	Lys	Tyr	Gly	Asp	Thr	Val	Val	Pro	Leu	Thr
				485					490					495	
Arg	Val	Leu	Cys	Arg	Pro	Glu	Val	Ser	Tyr	Gln	Gln	Leu	Leu	Thr	Glu
			500					505					510		
Phe	Pro	Ala	Asp	Val	Arg	Asp	Leu	Gly	Pro	Ile	Val	Gly	Ala	Ser	Leu
		515					520					525			
Glu	Met	Glu	Ile	Lys	Tyr	Ser	Gly	Tyr	Ile	Ser	Arg	Gln	Gln	Thr	Leu
	530					535					540				
Ile	Arg	Ser	Met	Glu	Arg	Ser	Glu	Asn	Ile	Ser	Ile	Pro	Glu	Asp	Ile
545					550					555					560
Asp	Tyr	His	Ser	Ile	Ser	Ala	Leu	Ser	Leu	Glu	Ala	Arg	Glu	Lys	Leu
				565					570					575	
Ser	Lys	Phe	Thr	Pro	Arg	Thr	Ile	Gly	Ser	Ala	Ala	Arg	Ile	Ser	Gly
			580					585					590		
Ile	Ser	Val	Ala	Asp	Ile	Gln	Val	Leu	Met	Val	Ser	Leu	Lys	Lys	Asp

Ala His
610

600

605

(2) INFORMATIONS POUR LA SEQ ID NO: 975:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 466 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(936666..938063)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 975:

Lys	Pro	Gln	Pro	Thr	Gln	Leu	Leu	Ser	Leu	Pro	Asn	Ser	Lys	Glu	Ser	1	5	10	15
Glu	Met	Ile	Val	Leu	Gly	Cys	Met	Leu	Thr	Ser	Val	Asn	His	Leu	Asn	20	25	30	
Leu	Ala	Ala	Asn	Leu	Leu	Gln	Glu	Asp	Asp	Phe	Tyr	Phe	Leu	Glu	His	35	40	45	
Arg	Ile	Ile	Phe	Arg	Val	Leu	Gln	Asp	Ala	Phe	Lys	Ser	Asp	Arg	Pro	50	55	60	
Met	Asp	Pro	His	Leu	Thr	Gly	Glu	Glu	Leu	Lys	Arg	Arg	Asp	Gln	Leu	65	70	75	80
Asn	Ile	Ile	Gly	Gly	Pro	Ser	Tyr	Leu	Ile	Thr	Leu	Ser	Glu	Phe	Ala	85	90	95	
Gly	Thr	Ser	Ala	Tyr	Ile	Glu	Glu	Tyr	Ala	Glu	Ile	Ile	Arg	Ser	Lys	100	105	110	
Ser	Ile	Leu	Arg	Lys	Met	Ile	Gln	Ala	Ala	Lys	Asp	Ile	Glu	Lys	Lys	115	120	125	
Ala	Ala	Glu	Glu	Pro	Arg	Asp	Val	Thr	Thr	Ala	Leu	Asp	Asp	Ala	Gln	130	135	140	
Asn	Leu	Leu	Phe	Arg	Ile	Ser	Gln	Thr	Thr	Asn	Leu	Ala	Pro	Tyr	Val	145	150	155	160
Leu	Val	Ala	Asp	Lys	Leu	Lys	Gly	Val	Ala	Ser	Ser	Lys	Asp	Lys	Ser	165	170	175	
Phe	Leu	Leu	Ala	Leu	Gln	Glu	Arg	Gln	Glu	Ala	Phe	Gln	Ala	Ser	Ala	180	185	190	
His	Asp	Ser	Ser	Ser	Pro	Met	Leu	Ser	Gly	Phe	Pro	Thr	His	Phe	Leu	195	200	205	
Asp	Leu	Asp	Arg	Met	Ile	Ser	Gly	Phe	Ser	Pro	Ser	Asn	Leu	Ile	Ile	210	215	220	
Leu	Ala	Ala	Arg	Pro	Ala	Met	Gly	Lys	Thr	Ala	Leu	Ala	Leu	Asn	Ile	225	230	235	240
Val	Glu	Asn	Phe	Cys	Phe	Asp	Ser	Arg	Leu	Pro	Val	Gly	Ile	Phe	Ser	245	250	255	
Leu	Glu	Met	Thr	Val	Asp	Gln	Leu	Ile	His	Arg	Ile	Ile	Cys	Ser	Arg	260	265	270	
Ser	Glu	Val	Glu	Ala	Lys	Lys	Ile	Ser	Val	Gly	Asp	Ile	Ser	Gly	Arg	275	280	285	
Asp	Phe	Gln	Arg	Val	Val	Ser	Val	Val	Arg	Glu	Met	Glu	Glu	His	Thr	290	295	300	
Leu	Leu	Ile	Asp	Asp	Tyr	Pro	Gly	Leu	Lys	Ile	Thr	Asp	Leu	Arg	Ala	305	310	315	320

```

Arg Ala Arg Arg Met Lys Glu Ser Tyr Asp Ile Gln Phe Leu Val Ile
      325                      330                      335
Asp Tyr Leu Gln Leu Ile Ser Ser Ser Gly Asn Leu Arg Asn Ser Asp
      340                      345                      350
Ser Arg Asn Gln Glu Ile Ser Xaa Ile Ser Arg Met Leu Xaa Asn Leu
      355                      360                      365
Ala Arg Glu Leu Asn Ile Pro Ile Leu Cys Xaa Ser Gln Leu Ser Arg
      370                      375                      380
Glu Val Glu Asp Arg Ala Asn His Arg Pro Leu Met Ser Asp Leu Arg
385                      390                      395                      400
Glu Ser Gly Ser Ile Glu Gln Asp Ala Asp Gln Ile Met Phe Leu Leu
      405                      410                      415
Arg Arg Glu Tyr Tyr Asp Pro Asn Asp Lys Pro Gly Thr Ala Glu Leu
      420                      425                      430
Ile Val Ala Lys Asn Arg His Gly Ser Ile Gly Ser Ile Gln Leu Val
      435                      440                      445
Phe Glu Lys Asp Phe Ala Arg Phe Arg Asn Tyr Ala Gly Cys Glu Phe
450                      455                      460
Pro Gly
465

```

(2) INFORMATIONS POUR LA SEQ ID NO: 976:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 187 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 938538..939098

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 976:

```

Tyr Val Ser Leu Arg Trp Arg Leu Arg Ile Phe Lys Thr Ser Phe Arg
1      5      10      15
Ile Asn Val Met Arg Gln Phe Cys Asn Leu Leu Ser Leu Ser Arg Val
      20      25      30
Trp Leu Ala Leu Leu Phe Cys Gln Glu Arg Ile Ile Thr Arg Leu Leu
      35      40      45
Val Ile Phe Ala Ala Met Val Ser Asp Val Leu Asp Gly Tyr Leu Ala
50      55      60
Arg Arg Tyr Asn Ala Thr Ser Arg Leu Gly Ser Ile Leu Asp Pro Ala
65      70      75      80
Thr Asp Lys Ile Phe Phe Leu Ile Cys Val Gly Val Leu Phe Trp Glu
      85      90      95
Asn Ser Leu Gly Leu Thr His Leu Ala Leu Ile Phe Ser Arg Asp Ile
      100     105     110
Phe Leu Val Phe Phe Gly Phe Tyr Leu Ser Trp Val Arg Gly Trp Lys
      115     120     125
Gly Tyr Asp Tyr Arg Ala Leu Ser Phe Gly Lys Phe Phe Thr Val Val
130     135     140
Gln Phe Phe Ile Leu Phe Gly Val Thr Ile Gly Met Glu Ile Pro Val
145     150     155     160
Leu Trp Leu Ala Pro Leu Val Ile Leu Gly Ala Leu Tyr Phe Leu Glu
      165     170     175
Arg Val Leu Asp Tyr Arg Arg His Cys Leu Glu

```

180

185

(2) INFORMATIONS POUR LA SEQ ID NO: 977:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 535 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 939329..940933

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 977:

Asn Pro Phe Arg Ser Ser Gly Asp Xaa Phe Phe Pro Ile Tyr Arg Ser
 1 5 10 15
 Glu Phe Ser Lys Phe Ile Pro Leu Phe Phe Leu Ala Phe Phe Val Gly
 20 25 30
 Val Asn Tyr Ala Leu Leu Lys Thr Thr Lys Asp Ser Leu Val Leu Val
 35 40 45
 Gly Ser Arg Ala Gly Ala Glu Val Ile Pro Phe Leu Lys Val Trp Gly
 50 55 60
 Ile Val Pro Gly Ala Val Ile Val Thr Met Ile Tyr Gly Trp Met Ser
 65 70 75 80
 Arg Arg Tyr Ser Arg Gly Thr Val Phe Ile Ser Leu Val Gly Gly Phe
 85 90 95
 Leu Gly Phe Phe Ala Leu Phe Ala Thr Val Ile Tyr Pro Ile Gly Asp
 100 105 110
 Ala Leu His Leu Asn Lys Leu Ala Ala Lys Leu Gln Ser Ile Leu Pro
 115 120 125
 Pro Gly Gly Arg Gly Phe Val Val Met Val Gln Tyr Trp Ser Tyr Ser
 130 135 140
 Leu Tyr Tyr Val Met Ser Glu Leu Trp Ser Ser Val Val Leu Ser Thr
 145 150 155 160
 Leu Phe Trp Gly Val Ala Asn His Ile Thr Ser Val Arg Glu Ala Gly
 165 170 175
 Arg Phe Tyr Ala Leu Ile Asn Thr Gly Leu Asn Leu Ser Ser Val Phe
 180 185 190
 Ala Gly Glu Val Ser Leu Trp Leu Gly Arg Ser Pro Val Ile Ala Phe
 195 200 205
 Pro Met Ala Val Asp Pro Trp His Glu Met Leu Leu Asn Ile Thr Leu
 210 215 220
 Leu Ile Val Leu Ala Gly Gly Val Ile Leu Tyr Leu Tyr Gln Lys Leu
 225 230 235 240
 Asp Arg Leu Met Asp Glu Thr Ser Met Leu Glu Glu Gly Leu Ala Ala
 245 250 255
 Glu Met Ser Val Ala Gln Leu Lys Lys Glu Lys Lys Arg Ser Lys Ala
 260 265 270
 Lys Ala Lys Ser Leu Phe Ala Leu Leu Arg Ser Arg Tyr Leu Leu
 275 280 285
 Gly Ile Ala Val Val Val Leu Ser Tyr Asn Leu Val Ile His Leu Phe
 290 295 300
 Glu Val Val Trp Lys Asp Gln Val Cys Arg Ile Tyr Ala Ser Arg Val
 305 310 315 320
 Glu Phe Asn Ser Tyr Met Ser Arg Ile Thr Leu Thr Gly Ile Val
 325 330 335

```

Ser Ala Leu Ala Gly Ile Phe Ala Ala Gly Gln Thr Ile Arg Arg Trp
      340                      345                      350
Gly Trp Thr Val Gly Ala Leu Val Pro Pro Leu Thr Ile Leu Ile Thr
      355                      360                      365
Gly Ala Leu Phe Phe Gly Ala Ile Tyr Ala Val Lys Gly Asp Ala Met
      370                      375                      380
Ile Phe Gly Gly Ile Leu Gly Ile Ser Pro Leu Val Leu Thr Ala Trp
385      390                      395                      400
Leu Gly Gly Val Gln Asn Val Phe Ser Arg Ala Ile Lys Phe Thr Tyr
      405                      410                      415
Phe Asp Gln Thr Lys Glu Met Ala Phe Ile Pro Leu Glu Asp Asp Glu
      420                      425                      430
Lys Asn Tyr Gly Lys Ala Ala Ile Asp Gly Val Ile Ser Arg Val Gly
      435                      440                      445
Lys Ser Gly Gly Ser Leu Val Tyr Gln Gly Leu Leu Ile Ile Phe Ser
      450                      455                      460
Ser Val Ala Ala Ser Leu Asn Ala Ile Thr Ile Val Leu Leu Leu Ala
465      470                      475                      480
Leu Gly Ser Trp Ile Phe Val Ile Ala Trp Leu Gly Arg Glu Tyr Thr
      485                      490                      495
Ala Lys Thr Glu Thr Leu Val Arg Val Asn Ala Ser Glu Glu Asp Val
      500                      505                      510
Leu Gln Glu Glu Arg Glu Ala Ser Ser Leu Val Asp Ala Glu Ser Arg
      515                      520                      525
Glu Glu Pro Ala Thr Thr Leu
      530                      535

```

(2) INFORMATIONS POUR LA SEQ ID NO: 978:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 331 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 941076..942068

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 978:

```

Met Lys Asn Phe Phe Arg Phe Leu Leu Lys Gly Phe Leu Ser Ala Cys
1      5      10      15
Gly Leu Phe Leu Gly Val Ile Gly Ala Ala Gly Phe Ile Phe Val Leu
      20      25      30
Ser Ala Ser Val Leu Gly Ala Gly Asp Gly Val Leu Phe Val Asn Phe
      35      40      45
Pro Asn Ala Gln Gly Val Val Gln Glu Leu Gly Lys Thr Ala Pro Ile
      50      55      60
Ile Ala Val Ile Asp Ile Asn Asp Ala Ile Ile Ala Ser Ser Gly Ala
65      70      75      80
Ala Lys Arg Leu Gln Ser Ala Leu Gln Pro Leu Asn Glu Ala Pro Tyr
      85      90      95
Lys Gly Arg Val Lys Gly Ile Leu Val Lys Ile Asp Cys Pro Gly Gly
      100     105     110
Glu Val Phe Glu Ile Asp Arg Met Cys Ala Thr Leu Ser Phe Trp Lys
      115     120     125
Lys Gln Trp Gly Ile Pro Val His Val Phe Val Ser Gly Leu Cys Ala

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      130      135      140
Ser Gly Gly Tyr Tyr Val Ala Cys Ile Ala Asp Lys Ile Gly Thr Thr
145      150      155      160
Ser Ser Ser Leu Ile Gly Ser Ile Gly Val Arg Ser Gly Pro Tyr Phe
      165      170      175
Asn Val Lys Glu Gly Leu Gln Arg His Gly Val Glu Thr Ala Ile Leu
      180      185      190
Thr Ala Gly Asp Asp Lys Ala Pro Leu Asn Pro Phe Ser Ser Trp Thr
      195      200      205
Glu Glu Glu Tyr Ala Glu Arg Gln Gly Ile Val Asp Ala Phe Tyr Glu
      210      215      220
Gln Phe Val Asp His Val Val Lys Tyr Arg Ser Lys Leu Ser Lys Glu
225      230      235      240
Lys Leu Thr Lys Val Leu Gly Ala Arg Val Phe Ile Ala Lys Gln Ala
      245      250      255
Leu Glu Glu Gly Leu Val Asp Ala Ile Asn Gln Thr Gln Glu Gln Ala
      260      265      270
Leu Glu Glu Leu Ala Glu Ala Cys Gly Ile Lys Asp Asn Tyr Arg Val
      275      280      285
Ile Gly Leu Gly Ser Gly His Phe Leu Lys Arg Phe Ser Ser Tyr Leu
      290      295      300
Ser Asn Ser Pro Leu Val Thr Gly Lys Leu Gln Val Thr Ala Leu Pro
305      310      315      320
Asp Gln Gln Gln Lys Ser Leu Trp Tyr Met Gly
      325      330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 979:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 866 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 942088..944685

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 979:

```

Met Lys Lys Leu Phe Val Leu Asp Val Ser Gly Phe Val Phe Arg Ala
1      5      10      15
Tyr Phe Ala Leu Pro Glu Met Arg Gly Pro Asn Gly Glu Ser Thr Gln
      20      25      30
Xaa Val Phe Gly Phe Ile Arg Ser Leu Asp Lys Leu Ile Lys Asp Leu
      35      40      45
Ser Pro Glu Tyr Val Val Ala Val Phe Asp Gly Pro Asn Asn Lys Gln
      50      55      60
Ser Arg Gln Glu Leu Tyr Ala Asp Tyr Lys Ser Asn Arg Asp Arg Gln
65      70      75      80
Leu Glu Asp Leu Pro Glu Gln Ile Arg Leu Val Lys Gln Tyr Cys Glu
      85      90      95
Leu Leu Gly Ile Ser Cys Leu Glu Glu Lys Gly Val Glu Ala Asp Asp
      100      105      110
Val Ile Ala Ser Ile Thr Lys Lys Ala Val Ala Asp Gly Phe Glu Val
      115      120      125
Cys Ile Cys Thr Ala Asp Lys Asp Leu Leu Gln Leu Val Ser Ser Arg
130      135      140

```

Val	Ser	Val	Phe	Asn	Pro	Trp	Lys	Glu	Gln	Glu	Ile	Gln	Tyr	Asn	Glu
145					150					155					160
Val	Leu	Leu	Gln	Phe	Gly	Val	Pro	Pro	Glu	Gln	Ile	Ala	Asp	Tyr	Leu
				165					170						175
Ala	Leu	Val	Gly	Asp	Ser	Ser	Asp	Asn	Ile	Pro	Gly	Val	Ser	Gly	Cys
			180					185					190		
Gly	Pro	Lys	Lys	Ala	Gln	Ala	Leu	Lys	Glu	Phe	Gln	Ser	Val	Glu	
		195					200				205				
Glu	Leu	Val	Ala	Asn	Thr	Glu	Arg	Leu	Ser	Gly	Lys	Thr	Lys	Gln	Met
	210					215					220				
Ile	Glu	Asp	Gln	Lys	Glu	Thr	Leu	Leu	Leu	Ser	Lys	Arg	Leu	Ala	Thr
225					230					235					240
Leu	His	Met	Asp	Leu	Ala	Phe	Pro	Leu	Thr	Thr	Glu	Glu	Phe	Ala	Phe
				245					250					255	
Ser	Pro	Gln	Ala	Ile	Asp	Ser	Ala	Gln	Leu	Asn	Thr	Phe	Tyr	Leu	Gln
			260					265					270		
His	Gly	Phe	Lys	Ala	Leu	Val	Lys	His	Ser	Glu	Thr	Ala	Thr	Ser	Ser
		275					280					285			
Ile	Ala	Val	Gln	Thr	Val	Thr	Asp	Pro	Val	Thr	Leu	Lys	Thr	Val	Leu
	290					295					300				
Glu	Gln	Leu	Lys	Gly	Gly	Glu	Val	Gly	Tyr	Cys	Ala	Ala	Tyr	Thr	Gly
305					310					315					320
Glu	His	Leu	Pro	Ser	Leu	Gln	Leu	His	Gly	Val	Ala	Leu	Ala	Gly	Ala
				325					330					335	
Asn	Gln	Val	Phe	Tyr	Ile	Glu	Val	Ser	Gly	Val	Gln	Glu	Ile	Ala	Leu
			340					345					350		
Leu	Lys	Asp	Phe	Phe	Ala	Asp	Lys	Ala	Thr	Gln	Phe	Phe	Gly	Tyr	Arg
		355					360					365			
Ser	Lys	Arg	Asp	Asn	His	Ala	Leu	Arg	Asn	Ser	Gly	Ile	Asp	Val	His
	370					375					380				
Val	Thr	Ala	Asp	Leu	Val	Leu	Ala	Glu	His	Leu	Val	Ser	Gly	Gly	Ala
385					390					395					400
Lys	Ile	Ser	Phe	Gln	Thr	Leu	Leu	Met	Glu	Ser	Gly	His	Ile	Gln	Glu
				405					410					415	
Ala	Val	Phe	Phe	Ser	Lys	Glu	Trp	Gly	Ala	Gly	Ser	Leu	Pro	Val	Gln
			420					425					430		
Ser	Leu	Pro	Arg	Asp	Pro	Ala	Gln	Tyr	Phe	Gly	Met	Phe	Ala	Ser	Lys
		435				440						445			
Leu	Leu	Ala	Ile	Lys	Asn	Tyr	Leu	Phe	Val	Lys	Leu	Glu	Glu	Lys	Gly
	450					455					460				
Leu	Lys	Asp	Ile	Phe	Glu	Thr	Val	Glu	Gln	Pro	Leu	Glu	Ala	Val	Leu
465					470					475					480
Phe	Ala	Met	Glu	Cys	Val	Gly	Met	Pro	Leu	Asp	Ser	Gln	Gly	Leu	Ala
				485					490					495	
Val	Leu	Asp	Arg	Asp	Leu	Thr	Lys	Glu	Leu	Glu	Glu	Cys	Ser	Gln	Glu
			500					505					510		
Ile	Tyr	Asp	Leu	Thr	Gly	Cys	Glu	Phe	Asn	Ile	Lys	Ser	Pro	Lys	Gln
	515						520					525			
Leu	Ser	Asp	Ile	Leu	Tyr	Gln	Arg	Leu	Gly	Ile	Glu	Pro	Val	Asp	Lys
	530					535					540				
Ala	Lys	Ser	Thr	Lys	Ala	Glu	Val	Leu	Glu	Ala	Leu	Glu	Asp	Arg	His
545					550					555					560
Glu	Ile	Ile	Pro	Lys	Ile	Leu	Met	Phe	Arg	Ala	Thr	Glu	Lys	Met	Leu
				565					570					575	
Ser	Thr	Tyr	Val	Arg	Ala	Leu	Pro	Lys	Gln	Ile	Asn	Ala	Gly	Thr	Gln
			580					585					590		
Arg	Ile	His	Pro	Thr	Phe	Asn	Gln	Val	Gly	Thr	Val	Thr	Gly	Arg	Leu
		595					600						605		
Ser	Cys	Gln	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Ser	Glu	Arg

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        610                      615                      620
Gly Arg Ser Leu Arg Glu Ala Phe Arg Val Lys Lys Asp Asn Asp Tyr
625                      630                      635                      640
Phe Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Phe Leu Ala His
        645                      650                      655
Leu Ser Gln Asp Glu Thr Leu Lys Arg Ala Phe Asn Ser Gly Glu Asp
        660                      665                      670
Ile His Ala Phe Thr Ala Ser Gln Val Phe Asn Val Pro Leu Glu Gln
        675                      680                      685
Val Thr Lys Gln Glu Arg Tyr Gln Ala Lys Ala Val Asn Phe Gly Leu
        690                      695                      700
Val Tyr Gly Gln Gln Ala Tyr Gly Leu Ser Lys Ile Leu Lys Ile Ser
705                      710                      715                      720
Val Ser Glu Ala Gln Gly Leu Met Asp Ala Tyr Phe Ala Arg Tyr Pro
        725                      730                      735
Leu Ala Ala Glu Phe Ile Thr Gln Thr Ile Glu Gln Ala Ser Lys Asn
        740                      745                      750
Gln Lys Val Thr Thr Met Leu Gly Arg Glu Arg Ile Leu Ser Asp Trp
        755                      760                      765
Glu Ser Ser Pro Gly Ala Arg Ala Ala Ser Gly Arg Leu Ala Val Asn
        770                      775                      780
Thr Arg Ile Gln Gly Ser Ala Ala Glu Leu Ile Lys Leu Ala Met Leu
785                      790                      795                      800
Asn Ile Ser Asp Glu Met Arg Ser Arg Gly Leu Lys Ser Arg Leu Leu
        805                      810                      815
Leu Gln Ile His Asp Glu Leu Leu Phe Glu Val Pro Ala Glu Glu Leu
        820                      825                      830
Glu Glu Met Arg Ser Leu Val Gln Glu Lys Met Glu Ser Ala Met Glu
        835                      840                      845
Leu Ser Val Pro Leu Val Val Asn Val Leu Ile Gly Lys Asn Trp Ala
        850                      855                      860
Glu Cys
865

```

(2) INFORMATIONS POUR LA SEQ ID NO: 980:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 218 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 944634..945287

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 980:

```

Val Cys Ser Phe Ser Cys Glu Cys Leu Asn Trp Lys Lys Leu Gly Gly
1          5          10          15
Met Leu Asp Leu Leu Lys Ile Ser Val Thr Gly Asp Pro Ser Ser Gly
        20          25          30
Lys Thr Glu Ala Cys Gln Val Phe Glu Asp Leu Gly Ala Tyr Val Ile
        35          40          45
Ser Ala Asp Lys Val Ser His Ser Phe Leu Val Pro Tyr Thr Ser Val
        50          55          60
Gly Gln Arg Ile Ile Asp Leu Leu Gly Pro Glu Ile Ile Ile Glu Asn
65          70          75          80

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Thr Leu Ser Arg Lys Ala Ile Ala Glu Lys Val Phe Gly Asn Arg Asp
      85                      90                      95
Leu Leu Leu Ser Leu Glu Glu Ile Leu His Pro Glu Val Cys Arg Phe
      100                      105                      110
Val Glu Glu Lys Tyr Ala His Val Val Gln Glu Gln Lys Tyr Pro Leu
      115                      120                      125
Phe Ile Val Glu Phe Pro Leu Tyr Glu Ile Gln Tyr Ala Asp Trp
      130                      135                      140
Phe Asp Gln Val Ile Leu Ile Ser Ala Asp Thr Gly Ile Arg Lys Glu
      145                      150                      155                      160
Arg Phe Leu Lys Lys Thr Gly Gly Ser Asp Thr Ser Phe Asp Leu Arg
      165                      170                      175
Cys Ala Arg Phe Ser Ser Leu Glu Glu Lys Ile Leu Arg Ala Asp Val
      180                      185                      190
Val Ile Glu Asn Asn Gly Thr Lys Glu Glu Phe Arg Arg Lys Val Lys
      195                      200                      205
Gln Cys Phe Lys Ala Leu Lys Gly Thr Ile
      210                      215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 981:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 287 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 945434..946294

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 981:

```

Lys Ile Ala Lys Leu Gln Arg Met Gly Ile Asn Glu Leu Asn Val Leu
1      5      10      15
Ala Arg Gln Tyr Gly Val Lys Asn Val Gly Ser Leu Thr Lys Ser Gln
      20      25      30
Val Val Phe Glu Ile Val Lys Ala Lys Ser Glu Arg Pro Asp Glu Phe
      35      40      45
Leu Ile Gly Glu Gly Val Leu Glu Val Leu Pro Asp Gly Phe Gly Phe
      50      55      60
Leu Arg Ser Pro Thr Tyr Asn Tyr Leu Pro Ser Ala Glu Asp Ile Tyr
      65      70      75      80
Val Ser Pro Ala Gln Ile Arg Arg Phe Asp Leu Lys Lys Gly Asp Thr
      85      90      95
Ile Val Gly Thr Ile Arg Ser Pro Lys Glu Lys Glu Lys Tyr Phe Ala
      100     105     110
Leu Leu Lys Val Asp Lys Ile Asn Gly Ser Thr Pro Asp Lys Ala Lys
      115     120     125
Glu Arg Val Leu Phe Glu Asn Leu Thr Pro Leu His Pro Asn Glu Arg
      130     135     140
Leu Ile Met Glu Ile Gly Lys Glu Asn Leu Ala Glu Arg Val Leu Asp
      145     150     155                      160
Leu Thr Ala Pro Ile Gly Lys Gly Gln Arg Gly Leu Ile Val Ala Pro
      165     170     175
Pro Arg Ser Gly Lys Thr Val Ile Leu Gln Ser Ile Ala His Ala Ile
      180     185     190
Ala Val Asn Asn Pro Asp Ala Glu Leu Ile Val Leu Leu Ile Asp Glu

```

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          195                200                205
Arg Pro Glu Glu Val Thr Asp Met Ile Arg Gln Val Arg Gly Glu Val
      210                215                220
Val Ala Ser Thr Phe Asp Glu Gln Pro Asp Arg His Ile Gln Val Thr
225                230                235                240
Glu Met Val Ile Glu Lys Ala Arg Arg Leu Val Glu His Gly Lys Asp
      245                250                255
Val Val Ile Leu Leu Asp Ser Ile Thr Arg Leu Ala Arg Ala Tyr Asn
      260                265                270
Thr Val Gln Pro His Ser Gly Lys Ile Leu Thr Gly Gly Val Asp
      275                280                285

```

(2) INFORMATIONS POUR LA SEQ ID NO: 982:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 128 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 946293..946676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 982:

```

Thr Ser Ala Leu His Lys Pro Lys Arg Phe Phe Gly Ala Ala Arg Asn
1          5          10          15
Ile Glu Gly Gly Ser Leu Thr Ile Leu Ala Thr Ala Leu Ile Asp
      20          25          30
Thr Gly Ser Arg Met Asp Glu Val Ile Phe Glu Glu Phe Lys Gly Thr
      35          40          45
Gly Asn Met Glu Leu Val Leu Asp Arg His Leu Ser Asp Arg Arg Ile
      50          55          60
Tyr Pro Ala Ile Asp Leu Ile Lys Ser Gly Thr Arg Lys Glu Glu Leu
65          70          75          80
Leu Tyr His Pro Gly Glu Leu Glu Lys Val Arg Leu Phe Arg Gln Ala
      85          90          95
Ile Ala Gly Leu Thr Ala Ile Asp Ala Met His Leu Leu Leu Gly Arg
      100          105          110
Leu Lys Lys Thr Asn Ser Asn Thr Glu Phe Leu Leu Ser Leu Lys Asp
      115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 983:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 450 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 947105..948454

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 983:

Asn Tyr Phe Leu Trp Trp Arg Gly Gln Met Ala Gly Arg Arg Thr Lys
 1 5 10 15
 Glu Glu Gln Ile Asn Arg Lys Arg Ser His Phe Tyr Arg Asp Asn Val
 20 25 30
 Gly Val Ile Val Leu Cys Gly Gly Glu Gly Lys Arg Leu Ser Pro Leu
 35 40 45
 Thr Cys Trp Arg Cys Lys Pro Thr Val Ser Phe Gly Gly Arg Tyr Lys
 50 55 60
 Leu Ile Asp Val Pro Ile Ser His Ala Phe Ala Ser Glu Phe Ser Lys
 65 70 75 80
 Ile Phe Val Ile Gly Gln Tyr Leu Thr Tyr Thr Leu Gln Gln His Leu
 85 90 95
 Phe Lys Thr Tyr Phe Tyr His Gly Val Met Gln Asp Gln Ile His Leu
 100 105 110
 Leu Val Pro Glu Arg Arg Asp Gly Ser Gln Val Trp Tyr Gln Gly Thr
 115 120 125
 Ala Asp Ala Ile Arg Gln Asn Leu Leu Tyr Leu Gln Asp Ser Arg Val
 130 135 140
 Glu Tyr Phe Leu Ile Leu Ser Gly Asp Gln Leu Tyr Asn Met Asp Phe
 145 150 155 160
 Arg Ser Ile Val Asp Tyr Ala Ile Asp Ala Gln Ala Asp Met Val Ile
 165 170 175
 Ala Ser Gln Pro Val Ser Asp Lys Asp Val Ser Arg Phe Gly Val Leu
 180 185 190
 Lys Val Asp Asp Glu Ser Lys Leu Ile Asp Phe Tyr Glu Lys Pro Gln
 195 200 205
 Ser Glu Glu Ile Leu Lys His Phe Arg Leu Ser Asn Thr Ala Met Lys
 210 215 220
 Lys Phe Gly Leu Asp Pro Gln His Gly Asn Phe Leu Gly Ser Met Gly
 225 230 235 240
 Ile Tyr Leu Phe Arg Lys Asp Cys Leu Phe Gln Leu Leu Leu Glu Glu
 245 250 255
 Thr Gly Asp Asp Phe Gly Lys Glu Leu Ile His Arg Gln Met His Arg
 260 265 270
 Gly Lys Thr Val Ala Tyr Leu Tyr Asp Gly Tyr Trp Thr Asp Ile Gly
 275 280 285
 Thr Ile Glu Ser Tyr Tyr Glu Ala Asn Met Ala Leu Thr Gln Arg Pro
 290 295 300
 Ser His Asn Ile Arg Gly Phe Asn Cys Tyr Asp Asp Gly Gly Ile Ile
 305 310 315 320
 Tyr Ser Lys Asn Asn His Leu Pro Gly Ala Ile Ile Ser Asp Ser Arg
 325 330 335
 Ile Ser Ser Ser Leu Leu Cys Glu Gly Ala Met Ile Glu Ser Gly Gln
 340 345 350
 Val Ser Asn Ser Val Val Gly Val Arg Gly Val Ile Gly Gln Gly Ser
 355 360 365
 Val Phe Asp Arg Ser Ile Met Met Gly Ser Asp Ser Tyr Gly Ser Glu
 370 375 380
 Ser Phe Pro Leu Gly Ile Gly Lys Asn Cys Glu Ile His Lys Thr Ile
 385 390 395 400
 Ile Asp Glu Asn Cys Ile Gly Asn Gly Val Arg Leu Gln Asn Leu
 405 410 415
 Gln Gly His Lys Asp Tyr Asp Ser Pro Asp Gly Lys Leu Val Val Arg
 420 425 430
 Asp Gly Ile Ile Ile Val Pro Arg Gly Thr Gln Ile Pro Asp Asn Tyr
 435 440 445
 Val Phe
 450

(2) INFORMATIONS POUR LA SEQ ID NO: 984:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 252 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 948522..949277

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 984:

```

Phe Phe Tyr Gln Ala Arg Gly Phe Met Arg Ile Phe Ala Leu Ala Asp
1          5          10          15
Leu His Leu Ser Leu Gly Val Pro Glu Lys Thr Met Glu Val Phe Gly
20          25          30
Glu Pro Trp Val Gly Tyr His Gln Lys Ile Glu Lys His Trp Arg Asp
35          40          45
Ile Val Ser Ser Asp Asp Ile Val Cys Leu Pro Gly Asp Ile Ser Trp
50          55          60
Ala Met Arg Leu Glu Glu Ala Gln Val Asp Phe Arg Phe Leu Gly Ala
65          70          75          80
Leu Pro Gly Ile Lys Tyr Met Ile Arg Gly Asn His Asp Tyr Trp Ser
85          90          95
Ser Ala Ser Ser Ala Lys Leu Ala Asn Val Leu Pro Glu Thr Leu His
100          105          110
Tyr Leu Ser Lys Gly Tyr Val Leu Leu Asn Ala His Gln Ala Ile Val
115          120          125
Gly Val Arg Leu Trp Asp Ser Ser Asp Ile Cys Leu His Trp Glu Thr
130          135          140
Gln His Asp Gly Pro Gln Arg Val Leu Thr Glu Gln Asp Asp Lys Ile
145          150          155          160
Phe Leu Arg Glu Tyr Gly Arg Leu Glu Arg Ala Leu Lys Glu Leu Pro
165          170          175
Ala Ser Val Glu Asp Val Leu Val Met Thr His Tyr Pro Pro Val Ser
180          185          190
Asn Asp Gly Thr Pro Gly Arg Val Ser Asn Leu Leu Glu Met Asp Gly
195          200          205
Arg Val Ser Arg Cys Leu Phe Gly His Leu His Lys Val Pro Arg Pro
210          215          220
Phe Pro Gly Phe Gly Asn Ile Arg Gly Ile Glu Tyr Thr Leu Val Ala
225          230          235          240
Ala Asp Tyr Val Asp Phe Ile Pro Gln Val Val Ser
245          250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 985:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 106 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 949277..949594

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 985:

Leu	Lys	Ile	Leu	Ser	Gly	Lys	Phe	Lys	Gly	Lys	Ser	Leu	Lys	Thr	Phe
1				5					10					15	
Ser	Asn	Pro	Ser	Val	Arg	Pro	Thr	Cys	Gly	Val	Val	Lys	Glu	Ala	Val
			20					25					30		
Phe	Asn	Ile	Cys	Ala	Asn	His	Ile	Val	Gly	Ala	Arg	Phe	Leu	Asp	Leu
		35					40					45			
Phe	Ala	Gly	Ser	Gly	Ser	Met	Gly	Phe	Glu	Ala	Ile	Ser	Arg	Gly	Ala
	50					55					60				
Glu	Ser	Ala	Thr	Phe	Val	Asp	Ser	Ser	Val	Glu	Ala	Val	Arg	Leu	Ile
65					70					75					80
Arg	Ala	Asn	Leu	Ala	Leu	Leu	Asp	Ser	Asn	Leu	Pro	Val	His	Ile	Leu
			85						90					95	
Lys	Gln	Asp	Val	Arg	Ser	Ala	Phe	Tyr	Ala						
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 986:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 276 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 949849..950676

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 986:

Ala	Lys	Arg	Asn	His	Ser	Gly	Trp	Ile	Lys	Ile	Phe	Leu	Leu	Asn	Met
1				5					10					15	
Ile	Arg	Gly	Ser	Ser	Leu	Ile	Ser	Glu	Val	Arg	Val	Lys	Phe	Lys	Tyr
			20					25					30		
Leu	Arg	Pro	Leu	Ser	Phe	Leu	Val	Leu	Val	Ile	Val	Ala	Phe	Cys	Tyr
		35					40					45			
Gly	Cys	Ser	Arg	Glu	Lys	Gln	Glu	Val	Leu	Val	Gly	Arg	Asp	Ala	Thr
	50					55					60				
Trp	Phe	Pro	Gln	Gln	Phe	Gly	Ile	Tyr	Thr	Ser	Gly	Ile	Asn	Ala	Phe
65					70					75					80
Val	Asn	Asp	Leu	Val	Ser	Glu	Ile	Asn	Tyr	Lys	Glu	Gly	Leu	Asn	Ile
			85						90					95	
Ser	Ile	Val	Asn	Gln	Asp	Trp	Val	His	Leu	Phe	Glu	Asn	Leu	Asp	Asp
			100					105					110		
Lys	Lys	Thr	Ser	Gly	Ala	Phe	Thr	Ser	Ala	Ser	Pro	Ser	Ile	Glu	Met
		115					120						125		
Leu	Ala	Arg	Tyr	Gln	Phe	Ser	Asp	Pro	Val	Leu	Leu	Thr	Gly	Pro	Val
	130						135					140			
Leu	Val	Val	Leu	Glu	Asn	Ser	Pro	Tyr	His	Ser	Leu	Gln	Asp	Leu	Glu
145					150					155					160
Gly	Lys	Leu	Ile	Gly	Val	Tyr	Lys	Phe	Asp	Ser	Ser	Val	Leu	Ile	Ala
				165					170					175	
Gln	Asn	Val	Pro	Asn	Ala	Val	Ile	Asp	Ser	Tyr	Gln	His	Ile	Pro	Val
			180					185					190		
Ala	Leu	Glu	Ala	Leu	Ser	Thr	Gln	Arg	Tyr	Asp	Ala	Leu	Leu	Val	Pro

```

          195          200          205
Val Ile Glu Ala Thr Ala Leu Val Glu Thr Ala Tyr Lys Gly Arg Leu
      210          215          220
Arg Ile Ala Ser Glu Pro Leu Asn Glu Glu Gly Leu Arg Leu Val Val
225          230          235          240
Leu Arg Gly Gly Gly Ser Asp Ser Leu Leu Glu Gly Phe Asn Ala Gly
      245          250          255
Leu Ala Lys Ile Arg Arg Ser Gly Arg Tyr Lys Ala Ile Lys Met Gln
      260          265          270
Ser Arg Leu Pro
      275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 987:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 217 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 950680..951330

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 987:

```

Asn Lys Glu Phe Lys Glu Thr Val Val Thr Tyr Leu Leu Ala Asn Phe
1          5          10          15
Gly Gly Pro Arg Thr Ser Gln Glu Ile Val Ser Phe Leu Gln Ala Leu
      20          25          30
Leu Thr Asp Arg Asp Val Thr Gly Gly Met Ile Pro Ser Val Leu His
      35          40          45
Arg Pro Leu Phe Ser Tyr Ile Ala Lys Arg Arg Ala Pro His Val Ala
      50          55          60
Arg Gln Tyr Ala Tyr Leu Gly Gly Gly Ser Pro Ile Phe Gln Asp Thr
65          70          75          80
Glu Arg Leu Ala Gln Asn Leu Ser Gln Glu Leu Gln Ala Ser Val Ile
      85          90          95
Pro Phe His Thr Tyr Leu Pro Glu Thr His Arg Glu Thr Leu Gln Ala
      100          105          110
Leu Gln Glu Ser Gln Gly Ser Ile Val Gly Ile Pro Leu Phe Pro His
      115          120          125
Tyr Thr Phe Ala Val Thr Gly Ser Ile Ile Arg Phe Phe Leu Gln His
      130          135          140
Leu Pro Glu Lys Pro Ile Ser Trp Ile Thr Gln Phe Gly Val His Pro
145          150          155          160
Gln Phe Val Ser Cys Met Gln Gln His Ile Arg Asp Cys Leu Ala Ala
      165          170          175
Gln Xaa Ile Ala Val Glu Asp Cys Tyr Phe Leu Phe Ser Val His Gly
      180          185          190
Leu Pro Gln Arg His Ile Arg Leu Gly Asp Pro Tyr Ala Gln Gln Cys
      195          200          205
Gln Ala Ser Phe Glu Ala Leu Arg Arg
      210          215

```

(2) INFORMATIONS POUR LA SEQ ID NO: 988:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 121 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 951281..951643

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 988:

Glu	Ile	Leu	Met	Leu	Ser	Asn	Val	Arg	Leu	Leu	Ser	Lys	His	Tyr	Gly
1			5						10					15	
Gly	Glu	Leu	Glu	Gly	Glu	Ile	Ala	Phe	Gln	Ser	Lys	Phe	Gly	Ile	Gly
		20					25						30		
Lys	Trp	Leu	Asp	Pro	Ser	Thr	Gln	Glu	Val	Cys	Gln	Ser	Leu	Arg	Thr
	35					40					45				
Lys	Lys	Arg	Tyr	Ile	Val	Ile	Val	Pro	Phe	Gly	Phe	Val	Ser	Asp	His
	50				55						60				
Ile	Glu	Thr	Leu	Tyr	Glu	Ile	Asp	His	Leu	Tyr	Val	Pro	Ile	Leu	Leu
65					70					75					80
Gln	Lys	Glu	Tyr	Arg	Val	Val	Arg	Ile	Pro	Ala	Ile	Asn	Ala	Ser	Ser
			85						90					95	
Arg	Trp	Val	Ser	Ser	Leu	Ala	Ala	Ile	Val	Arg	Ser	Ser	Pro	Gln	Glu
		100						105					110		
Thr	Ser	Leu	Glu	Pro	Leu	Leu	Met	Pro							
		115					120								

(2) INFORMATIONS POUR LA SEQ ID NO: 989:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 337 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 951788..952798

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 989:

Glu	Cys	Gly	Ile	Ser	Met	Lys	Ser	Arg	Asn	Ala	Gln	Ser	Ile	Leu	Glu
1				5					10					15	
Ser	Leu	Cys	Lys	Lys	Thr	His	Arg	Leu	Leu	Leu	Arg	Tyr	Leu	Leu	Lys
		20					25						30		
Gln	Thr	Leu	Leu	Val	Ala	Leu	Gly	Met	Thr	Leu	Met	Val	Ala	Glu	Leu
	35					40					45				
Gly	Ile	Phe	Leu	Tyr	Phe	Phe	Leu	Phe	Ser	Gly	Lys	Thr	Leu	Leu	Pro
	50				55						60				
Ala	Phe	Cys	Leu	Ala	Cys	Phe	Val	Leu	Thr	Ile	Phe	Ile	Cys	Leu	Val
65				70					75						80
Ile	Arg	Leu	Tyr	Ile	Leu	Ser	Lys	Lys	Thr	Glu	Phe	Phe	Asp	Lys	Leu
			85					90					95		
Leu	Ala	Asp	Phe	Val	His	Gln	Ala	Gln	Val	Ile	Phe	Lys	Lys	Lys	Asn
		100					105						110		
Met	Met	Glu	Glu	His	Pro	Glu	Ile	Ala	Ala	Ala	Val	Thr	Gln	Leu	Ser

115 120 125
 Leu Val Met Gln Asn Gln Glu Tyr Phe Val Phe Cys Asn Leu Leu Lys
 130 135 140
 Ile Val Pro Pro Tyr Asp Ser Ile Lys Lys Phe Ser Cys Phe Cys Phe
 145 150 155 160
 Trp Lys Asp Tyr Phe Ser Phe Arg Glu Met Leu Leu Gln Lys Ala Ile
 165 170 175
 Asp Leu Tyr Leu Leu Val Val Gln Ala Ile Pro Thr Asp Leu Gly Ala
 180 185 190
 His Val Ser Leu Ala Asp Ala Tyr Val Ser Leu Ser Gly Leu Tyr Ala
 195 200 205
 Asp Pro Arg Lys Tyr Thr Glu Phe Asp Thr Lys Tyr Trp Val Pro Pro
 210 215 220
 Gly Arg Tyr Gly Glu Asp Ile Gln Glu Lys Phe Phe Ala Thr Ala His
 225 230 235 240
 Arg Ala Thr Glu Glu Phe Lys Ile Leu Asn Glu Tyr Ala Pro Gly Asn
 245 250 255
 Val Trp Val His Thr Gln Leu Ala Tyr Ser Tyr His Asp Leu Gln Met
 260 265 270
 Pro Lys Lys Glu Ile Arg Glu Tyr Glu Ile Val Leu Lys Leu Lys Pro
 275 280 285
 His Asp Ala Asn Thr Ile Met Lys Leu Gly Ile Leu Tyr Phe Gln Gln
 290 295 300
 Gly Met Asn Ala Lys Gly Leu Gln Val Tyr Glu Gln Leu Arg Lys Val
 305 310 315 320
 Asp Leu Lys Lys Ser Lys Lys Leu Ile Lys Phe Tyr Gly Val Val Ala
 325 330 335
 Lys

(2) INFORMATIONS POUR LA SEQ ID NO: 990:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 228 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 953581..954264

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 990:

Arg Thr Val Cys Phe Tyr Arg Val Arg Lys Thr Met Phe Glu Ile Leu
 1 5 10 15
 Arg Lys Lys Ile Ser Ser Tyr Ser Val Val Leu Phe Cys Leu Val Val
 20 25 30
 Leu Ser Ile Phe Leu Ser Gly Lys Ile Val Val Asn Val Lys Thr Tyr
 35 40 45
 Arg Val Glu Arg Gln Asn Ser Leu Val Leu Leu Ser Arg Ser Val Glu
 50 55 60
 Ala Ala Tyr Ser Arg Gly Ile Phe Pro Pro Glu Thr Ala Met Pro Met
 65 70 75 80
 Leu Glu Gln Ala Tyr Arg Arg Gly Gly Lys Glu Ala Val Ser Tyr Ala
 85 90 95
 Gly Phe Leu Ala Ser Cys Phe His Ile His Asn Asp Pro Leu Arg Gly
 100 105 110

Ala Tyr Tyr Ser Gly Leu Ala Tyr Gln His Gly Thr His Leu Gln Leu
 115 120 125
 Pro Ser Pro Gln His Ile Leu Leu Lys Glu Ile Ala Asp Ala His Ala
 130 135 140
 Thr Lys Gln Tyr Gln Glu Val Leu Asp Lys Ser Arg Glu Leu Leu Ser
 145 150 155 160
 Ser Ile Ser Ser Ser Lys Asp Phe Pro Met Leu Arg Phe Leu Thr Leu
 165 170 175
 Leu Arg Met Ile Glu Val Lys Glu Ser Leu Asn Gln Asp Phe Ser Leu
 180 185 190
 Glu Leu Thr Glu Leu Lys Ala Leu Pro Gly Phe Glu Asp Tyr Glu Gln
 195 200 205
 Leu Tyr Lys Asp Gly Val Trp Thr Ile Ser Lys Arg Tyr Ser Ser Leu
 210 215 220
 Arg Ala Leu Tyr
 225

(2) INFORMATIONS POUR LA SEQ ID NO: 991:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 244 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 954426..955157

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 991:

Ser Met Leu Arg Val Leu Ala Tyr Arg Gln Val Ser Phe Ser Lys Phe
 1 5 10 15
 Pro His Leu Phe Lys Ser Phe Val Ser Leu Leu Ser Ser Leu Lys Gln
 20 25 30
 His Tyr Ser Phe Met Leu Pro Gly Asp Pro Leu Pro Lys Lys Lys Ala
 35 40 45
 Leu Met Leu Thr Phe Asp His Ala Ser Val Asp Phe Tyr Thr His Val
 50 55 60
 Phe Pro Leu Leu Gln Asn Leu Gln Ile Pro Ala Val Ile Gly Val Ala
 65 70 75 80
 Trp Arg Tyr Val Ala Asp Leu Glu Gly Glu Asp Leu Pro Ile Asp Val
 85 90 95
 Arg Ile Ala Pro Ser Asp Phe Leu Ala Phe Gln Asp Glu Ile Phe Ser
 100 105 110
 Tyr His Gln Pro Phe Cys Ser Val Arg Glu Leu Cys His Met Ala Ala
 115 120 125
 Ser Pro Leu Val Arg Phe Ala Ser Ser Gly Phe Ala Ile Arg Asn Leu
 130 135 140
 Lys Tyr Ala Pro Pro Tyr Leu Asp Thr Glu Ile Leu Leu Ser Lys Ile
 145 150 155 160
 Leu Leu Glu Asn Ala Ile Gln Ser Pro Val Glu Ser Phe Phe Phe Pro
 165 170 175
 Leu Gly Lys Ser Asp Val Val Ser Gln His Phe Val Gln Glu Thr Tyr
 180 185 190
 Arg Tyr Ser Phe Val Leu Gly Asn Thr Ala Ser Phe Ser Tyr Pro Thr
 195 200 205
 Gln Ser Leu His Gly Ile Pro Arg Ile Asp Met Pro Leu Asp Ser Gln

	210				215				220						
Arg	Val	Pro	Ser	Leu	Tyr	Gln	Leu	Ser	Tyr	Arg	His	Leu	Lys	Gln	Phe
225					230					235					240
Leu	Val	Leu	Arg												

(2) INFORMATIONS POUR LA SEQ ID NO: 992:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 729 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 955754..957940

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 992:

Arg	Arg	Gln	Arg	Met	Ile	Asp	Lys	Ile	Ile	Arg	Thr	Val	Leu	Val	Leu
1				5					10					15	
Ser	Leu	Phe	Leu	Leu	Tyr	Trp	Ser	Ser	Asp	Leu	Leu	Glu	Lys	Asp	Val
			20				25						30		
Lys	Ser	Ile	Lys	Arg	Glu	Leu	Lys	Ala	Leu	His	Glu	Asp	Val	Leu	Glu
		35					40					45			
Leu	Val	Arg	Ile	Ser	His	Gln	Gln	Lys	Asn	Trp	Val	Gln	Ser	Ile	Asp
	50					55					60				
Phe	Ser	Val	Ser	Pro	Glu	Ile	Ser	Val	Leu	Lys	Asp	Cys	Gly	Asp	Pro
65					70					75				80	
Ala	Phe	Pro	Asn	Leu	Leu	Cys	Glu	Asp	Pro	Tyr	Val	Glu	Lys	Val	Val
			85						90					95	
Pro	Ser	Leu	Leu	Lys	Glu	Gly	Phe	Val	Pro	Lys	Gly	Ile	Leu	Arg	Thr
			100					105					110		
Ala	Gln	Val	Gly	Arg	Pro	Asp	Asn	Leu	Ser	Pro	Phe	Asn	Gly	Phe	Val
		115					120					125			
Asn	Ile	Val	Arg	Phe	Tyr	Glu	Leu	Cys	Val	Pro	Asn	Leu	Ala	Val	Glu
	130					135					140				
His	Val	Gly	Lys	Tyr	Glu	Glu	Phe	Ala	Pro	Ser	Leu	Ala	Leu	Lys	Ile
145					150					155				160	
Glu	Glu	His	Tyr	Val	Glu	Asp	Gly	Ser	Gly	Asp	Lys	Glu	Phe	His	Ile
			165						170					175	
Tyr	Leu	Arg	Pro	Asn	Met	Phe	Trp	Glu	Pro	Ile	Asp	Pro	Thr	Leu	Phe
			180					185					190		
Pro	Lys	Asn	Ile	Thr	Leu	Ala	Asp	Thr	Phe	Leu	Arg	Pro	His	Pro	Val
		195					200					205			
Thr	Ala	His	Asp	Val	Lys	Phe	Tyr	Tyr	Asp	Val	Val	Met	Asn	Pro	Tyr
	210					215					220				
Val	Ala	Glu	Met	Arg	Ala	Val	Ala	Met	Arg	Ser	Tyr	Phe	Glu	Asp	Met
225					230					235				240	
Val	Ser	Val	Arg	Val	Glu	Asn	Asp	Leu	Lys	Leu	Ile	Val	Arg	Trp	Arg
			245						250					255	
Ala	His	Thr	Val	Arg	Asn	Glu	Gln	Gly	Glu	Glu	Glu	Lys	Lys	Val	Leu
			260					265					270		
Tyr	Ser	Ala	Phe	Ala	Asn	Thr	Leu	Ala	Leu	Gln	Pro	Leu	Pro	Cys	Phe
		275				280						285			
Val	Tyr	Gln	Tyr	Phe	Ala	Asn	Gly	Glu	Lys	Ile	Val	Pro	Glu	Asp	Ser
	290					295					300				

Asp	Pro	Asp	Thr	Tyr	Arg	Lys	Asp	Ser	Val	Trp	Ala	Gln	Asn	Phe	Ser	305	310	315	320
Ser	His	Trp	Ala	Tyr	Asn	Tyr	Ile	Val	Ser	Cys	Gly	Ala	Phe	Arg	Phe	325	330	335	
Ala	Gly	Met	Asp	Asp	Glu	Lys	Ile	Thr	Leu	Val	Arg	Asn	Pro	Asn	Tyr	340	345	350	
His	Asn	Pro	Phe	Ala	Ala	Leu	Val	Glu	Lys	Arg	Tyr	Ile	Tyr	Met	Lys	355	360	365	
Asp	Ser	Thr	Asp	Ser	Leu	Phe	Gln	Asp	Phe	Lys	Ala	Gly	Lys	Val	Asp	370	375	380	
Ile	Ala	Tyr	Phe	Pro	Pro	Asn	His	Val	Asp	Asn	Leu	Ala	Ser	Phe	Met	385	390	395	400
Gln	Thr	Ser	Ala	Tyr	Lys	Glu	Gln	Ala	Ala	Arg	Gly	Glu	Ala	Ile	Leu	405	410	415	
Glu	Lys	Asn	Ser	Ser	Asp	Arg	Ser	Tyr	Ser	Tyr	Ile	Gly	Trp	Asn	Cys	420	425	430	
Leu	Ser	Leu	Phe	Phe	Asn	Asn	Arg	Ser	Val	Arg	Gln	Ala	Met	Asn	Met	435	440	445	
Leu	Ile	Asp	Arg	Asp	Arg	Ile	Ile	Glu	Gln	Cys	Leu	Asp	Gly	Arg	Gly	450	455	460	
Val	Ser	Val	Ser	Gly	Pro	Phe	Ser	Leu	Cys	Ser	Pro	Ser	Tyr	Asn	Arg	465	470	475	480
Asp	Val	Glu	Gly	Trp	Gln	Tyr	Ser	Pro	Glu	Glu	Ala	Ala	Arg	Lys	Leu	485	490	495	
Glu	Glu	Glu	Gly	Trp	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Ile	Arg	Glu	Lys	500	505	510	
Val	Ile	Asp	Gly	Val	Val	Val	Pro	Phe	Arg	Phe	Arg	Leu	Cys	Tyr	Tyr	515	520	525	
Val	Lys	Ser	Val	Thr	Ala	Arg	Thr	Ile	Ala	Glu	Tyr	Val	Ala	Thr	Val	530	535	540	
Cys	Lys	Glu	Val	Gly	Ile	Glu	Cys	Cys	Leu	Leu	Gly	Leu	Asp	Met	Ala	545	550	555	560
Asp	Tyr	Ser	Gln	Ala	Leu	Glu	Glu	Lys	Asn	Phe	Asp	Ala	Ile	Leu	Ser	565	570	575	
Gly	Trp	Cys	Leu	Gly	Thr	Pro	Pro	Glu	Asp	Pro	Arg	Ala	Leu	Trp	His	580	585	590	
Ser	Glu	Gly	Ala	Leu	Glu	Lys	Gly	Ser	Ala	Asn	Ala	Val	Gly	Phe	Cys	595	600	605	
Asn	Glu	Glu	Ala	Asp	Arg	Ile	Ile	Glu	Gln	Leu	Ser	Tyr	Glu	Tyr	Asp	610	615	620	
Ser	Asn	Lys	Arg	Gln	Ala	Leu	Tyr	His	Arg	Phe	His	Glu	Val	Ile	His	625	630	635	640
Glu	Glu	Ser	Pro	Tyr	Ala	Phe	Leu	Tyr	Ser	Arg	Gln	Tyr	Ser	Leu	Val	645	650	655	
Tyr	Lys	Glu	Phe	Val	Lys	Asn	Ile	Phe	Val	Pro	Thr	Glu	His	Gln	Asp	660	665	670	
Leu	Ile	Pro	Gly	Ala	Gln	Asp	Glu	Thr	Val	Asn	Leu	Ser	Met	Leu	Trp	675	680	685	
Val	Asp	Lys	Glu	Glu	Gly	Arg	Ser	Pro	Leu	Tyr	Leu	Lys	Thr	Ser	Ala	690	695	700	
Phe	Asp	Ser	Leu	Asn	Ala	Leu	Cys	Tyr	His	Leu	Cys	Glu	Phe	Cys	Asp	705	710	715	720
Ser	Gln	Cys	Cys	Ser	Arg	Arg	Pro	Ala								725			

(2) INFORMATIONS POUR LA SEQ ID NO: 993:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 492 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 957837..959312

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 993:

```

Asp Leu Arg Tyr Ile Leu Lys Arg Leu Leu Leu Ile Pro Leu Thr Leu
1      5      10      15
Phe Ala Ile Ile Ser Val Asn Phe Val Ile Leu Asn Ala Ala Pro Gly
      20      25      30
Asp Leu Leu Glu Glu His Ser Val Asp Ala Gln Gly Glu Ala Gly Arg
      35      40      45
Ser Asp Lys Ile Arg Thr Tyr Lys Gly Pro Asp Arg Tyr Leu Gln Phe
      50      55      60
Arg Glu His Tyr Gly Leu Thr Leu Pro Ile Phe Phe Asn Thr Arg Pro
      65      70      75      80
Gln Ile Ser Arg Ser Glu Leu Arg Ala Gly Ile Gln Glu Ile Ile Asp
      85      90      95
Gly Thr Ile His Lys Lys Ser Lys Thr Gly Ser Ile Thr Asn Ile Lys
      100     105     110
Val Tyr Trp Gly Asp Cys Ala Lys Phe Ile Met Pro Ala Leu Leu Ala
      115     120     125
Glu Ala Glu Asp Ser Ser Lys Glu Asp Ile Tyr Arg His Val Ala Ala
      130     135     140
Asp Leu Phe Ile Arg Gly Gly Ile Arg Gln Gly Ile Val Glu Pro Arg
      145     150     155     160
Leu Leu Glu Glu Gln Arg Glu Tyr Asn Gln Lys Val Ser Lys Ser Asn
      165     170     175
Ala Glu Leu Val Arg Leu Leu Asn Glu Asp Asn Ile Glu Val Lys Val
      180     185     190
Ala Ala Leu Gln Glu Trp Val Glu Gln Glu Gly Gly Arg Gly Gln Leu
      195     200     205
Met Arg Arg Asp Leu Trp Arg Ile Phe Phe Leu Glu Thr Arg Phe Ala
      210     215     220
Lys Tyr Leu Ser Arg Ile Val Arg Leu Asp Phe Gly Thr Leu Arg Asn
      225     230     235     240
Asp Cys His Lys Thr Val Val Ser Glu Val Ile Lys Arg Leu Gly Ser
      245     250     255
Ser Leu Ile Leu Ser Leu Leu Pro Met Ile Val Val Phe Ile Leu Cys
      260     265     270
Gln Val Phe Gly Met Ile Met Ala Val Asn Lys Asn His Trp Ile Asp
      275     280     285
His Leu Leu Asn Phe Leu Phe Leu Ile Leu Phe Ser Ile Pro Val Phe
      290     295     300
Val Ala Val Pro Trp Ile Ile Asp Asn Phe Val Leu Asn Lys Thr Val
      305     310     315     320
Pro Phe Thr Ser Ile Ser Met Pro Tyr Ser Gly Leu Cys Ser Ser Pro
      325     330     335
Glu Ile Phe Lys Glu Met Thr Ser Phe Glu Lys Leu Thr Asp Ile Val
      340     345     350
Leu His Ser Phe Leu Pro Phe Cys Ala Val Ser Tyr Gly Ala Phe Ala
      355     360     365
Ala Gln Ser Arg Leu Ser Arg Ala Val Phe Leu Glu Val Leu Gly Glu
      370     375     380

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Asp His Ile Ser Ala Leu Arg Ala Arg Gly Ile Ser Gln Tyr Asp Ile
385          390          395          400
Leu Val Arg His Val Gly Lys Asn Ser Ala Ala Thr Leu Ile Thr Ser
          405          410          415
Leu Ala Ser Ser Leu Ser Ala Leu Leu Gly Gly Ala Leu Val Val Glu
          420          425          430
Thr Leu Phe Asp Ile Asp Gly Phe Gly Lys Phe Phe Tyr Gln Ala Ile
          435          440          445
Leu Asn Arg Asp His Asn Val Val Met Phe Ser Val Ile Met Gly Ser
          450          455          460
Val Ile Ser Leu Ile Gly Tyr Leu Ile Gly Asp Ile Cys Tyr Val Leu
465          470          475          480
Leu Asp Pro Arg Val Gln Leu Glu Glu Arg Lys Val
          485          490

```

(2) INFORMATIONS POUR LA SEQ ID NO: 994:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 584 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 959299..961050

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 994:

```

Lys Lys Gly Arg Cys Glu Met Lys Glu Pro Gln Thr Ser Tyr Gln Arg
1          5          10          15
Phe Phe Arg Ala Tyr Asn Arg Arg Ala Leu Pro Ser Ile Ala Leu Lys
          20          25          30
Phe Phe Ile Gly Leu Met Leu Ile Gly Ile Tyr Ala Pro Leu Phe Ala
          35          40          45
Ser Ser Lys Pro Ile Leu Val Arg Trp His Gly Glu Trp Tyr Ser Pro
          50          55          60
Leu Phe Arg Tyr Leu Leu Phe Pro Gly Phe Tyr Thr Lys Ser Ile Asp
65          70          75          80
Leu Phe Phe Asn Val Leu Met Leu Thr Leu Pro Phe Phe Ile Leu Gly
          85          90          95
Phe Arg Tyr Leu Ser Gly Val Trp Lys Lys Leu Phe Leu Gly Val Val
          100          105          110
Thr Gly Ile His Ile Ala Val Phe Ser Phe Ala Leu Ser Gly Arg Val
          115          120          125
Gln Asp Pro Cys Arg Asp Glu Leu Leu Lys Gln Lys Arg Ala Lys His
          130          135          140
Leu Gln Gln Glu Leu Lys Thr Thr Pro Lys Thr Glu Phe Leu Pro Thr
145          150          155          160
Ile Ala Lys Arg Thr Arg Thr Trp Glu Ser Glu Arg Ala Tyr Met Ser
          165          170          175
Lys Tyr Glu Gln Leu Gly Met Leu Val Lys Ala Lys Tyr Arg Lys Met
          180          185          190
Gln His Asp His Leu Glu Lys Gln Arg Glu Ala Tyr Glu Leu Cys Lys
          195          200          205
Gln Ser Pro Met Pro Thr Leu Arg Phe Leu Glu Met Lys Asn Glu Thr
          210          215          220
Ala Ser Leu Arg Phe Phe Lys Asn Lys Ile Asn Lys Leu Lys Ala Ser

```

(2) INFORMATION POUR LA SEQ ID NO: 995:

(A) LONGUEUR: 154 acides aminés
(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(961053..961514)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 995:

Ala	Gln	Ala	Cys	Ser	Gln	Gly	Leu	Pro	Ile	Asn	Arg	Thr	Pro	Pro	Ile
1				5					10					15	
Gln	Ile	Ile	Val	His	Phe	Arg	Gly	Asp	Ser	Ile	Phe	His	Ser	Arg	Leu
			20					25					30		
Ser	Pro	Ala	Pro	Val	Phe	Thr	Cys	Leu	Phe	Leu	Gly	Pro	Gly	Ala	His
		35					40					45			
Lys	Ala	Met	Glu	Gly	Leu	Val	Arg	Trp	Cys	Glu	Ala	Tyr	Ala	Asn	Lys
	50					55					60				
Met	Pro	Pro	Lys	Leu	Ser	Phe	Leu	Asp	Leu	Ser	Ser	Phe	Lys	Glu	Lys
65					70					75					80
Arg	Leu	Ala	Ile	Leu	Gln	Glu	Ile	Arg	Gln	Ile	Pro	Phe	Gly	Thr	Arg
				85					90					95	
His	Thr	Cys	Glu	Glu	Ile	Ala	Glu	Arg	Thr	Lys	Thr	His	Thr	Glu	Glu
			100					105					110		
Val	Leu	Ile	Ala	Cys	Gln	Glu	Asn	Pro	Leu	Pro	Leu	Leu	Ile	Pro	Cys
		115					120						125		
His	Arg	Val	Leu	Ser	Ile	His	Asp	Tyr	Pro	Gly	Gly	Glu	Lys	Leu	Tyr
	130					135						140			
Lys	Ala	Leu	Thr	Glu	Phe	Glu	Glu	Leu	Ser						
145						150									

(2) INFORMATIONS POUR LA SEQ ID NO: 996:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 363 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(961487..962575)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 996:

Glu	Ile	Ser	Gln	His	Arg	Thr	Arg	Gln	Leu	Met	Lys	Arg	Leu	Phe	Phe
1				5					10					15	
Ile	Cys	Ala	Leu	Ala	Leu	Ser	Pro	Leu	Ala	Tyr	Gly	Ala	Val	Gln	Lys
			20					25					30		
Asp	Pro	Met	Leu	Met	Lys	Glu	Thr	Phe	Arg	Asn	Asn	Tyr	Gly	Ile	Ile
		35					40					45			
Val	Phe	Lys	Gln	Glu	Trp	Asn	Lys	Arg	Gly	Cys	Asp	Gly	Ser	Ile	Thr
	50					55					60				
Arg	Val	Phe	Lys	Asp	Gly	Thr	Thr	Thr	Leu	Glu	Val	Tyr	Ala	Gln	Gly
65					70					75					80
Ala	Leu	His	Gly	Glu	Val	Thr	Arg	Thr	Phe	Pro	His	Ser	Thr	Thr	Leu
				85					90					95	
Ala	Val	Ile	Glu	Thr	Tyr	Asp	Gln	Gly	Arg	Leu	Leu	Ser	Lys	Lys	Thr
			100					105					110		
Phe	Phe	Pro	Asn	Ala	Leu	Pro	Ala	Lys	Glu	Ala	Val	Tyr	His	Glu	Asp
		115					120					125			
Gly	Ser	Phe	Ser	Leu	Thr	Arg	Trp	Pro	Asp	Asn	Asn	Asn	Ser	Asp	Thr
	130					135						140			
Ile	Thr	Asp	Pro	Cys	Phe	Val	Glu	Lys	Thr	Tyr	Gly	Gly	Arg	Val	Leu
145					150					155					160
Glu	Gly	His	Tyr	Thr	Ser	Phe	Asn	Gly	Lys	Tyr	Ser	Ser	Lys	Ile	Leu

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          165          170          175
Asn Gly Glu Gly Val Arg Ser Thr Phe Ser Ser Asp Ser Ile Leu Leu
          180          185          190
Thr Glu Glu Ser Phe Asn Asp Gly Val Met Val Lys Lys Thr Thr Phe
          195          200          205
Tyr Ser Thr Arg Glu Pro Glu Thr Val Thr His Tyr Val Asn Gly Tyr
          210          215          220
Leu Thr Glu Phe Gly Leu Pro Ile Phe Leu Val Gly Phe Gln Ile Arg
          225          230          235          240
Leu Lys Asn Gly Asp Met Asp Ile Lys Thr Ala Leu Gln Ser Tyr Leu
          245          250          255
Lys Met Val Val Arg Leu Leu Lys Ser His Leu Tyr Ala Glu Gln Lys
          260          265          270
Met Glu Ser Asn Ser Asp Thr Met Asn Lys Arg Ile Ser Leu Lys Arg
          275          280          285
Phe Leu Gly Ser Thr Thr Ser Cys Met Glu Ser Ala Lys Ser Met Arg
          290          295          300
Arg Gly Tyr Ala Asn Pro Asn Gly Ile Thr Lys Ala Asn Leu Ser Arg
          305          310          315          320
Lys Ser Ser Leu Asn Asp Ser Val Pro Pro Asp Asn Ser Thr Leu Gly
          325          330          335
Ala Ser Trp Leu Lys Ser Ser Leu Leu Ser Leu Gln Arg Pro Arg Thr
          340          345          350
Val Trp Pro Arg Leu Ala Leu Lys Gly Phe Leu
          355          360

```

(2) INFORMATIONS POUR LA SEQ ID NO: 997:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 132 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(961584..961979)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 997:

```

Trp Arg Asn Gly Gln Lys Asn Asp Ile Leu Leu Asp Ser Arg Thr Arg
1          5          10
Asn Arg His Ser Leu Cys Gln Trp Val Pro His Gly Val Arg Phe Thr
          20          25          30
Tyr Leu Pro Gly Gly Ile Pro Asn Thr Ile Glu Glu Trp Arg Tyr Gly
          35          40          45
His Gln Asp Gly Leu Thr Ile Leu Phe Lys Asn Gly Cys Lys Ile Ala
          50          55          60
Glu Val Pro Phe Val Arg Gly Ala Lys Asn Gly Ile Glu Leu Arg Tyr
          65          70          75          80
Asn Glu Gln Glu Asn Ile Ala Glu Glu Ile Ser Trp Gln His Asn Ile
          85          90          95
Leu His Gly Val Arg Lys Ile His Ala Ala Gly Val Cys Lys Ser Glu
          100          105          110
Trp Tyr Tyr Lys Gly Lys Pro Val Ser Gln Ile Lys Phe Glu Arg Leu
          115          120          125
Ser Ala Ala Arg
          130

```


(2) INFORMATIONS POUR LA SEQ ID NO: 998:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 790 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(962545..964914)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 998:

Met	Leu	Val	Pro	Leu	Ser	Leu	Leu	Gln	Lys	Phe	Phe	Ser	Ser	Pro	Leu
1				5					10					15	
Ser	Ile	Glu	Glu	Ile	Leu	Gln	Ala	Cys	Asp	Arg	Ile	Gly	Ile	Glu	Ala
			20					25					30		
Glu	Cys	Ser	Asn	Val	Phe	Pro	Asp	Ser	Leu	Asn	Thr	Val	Val	Thr	Gly
		35					40					45			
Lys	Ile	Leu	Ser	Ala	Ser	Pro	His	Pro	Asp	Ala	Glu	Arg	Leu	Thr	Val
	50					55					60				
Ala	Ile	Val	Phe	Asp	Gly	Lys	Gly	Lys	Arg	Gln	Ile	Ile	Cys	Gly	Ala
65					70					75					80
Pro	Asn	Cys	Arg	Ala	Gly	Ile	Ile	Val	Pro	Ile	Ala	Leu	Pro	Gly	Ala
			85						90					95	
Lys	Leu	Arg	Asn	Ala	Ser	Gly	Glu	Ile	Thr	Thr	Ile	Lys	Lys	Ala	Lys
			100					105					110		
Ile	Arg	Gly	Leu	Glu	Ser	Gln	Gly	Met	Cys	Cys	Gly	Ala	Asp	Glu	Leu
		115					120					125			
Gly	Phe	Pro	His	Leu	Gln	Lys	Ala	Gln	Arg	Gly	Ile	Phe	Glu	Phe	Pro
		130				135					140				
Ala	Asp	Thr	Pro	Leu	Gly	Glu	Ser	Ala	Cys	Met	Leu	Leu	Ala	Gly	Ala
145					150					155					160
Ser	Leu	Glu	Cys	Ser	Leu	Thr	Pro	Asn	Leu	Gly	His	Cys	Ala	Ser	Leu
			165						170					175	
Leu	Gly	Leu	Ala	Arg	Glu	Ile	Ser	Phe	Leu	Ser	Pro	Val	Ser	Leu	Asn
			180					185					190		
Ile	Pro	Glu	Phe	Ser	Phe	Ala	Ser	Leu	Pro	Gln	Glu	Thr	Ser	Ile	
		195				200						205			
Cys	Asp	Met	His	Asp	Ala	Gly	Ala	Cys	Pro	Val	Phe	Tyr	Ser	Val	Lys
	210					215					220				
Ile	Ser	Gly	Leu	Ser	Cys	Arg	Arg	Ser	Pro	Glu	Tyr	Leu	Gln	Ala	Ala
225					230					235					240
Leu	Thr	Ala	Leu	Gly	Gln	Lys	Pro	Leu	Asn	Ala	Ile	Val	Asp	Ile	Thr
			245						250					255	
Asn	Tyr	Val	Met	Leu	Ser	Leu	Gly	Gln	Pro	Leu	His	Ala	Tyr	Asp	Ser
			260					265					270		
Gln	Ala	Val	Glu	Gln	Lys	Ser	Leu	His	Ala	Ala	Thr	Leu	Gln	Ser	Ala
		275					280					285			
Gln	Pro	Leu	Thr	Leu	Leu	Asn	Gln	Glu	Thr	Tyr	Thr	Leu	Pro	Ala	Gly
	290					295					300				
Ser	Leu	Val	Val	Ala	Asp	Gln	His	Asn	Ile	Leu	Gly	Leu	Ala	Gly	Val
305					310					315					320
Met	Gly	Ser	Ala	Ala	Ser	Ser	Cys	Ser	Glu	Asn	Thr	Thr	Glu	Ile	Ile
			325						330					335	
Leu	Glu	Ala	Ala	Tyr	Phe	Gln	Pro	Gln	Ala	Val	Arg	Lys	Tyr	Gln	Arg

340 345 350
 Thr Ile Gln Leu His Thr Glu Ala Tyr Arg Phe Thr Arg Gly Val
 355 360 365
 Asp Pro Gln Gly Val Leu Pro Ala Leu His Ala Ala Ile His Met Ile
 370 375 380
 Gln Ser Leu Phe Pro Asp Ala Gln Ile Ser Pro Ile Gln Lys Ile Gly
 385 390 395 400
 Asp Asp Ser Phe Phe Pro Leu Ser Leu Ser Val Arg Pro Lys Thr Ile
 405 410 415
 Lys Arg Leu Leu Asp Ile Glu Leu Ser Thr Ala Glu Ile Val Ala Lys
 420 425 430
 Leu Phe Ser Leu Gly Phe Gln Thr Ala Val Glu Glu Gln Ala Val Arg
 435 440 445
 Val Glu Val Pro Ser Tyr Arg His Asp Ile Gln Glu Glu Thr Asp Leu
 450 455 460
 Val Glu Glu Ile Cys Arg Thr Thr Pro Phe Val Gln Lys Thr Gln Lys
 465 470 475 480
 Ile Leu Pro Thr Tyr Thr Pro Ile Tyr Ser Leu Lys Arg Glu Leu Thr
 485 490 495
 Ala Phe Leu Ala Asn Gly Gly Leu Gln Gln Phe Phe Thr Cys Ser Leu
 500 505 510
 Leu Asp Thr Glu Val Ser Ser Leu Ser Leu Gln Glu Ser Ser Leu Ile
 515 520 525
 Pro Val Gln Asn Ser Ser Trp Lys Leu Arg Asp Ser Leu Leu Pro Gly
 530 535 540
 Met Leu Lys Ser Ala Ala Thr Asn Leu His Arg Gln Ala Pro Tyr Val
 545 550 555 560
 Tyr Ala Phe Glu Ile Gly Asn Val Tyr Ser Lys Glu Gln Asn Arg Tyr
 565 570 575
 Gln Glu Glu Glu Arg Val Ala Ile Leu Leu Ser Arg Gln Val Met Asp
 580 585 590
 Asp Ser Trp Gln Gly Lys Thr Pro Leu Ser Phe Tyr Thr Ile Lys Gly
 595 600 605
 Trp Val Glu Lys Leu Leu Cys Gln Ser Gly Ala Ser Ile Glu Asp Phe
 610 615 620
 Ser Leu Gln Pro Ser Gln His Pro Asn Phe His Pro Tyr Gln Gln Ala
 625 630 635 640
 Ala Leu Tyr Gln Lys Lys His Leu Leu Gly Ile Phe Gly Thr Leu His
 645 650 655
 Pro Gln Leu Cys Arg Lys Ala Gln Ile Lys His Asp Val Val Phe Ala
 660 665 670
 Glu Leu Ser Leu Asn Val Leu Leu Ser Leu Lys Lys Lys Ser Gly Pro
 675 680 685
 His Tyr Val Pro Tyr Pro Ile Tyr Pro Ala Ser Ser Arg Asp Ile Thr
 690 695 700
 Ile Thr Ile Asp Arg Asp Leu Pro Ala Asp Leu Val Arg Arg Glu Leu
 705 710 715 720
 Leu Ser Phe Glu Ser Lys Trp Leu Glu Ser Val His Ile Val Ser Val
 725 730 735
 Tyr Gln Gly Arg Asp Ser Ala Ser Gln Ser Lys Asn Val Ser Leu Arg
 740 745 750
 Met Val Phe Arg Asp His Glu Arg Thr Leu Ser Gly Gln Glu Ile Glu
 755 760 765
 Glu Glu Tyr Glu Arg Leu Thr Ala Leu Leu Asp Lys Lys Leu Ala Asn
 770 775 780
 Ile Gly Gln Gly Asn Ser
 785 790

(2) INFORMATIONS POUR LA SEQ ID NO: 999:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 256 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 964941..965708

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 999:

```

Ile Leu Arg Ser Gly Val Tyr Ser Ser Lys Tyr Phe Glu Gly Glu Gly
1      5      10      15
Cys Arg Ser Phe Met Gly Ile Glu Gly Arg Gly Ser Gly Ala Met Gln
      20      25      30
Ser Lys Lys Thr Ile Lys Trp Leu Lys Gln Ala Leu Val Leu Ser Ser
      35      40      45
Ile Val Asn Ile Leu Leu Leu Leu Ile Tyr Ser Thr Val Phe Arg
      50      55      60
Lys Asp Ile Tyr Lys Leu Arg Val Phe Pro Gly Asn Leu Ile Ala Lys
65      70      75      80
Ser Ser Arg Ile Gly Lys Ile Pro Glu Asp Ile Leu Glu Arg Leu Glu
      85      90      95
Asn Ala Ser Phe Ala Asp Leu Leu Ala Leu Leu Xaa Glu Glu Arg Met
      100      105      110
Val Phe Gly His Pro Leu Lys Ser Trp Ala Gln Gly Val Ser Ile Gln
      115      120      125
Lys Tyr Phe Val Asp Ile Ala Pro Met Leu Xaa His Xaa Leu Thr Phe
130      135      140
Ile Lys Leu Lys Ser Pro Glu Arg Thr Trp Leu Leu Pro Asp Ile Asn
145      150      155      160
Asp Gln Glu Phe Thr Arg Ile Cys Gln Tyr Leu Leu Thr Xaa Arg Phe
      165      170      175
Pro Phe Ser Ser Arg Gly Phe Phe Arg Ile Met Val Arg Asp Cys Glu
      180      185      190
Ala Gly Val Val Asp Glu Asp Val Leu Tyr Arg Phe Cys His Leu Pro
195      200      205
Glu Phe Leu Tyr Val Arg Ser Leu Leu Phe Gly Ala Glu Ile Glu Ala
210      215      220
Ala Ser Val Ala Ser Leu Ala Arg Met Ile Ile Gln Gly Gly Glu Asp
225      230      235      240
Leu Phe Phe Ser Leu Cys Cys Leu Glu Asn Arg Gln Thr Ala Asp Phe
      245      250      255

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1000:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 277 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(966193..967023)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1000:

```

Asp Thr Leu Pro Phe Asn Asp Ile Asp Val Ile Ser Thr Met Arg Cys
1      5      10      15
Ser Ala Tyr Cys Thr Ala Ser Ser Tyr His Leu His Val Leu Phe His
20      25      30
Leu Leu Lys Val Asn Tyr Pro Ser Val Leu Ser Arg Glu Tyr Val Leu
35      40      45
Ile Ser Ser Glu Glu Leu Asp Glu Ser Asp Lys Ala Ala Val Phe Phe
50      55      60
Pro Phe Gly Val Cys Val Phe Trp Gly Trp Glu Glu Thr Glu Glu Leu
65      70      75      80
Gln Val Ile Arg Ala Ile Thr Pro Ser Ala Val Asn Pro Leu Pro Asn
85      90      95
Pro Glu Ile Asp Ser Tyr Asp Phe His Tyr Gly Glu Lys Leu Gln Ile
100     105     110
Arg Arg Asp Arg Leu Val Leu Thr Asn Ser Asn Leu Asn Thr Lys Leu
115     120     125
Ala Ile Ser Phe Gly Leu Ala Gln Ser Ile Lys Leu Thr Val Phe Glu
130     135     140
Glu Thr Ile Tyr Lys Thr Val Glu Asn Ser Lys Ser Leu Pro Gln Glu
145     150     155     160
Leu Ala Ser Lys Gly Lys Ile Ser Leu Ser Arg Lys Thr Ile Ala Lys
165     170     175
Lys Ile Gly Glu Leu Phe Leu Asp Lys Ala Ser Val Asn Leu His Ser
180     185     190
Asp Ile Leu Asp Glu Pro Asp Phe Trp Glu His Pro Glu Thr Gln
195     200     205
Pro Phe Tyr Ile Asn Val Leu Thr Cys Leu Asp Val Asn Ala Arg Val
210     215     220
Asn Val Leu Asn His Arg Leu Ala Ile Leu Gly Asp Val Leu Glu Ile
225     230     235     240
Leu Asn Asp Gln Leu Asn His Gln His Ser Ser Ala Leu Glu Trp Thr
245     250     255
Val Ile Trp Leu Ile Ala Leu Glu Val Leu Val Thr Leu Leu Lys Asp
260     265     270
Val Phe Asn Ile Ile
275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1001:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 206 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 967444...968061

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1001:

```

Ser Phe Val Ser Phe Val Met Glu Lys Arg Gly Val Ile Val His Ile
1      5      10      15
Leu Val Cys Leu Leu Thr Ile Phe Gly Thr Leu Ser Leu Pro Ala Phe
20      25      30

```

(2) INFORMATION POUR LA SEQ ID NO: 1002:

(A) LONGUEUR: 280 acides aminés

(D) CONFIGURATION: linéaire

(viii) POSITION DANS LE GENOME: complement(968064..968903)

Arg 1	Lys	Leu	Ser	Ala 5	His	Arg	Phe	Phe	Ile 10	Pro	Lys	Asp	Lys	Asn 15	Ile
Arg	Phe	Leu	Pro 20	Arg	Asp	Ser	Phe	Ile 25	Phe	Ser	Thr	Asp	Glu 30	Leu	Leu
Tyr	Pro	Tyr 35	Ile	Phe	Met	Gln	Ile 40	Thr	Leu	Pro	Gly	Val 45	Val	Leu	Thr
Asn 50	Ser	Pro	Ala	Glu	Lys	Gln 55	His	Val	Ile	Val	Lys 60	Ile	Phe	Ser	Pro
Ala 65	Gly	Leu	Leu	Ser 70	Ala	Phe	Ala	Lys	Asn 75	Gly	Ala	Ser	Leu	Ser	Cys 80
Asp	Phe	Arg	Glu	Ser 85	Leu	Phe	Pro	Ile	Ser 90	Phe	Ser	Leu	Phe	Thr 95	Ile
Gln	Gln	Ser	Pro 100	Pro	Lys	Met	Arg	Lys 105	Val	Ile	Gln	Gly	Glu 110	Leu	Gln
Asn	Pro	Phe 115	Thr	Thr	Ile	Lys	Ser 120	Ser	Tyr	Pro	Leu	Leu 125	Gln	Ser	Ala
Gly	Lys 130	Met	Ile	Gln	Ala	Ile 135	Leu	Lys	Thr	Gln	Trp 140	His	Glu	Lys	Pro
Ser 145	Pro	His	Leu	Phe	Ser 150	Leu	Phe	Phe	Asn 155	Phe	Leu	Gln	Arg	Ile	Pro 160
Glu	Thr	Gln	Tyr	Pro	Asn	Phe	Phe	Ser	Ser	Met	Phe	Leu	Leu	Lys	Leu


```

Lys Lys Val Gly Arg Phe Glu Leu Ala His Gln Gly Thr Leu Leu Leu
225                230                235                240
Asp Glu Ile Thr Glu Ile Pro Ile His Leu Gln Ala Lys Leu Leu Arg
                245                250                255
Ala Ile Gln Glu Gln Glu Phe Xaa His Ile Gly Gly Ile Lys Thr Leu
                260                265                270
Pro Val Asn Ile Arg Phe Leu Ala Thr Ser Asn Arg Asp Leu Glu Glu
                275                280                285
Ala Ile Glu Thr Lys Val Leu Arg Gln Asp Leu Tyr Tyr Arg Leu Ser
                290                295                300
Val Ile Ser Leu His Ile Pro Pro Leu Arg Asp Arg Lys Glu Asp Ile
305                310                315                320
Leu Pro Leu Ala His Tyr Tyr Leu Glu Lys Phe Cys Lys Met Asn Asn
                325                330                335
Lys Pro Pro Lys Thr Leu Ser Leu Glu Ala Gln Arg Asn Leu Leu Asp
                340                345                350
Tyr Ser Trp Pro Gly Asn Val Arg Glu Leu Ser Asn Val Leu Glu Arg
                355                360                365
Thr Val Ile Leu Glu Asn Asp Pro Ala Ile Thr Pro Ser Met Leu Ala
                370                375                380
Leu Leu
385

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1004:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(971024..971806)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1004:

```

Glu Lys Glu Asn Trp Glu Leu Met Pro Lys Ile Asp Thr Cys Asp Ser
1                5                10                15
Cys Val Ser Asn Thr Glu Leu Leu Ala Ile Arg Thr Arg Val Thr Gln
                20                25                30
Ser Tyr Asn Glu Ala Gln Thr Ile Leu Ser Ser Ile Pro Asp Gly Ile
                35                40                45
Phe Leu Leu Ser Glu Ser Gly Glu Ile Leu Ile Cys Asn Pro Gln Ala
                50                55                60
Arg Ala Ile Leu Gly Ile Pro Lys Asp Ile Gln Leu Val Thr Arg Arg
65                70                75                80
Phe His Asp Phe Phe Pro Asp Thr Phe Phe Gly Phe Ser Val Gln Glu
                85                90                95
Ala Leu Glu Lys Glu Val Pro Pro Lys Thr Ile Arg Leu Thr Leu Ser
                100                105                110
Gln Glu Leu Ser Gln Lys Glu Val Glu Val Phe Val Arg Lys Asn Ile
                115                120                125
Ser His Gly Phe Leu Phe Leu Leu Ile Arg Asp Arg Ser Asp Tyr Arg
130                135                140
Gln Leu Glu Gln Ala Ile Glu Lys Tyr Arg Ser Ile Ser Glu Leu Gly
145                150                155                160
Lys Ile Ala Ala Thr Leu Ala His Glu Ile Arg Asn Pro Leu Thr Ser

```



(2) INFORMATIONS POUR LA SEQ ID NO: 1006:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 267 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(973746..974546)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1006:

```

Met Thr Lys Lys Ile Val Leu Gln Ile Ala Tyr Gln Gly Thr Ser Tyr
1      5      10      15
Ser Gly Trp Gln Tyr Gln Pro Asn Ala Leu Ser Ile Gln Glu Val Leu
      20      25      30
Lys Thr Ile Leu Lys Lys Ile Ala Gly Phe Arg Ile Ser Val Ile Ser
      35      40      45
Ser Gly Arg Thr Asp Ala Gly Val His Ala Gln Gly Gln Ile Ala His
      50      55      60
Phe His Cys Pro Asp His Pro His Phe Thr Asp Pro Arg Gln Ile Gln
      65      70      75      80
Lys Met Leu Asn Ala Leu Leu Pro His Asp Ile Val Ile Arg Asp Ala
      85      90      95
Val Met Thr Asp Gly Asp Phe His Ser Arg Phe Ser Ala Ile Ala Lys
      100     105     110
Glu Tyr Arg Tyr Thr Leu Ser Leu Leu Pro Lys Pro Leu Pro His His
      115     120     125
Arg Leu Phe Cys Phe Ser Pro Arg Tyr Lys Leu Asn Ile Ala Arg Met
      130     135     140
Gln Glu Ala Ala Gln Tyr Leu Val Gly Thr His Asp Phe Ala Ser Phe
      145     150     155     160
Ala Asn Leu Gly Arg Glu Tyr Ser Ser Thr Ile Arg Thr Leu Tyr Thr
      165     170     175
Leu Asp Leu Ser Glu Gln Glu His Leu Val Thr Val Ile Cys Arg Gly
      180     185     190
Asn Gly Phe Leu Tyr Lys Met Val Arg Asn Ile Val Gly Ala Leu Leu
      195     200     205
Asp Ile Gly Lys Gly Lys Tyr Pro Pro Glu His Leu Leu Asp Met Leu
      210     215     220
Ala Thr Lys Asp Arg Arg Lys Gly Pro Pro Ser Ala Pro Pro Tyr Gly
      225     230     235     240
Leu Ser Leu His His Val Cys Tyr Pro Pro Pro Tyr Gln Trp Phe Cys
      245     250     255
Lys His Glu His Asn Asn Ser Ser Glu Gly Lys
      260     265

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1007:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 222 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(974558..975223)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1007:

```

Gly Ala Ser Met Asn Leu Ser Cys Ser Leu Val Leu Leu Gly Gly Gly
1      5      10      15
Lys Gly Glu Arg Phe Asn Ser Leu Gln Pro Lys Gln Tyr Thr His Leu
20      25      30
Cys Gly Glu Pro Leu Ile Leu His Ala Leu His Ala Tyr Gln Arg Leu
35      40      45
Pro Phe Val Gln Glu Val Val Val Val Cys Glu Glu Gln Tyr Arg Glu
50      55      60
Leu Phe Leu Pro Tyr Ser Val Lys Phe Ala Ser Pro Gly Thr Leu Arg
65      70      75      80
Gln Asp Ser Val Phe Ser Gly Leu Gln Gln Val Phe Thr Pro Trp Val
85      90      95
Cys Ile His Asp Gly Val Arg Pro Phe Val Tyr Ala Asp Glu Val Ile
100     105     110
Glu Val Cys Ser Ala Ala Arg Lys Thr Gly Ala Ala Ala Leu Ala Ser
115     120     125
Pro Ala Thr Tyr Thr Ile Lys Ser Cys Ala Pro Val Arg Thr Leu Asp
130     135     140
Arg Asp Ala Leu Ala Val Ile His Thr Pro Gln Cys Leu Asp Thr Glu
145     150     155     160
Val Leu Arg Glu Gly Leu Leu Leu Ala Arg Ala Met Asp Phe Ser Leu
165     170     175
Ser Asp Asp Thr Glu Ala Ala Glu Leu Leu Gly Ile Glu Pro Thr Leu
180     185     190
Val Phe Ser Asn Arg Val Gln Ile Lys Val Thr Tyr Pro Glu Asp Leu
195     200     205
Leu Phe Ala Glu Thr Leu Leu Ser Lys Ser Ser Thr Tyr Lys
210     215     220

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1008:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 261 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(975207..975989)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1008:

```

Ala Phe Leu Lys Lys Val Ser Arg Lys Ile Ser Ser Leu Ser Pro Asp
1      5      10      15
Ile Leu Val Phe Thr Gly Asp Phe Val Cys Arg Ala Lys Val Glu Thr
20      25      30
Pro Glu Arg Leu Lys His Phe Leu Cys Ser Leu His Ala Pro Leu Gly
35      40      45
Cys Phe Ala Cys Leu Gly Asn His Asp Tyr Ala Thr Tyr Val Ser Arg
50      55      60
Asp Ile His Gly Lys Ile Asn Thr Ile Ser Ala Met Asn Ser Arg Pro
65      70      75      80

```

```

Leu Lys Arg Ala Phe Thr Ser Val Tyr Gln Ser Leu Phe Ala Ser Ser
      85                      90                      95
Arg Asn Glu Phe Ala Asp Thr Leu Asn Pro Gln Ile Pro Asn Pro His
      100                    105                    110
Leu Val Ser Ile Leu Arg Asn Thr Pro Phe Gln Leu Leu His Asn Gln
      115                    120                    125
Ser Ala Thr Leu Ser Asp Thr Ile Asn Ile Val Gly Leu Gly Asp Phe
      130                    135                    140
Phe Ala Lys Gln Phe Asp Pro Lys Lys Ala Phe Thr Asn Tyr Asn Pro
145                      150                      155                      160
Thr Leu Pro Gly Ile Ile Leu Ser His Asn Pro Asp Thr Ile His His
      165                    170                    175
Leu Gln Asp Tyr Pro Gly Asp Val Val Phe Ser Gly His Ser His Gly
      180                    185                    190
Pro Gln Ile Ser Leu Pro Trp Pro Lys Phe Ala Asn Thr Ile Thr Asn
      195                    200                    205
Lys Leu Ser Gly Leu Glu Asn Pro Glu Leu Ala Arg Gly Leu Phe Ser
      210                    215                    220
Phe Pro Glu Glu Ser Arg Leu Leu Tyr Val Asn Arg Gly Leu Gly Gly
225                      230                      235                      240
Trp Lys Arg Ile Arg Phe Cys Ser Pro Pro Glu Ile Cys Leu Met Arg
      245                    250                    255
Cys Leu Tyr Glu Pro
      260

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1009:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 89 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(976254..976520)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1009:

```

Glu Ser Ser Met Ser Gln Asn Lys Asn Ser Ala Phe Met Gln Pro Val
1      5      10      15
Asn Val Ser Ala Asp Leu Ala Ala Ile Val Gly Ala Gly Pro Met Pro
      20      25      30
Arg Thr Glu Ile Ile Lys Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser
      35      40      45
Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu
      50      55      60
Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr
65      70      75      80
Lys Met Val Ser Gln His Ile Ile Lys
      85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1010:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 104 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 976588..976899

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1010:

Val	Tyr	Arg	Gln	Asn	Lys	Lys	His	Ser	Gln	Val	Phe	Ser	Lys	Lys	Arg
1				5					10					15	
Gly	Lys	Ser	Glu	Leu	Glu	Asn	Asp	Leu	Phe	Leu	Gly	Leu	Leu	Arg	Lys
			20					25					30		
Lys	Leu	Ile	Pro	Lys	Arg	Arg	Ser	Cys	Tyr	His	Glu	Arg	Val	Leu	Ala
		35					40					45			
Val	Thr	Ala	Thr	Val	Ile	Val	Glu	Ile	Thr	Gly	Lys	Glu	Asn	Ser	Ser
50					55					60					
Leu	Lys	Lys	Lys	Ser	Leu	Lys	Leu	Asp	Ile	Leu	Arg	Lys	Val	Ser	Lys
65				70					75					80	
Ile	Met	His	Glu	Asn	Phe	Asp	Lys	Arg	Leu	Glu	Val	Leu	Leu	Glu	Gly
			85					90						95	
Leu	Ala	Leu	Thr	Arg	Arg	Ser	Leu								
			100												

(2) INFORMATIONS POUR LA SEQ ID NO: 1011:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 976886..977635

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1011:

Leu	Gly	Gly	Leu	Phe	Asp	Pro	Glu	Gly	Lys	Glu	Asn	Glu	Leu	Lys	Glu
1			5					10						15	
Leu	Glu	Gln	Gln	Ala	Val	Gln	Asp	Gly	Phe	Trp	Asp	Asp	Val	Ala	Arg
		20						25					30		
Ala	Gly	Lys	Ile	Ser	Glu	Arg	Ile	Ala	Arg	Leu	Lys	Gln	Gln	Leu	Ser
		35					40					45			
Glu	Phe	Asn	Glu	Leu	Lys	Asn	Lys	Val	Ser	Thr	Ile	Gln	Phe	Phe	Leu
50					55					60					
Glu	Asp	Glu	Glu	Ser	Ser	Lys	Asp	Leu	Glu	Met	Gln	Lys	Glu	Leu	Glu
65				70					75					80	
Lys	Glu	Phe	Val	Phe	Cys	Glu	Lys	Lys	Ile	Thr	Glu	Trp	Glu	Thr	Leu
			85					90						95	
Arg	Leu	Leu	Ser	Gly	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Phe	Leu	Ser	Ile
		100						105					110		
Asn	Ala	Gly	Ala	Gly	Gly	Thr	Glu	Ser	Cys	Asp	Trp	Val	Glu	Met	Cys
		115					120					125			
Cys	Ala	Cys	Ile	Cys	Asp	Gly	Leu	Val	Val	Ile	Ser	Trp	Arg	Val	Glu
		130				135				140					
Val	Ile	Asp	Arg	Leu	Asp	Gly	Glu	Val	Ala	Gly	Ile	Lys	His	Ile	Thr
145					150					155					160

```

Leu Lys Leu Val Gly Glu Tyr Ala Tyr Gly Tyr Ala Lys Ala Glu Ser
                      165                      170                      175
Gly Val His Arg Leu Val Arg Ile Ser Pro Phe Asp Ser Asn Ala Lys
                      180                      185                      190
Arg His Thr Ser Phe Ala Ser Val Glu Val Phe Pro Glu Ile Asp Asp
                      195                      200                      205
Lys Ile Glu Val Glu Ile His Pro Gly Asp Ile Arg Ile Asp Thr Tyr
                      210                      215                      220
Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn Val Thr Asp Ser Ala
225                      230                      235                      240
Val Arg Ile Thr Gln Xaa Leu Arg Glu Leu
                      245                      250

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1012:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 91 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 977661..977933

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1012:

```

Ser Asn Ser Lys Pro Arg Ser Leu Tyr Glu Tyr Leu Arg Ala Arg Ile
1                      5                      10                      15
Tyr Gln Lys Leu Gln Glu Arg Leu Glu Lys Gln Asn Ile Asp Arg
                      20                      25                      30
Lys Asn Lys Lys Glu Ile Ser Trp Gly Ser Gln Ile Arg Asn Tyr Val
                      35                      40                      45
Phe Gln Pro Tyr Thr Leu Val Lys Asp Val Arg Thr Gly Tyr Glu Val
                      50                      55                      60
Gly Asn Ile Gln Ala Met Met Asp Gly Glu Leu Leu Asp Ala Phe Ile
65                      70                      75                      80
Lys Ala Tyr Leu Val Asp Tyr Gly Glu Ile Thr
                      85                      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1013:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 172 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 977918..978433

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1013:

```

Leu Trp Arg Asn Tyr Met Thr Thr Met Arg Asp Pro Leu Leu Glu Ile
1                      5                      10                      15
Arg Tyr Thr Val Pro Glu Asp Ala His Tyr Met Arg Leu Trp Leu Asn

```

(2) INFORMATION POUR LA SEQ ID NO: 1014:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 122 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 978619..978984

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1014:

(2) INFORMATION POUR LA SEQ ID NO: 1015:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 133 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 978933..979331

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1015:

```

Glu Pro His Ser Leu Gly Tyr Ala Arg Thr Val Asn Lys Arg Gly Gly
1          5          10          15
Ala Leu Val Glu Pro Gly Ser Val Leu Tyr Asn Phe Ser Arg Lys Gly
20          25          30
Ala Cys Tyr Val Pro Lys His Ser Ile Asp Glu Ala Ser Leu Leu Thr
35          40          45
His Val Ile Asp Cys Gly Gly Glu Asp Leu Asp Ser Asp Asp Glu Glu
50          55          60
Phe Phe Leu Val Leu Cys Glu Pro Thr Asp Leu Ala Ser Val Lys Glu
65          70          75          80
Ala Leu Leu Ala Lys Gly Val Thr Cys Ser Glu Glu Arg Leu Ile Tyr
85          90          95
Val Pro Leu Arg Leu Val Asp Cys Asp Glu Glu Thr Gly Lys Ser Asn
100         105         110
Leu Ala Leu Ile Glu Trp Leu Glu Asn Ile Asp Asp Val Asp Asp Val
115         120         125
Tyr His Asn Met Ala
130

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1016:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 603 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(979389..981197)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1016:

```

Val Thr Gln Lys Ile Arg Val Val Val Gln Gln Gln His Ser Ile Leu
1          5          10          15
Tyr Arg Gly Ser Ser Tyr Thr Thr Gly Pro Arg Asn Glu Gly Val Phe
20          25          30
Gly Pro Gly Pro Glu Gly Leu Pro Asp Met Ser Leu Pro Ser Tyr Asp
35          40          45
Pro Thr Asn Lys Thr Ser Leu Leu Thr Phe Leu Ser Asn Pro His Val
50          55          60
Lys Xaa Lys Met Leu Glu Asn Ser Gly His Phe Val Phe Ile Asp Thr
65          70          75          80
Asp Arg Ser Ser Phe Ile Leu Val Pro Asn Gly Asn Trp Asp Gln Val
85          90          95
Cys Ser Ile Lys Val Gln Asn Gly Lys Thr Lys Glu Asp Leu Asp Ile
100         105         110
Lys Asp Leu Glu Asn Met Cys Ala Lys Phe Cys Thr Gly Phe Asn Lys
115         120         125
Phe Ser Gly Asp Trp Asp Ser Arg Val Glu Pro Met Met Ser Ala Lys

```

130 135 140
 Ala Gly Val Ala Ser Gly Gly Asn Leu Pro Asn Thr Val Ile Ile Asn
 145 150 155 160
 Asn Lys Phe Lys Thr Cys Val Ala Tyr Gly Pro Trp Asn Ser Arg Glu
 165 170 175
 Ala Ser Ser Gly Tyr Thr Pro Ser Ala Trp Arg Arg Gly His Gln Val
 180 185 190
 Asn Phe Gly Glu Ile Phe Glu Lys Ala Asn Asp Phe Asn Lys Ile Asn
 195 200 205
 Trp Gly Thr Gln Ala Gly Pro Ser Ser Glu Asp Asp Gly Ile Ser Phe
 210 215 220
 Ser Asn Glu Thr Pro Gly Ala Gly Pro Ala Ala Ala Pro Ser Pro Thr
 225 230 235 240
 Pro Ser Ser Ile Pro Val Ile Asn Val Asn Val Asn Val Gly Gly Thr
 245 250 255
 Asn Val Asn Ile Arg Asp Thr Asn Val Asn Thr Thr Asn Thr Thr Pro
 260 265 270
 Thr Thr Gln Ser Thr Asp Ala Ser Thr Asp Thr Ser Asp Ile Asp Asn
 275 280 285
 Ile Asn Thr Asn Asn Gln Thr Asp Asp Ile Asn Thr Thr Asp Lys Asp
 290 295 300
 Ser Asp Gly Ala Gly Gly Val Asn Gly Asp Ile Ser Glu Thr Glu Ser
 305 310 315 320
 Ser Ser Gly Asp Asp Ser Gly Ser Val Ser Ser Ser Glu Ser Asp Lys
 325 330 335
 Asn Ala Ser Val Gly Asn Asp Gly Pro Ala Met Lys Asp Ile Leu Ser
 340 345 350
 Ala Val Arg Lys His Leu Asp Val Val Tyr Pro Gly Asp Asn Gly Gly
 355 360 365
 Ser Thr Glu Gly Pro Leu Gln Ala Asn Gln Thr Leu Gly Asp Ile Val
 370 375 380
 Gln Asp Met Glu Thr Thr Gly Thr Ser Gln Glu Thr Val Val Ser Pro
 385 390 395 400
 Trp Lys Gly Ser Thr Ser Ser Thr Gly Ser Ala Gly Gly Ser Gly Ser
 405 410 415
 Val Gln Thr Leu Leu Pro Ser Pro Pro Pro Thr Pro Ser Thr Thr Thr
 420 425 430
 Leu Arg Thr Gly Thr Gly Ala Thr Thr Thr Ser Leu Met Met Gly Gly
 435 440 445
 Pro Ile Lys Ala Asp Ile Ile Thr Thr Gly Gly Gly Arg Ile Pro
 450 455 460
 Gly Gly Gly Thr Leu Glu Lys Leu Leu Pro Arg Ile Arg Ala His Leu
 465 470 475 480
 Asp Ile Ser Phe Asp Gly Gln Gly Asp Leu Val Ser Thr Glu Glu Pro
 485 490 495
 Gln Leu Gly Ser Ile Val Asn Lys Phe Arg Lys Glu Thr Gly Ser Gly
 500 505 510
 Gly Ile Val Ala Ser Val Glu Ser Ala Pro Gly Lys Pro Gly Ser Ala
 515 520 525
 Gln Val Leu Thr Gly Thr Gly Gly Asp Lys Gly Asn Leu Phe Gln Ala
 530 535 540
 Ala Ala Ala Val Thr Gln Ala Leu Gly Asn Val Ala Gly Lys Val Asn
 545 550 555 560
 Leu Ala Ile Gln Gly Gln Lys Leu Ser Ser Leu Val Asn Asp Asp Gly
 565 570 575
 Lys Gly Ser Val Gly Arg Asp Leu Phe Gln Ala Ala Thr Gln Thr Thr
 580 585 590
 Gln Ala Leu Ser Ser Leu Ile Asp Thr Val Gly
 595 600

(2) INFORMATIONS POUR LA SEQ ID NO: 1017:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 134 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 979711..980112

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1017:

Gly	Ser	Ser	Val	Leu	Thr	Arg	Ser	Pro	Cys	Pro	Ser	Lys	Asp	Met	Ser
1				5					10					15	
Lys	Cys	Ala	Arg	Ile	Arg	Gly	Ser	Ser	Phe	Ser	Asn	Val	Pro	Pro	Pro
			20					25					30		
Gly	Ile	Arg	Pro	Pro	Pro	Pro	Val	Val	Ile	Met	Ser	Ala	Leu	Ile	Gly
			35				40					45			
Pro	Pro	Ile	Ile	Lys	Asp	Val	Val	Val	Ala	Pro	Val	Pro	Val	Leu	Asn
			50			55					60				
Val	Val	Val	Asp	Gly	Val	Gly	Gly	Gly	Glu	Gly	Ser	Ser	Val	Cys	Thr
65					70					75					80
Leu	Pro	Leu	Pro	Pro	Ala	Asp	Pro	Val	Glu	Glu	Val	Leu	Pro	Phe	His
				85					90					95	
Gly	Asp	Thr	Thr	Val	Ser	Trp	Asp	Val	Pro	Val	Val	Ser	Ile	Ser	Trp
			100					105					110		
Thr	Ile	Ser	Pro	Arg	Val	Trp	Leu	Ala	Trp	Arg	Gly	Pro	Ser	Val	Glu
			115				120						125		
Pro	Pro	Leu	Ser	Pro	Gly										
															130

(2) INFORMATIONS POUR LA SEQ ID NO: 1018:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 323 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(981148..982116)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1018:

Phe	Val	Val	Met	Thr	Asn	Ser	Ile	Ser	Gly	Asp	Gln	Pro	Thr	Val	Thr
1				5					10					15	
Thr	Phe	Thr	Ser	Ser	Thr	Thr	Ser	Ala	Ser	Gly	Ala	Ser	Gly	Ser	Leu
			20					25					30		
Gly	Ala	Ser	Ser	Val	Ser	Thr	Thr	Ala	Asn	Ala	Thr	Val	Thr	Gln	Thr
			35					40				45			
Ala	Asn	Ala	Thr	Asn	Ser	Ala	Ala	Thr	Ser	Ser	Ile	Gln	Thr	Thr	Gly
			50			55					60				
Glu	Thr	Val	Val	Asn	Tyr	Thr	Asn	Ser	Ala	Ser	Ala	Pro	Thr	Val	Thr

```

65              70              75              80
Val Ser Thr Ser Ser Ser Ser Thr Gln Ala Thr Ala Thr Ser Asn Lys
              85              90
Thr Ser Gln Ala Val Ala Gly Lys Ile Thr Ser Pro Asp Thr Ser Glu
              100              105              110
Ser Ser Glu Thr Ser Ser Thr Ser Ser Ser Asp His Ile Pro Ser Asp
              115              120              125
Tyr Glu Pro Ile Ser Thr Thr Glu Asn Ile Tyr Glu Asn Ile Tyr Glu
              130              135              140
Ser Ile Asp Asp Ser Ser Thr Ser Gly Pro Glu Asn Thr Ser Gly Gly
145              150              155              160
Ala Ala Ala Leu Asn Ser Leu Arg Gly Ser Ser Tyr Ser Asn Tyr Asp
              165              170              175
Asp Ala Ala Ala Asp Tyr Glu Pro Ile Ser Thr Thr Glu Asn Ile Tyr
              180              185              190
Glu Ser Ile Asp Asp Ser Ser Thr Ser Asp Pro Glu Asn Thr Ser Gly
              195              200              205
Gly Ala Ala Ala Leu Asn Ser Leu Arg Gly Ser Ser Tyr Ser Asn Tyr
              210              215              220
Asp Asp Ala Ala Ala Asp Tyr Glu Pro Ile Ser Thr Thr Glu Asn Ile
225              230              235              240
Tyr Glu Asn Ile Tyr Glu Ser Ile Asp Asp Ser Ser Thr Ser Gly Pro
              245              250              255
Glu Asn Thr Ser Gly Gly Ala Ala Ala Leu Asn Ser Leu Arg Gly Ser
              260              265              270
Ser Tyr Ser Asn Tyr Asp Asp Ala Ala Ala Asp Tyr Glu Pro Ile Ser
              275              280              285
Thr Thr Glu Ser Ile Tyr Glu Asn Ile Tyr Glu Ser Ile Asp Gly Ser
              290              295              300
Ser Ile Ser Asp Pro Glu Asn Thr Ser Gly Gly Ala Ala Ala Ala Leu
305              310              315              320
Asn Ser Leu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1019:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 426 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 982321..983598

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1019:

```

Met Pro Gly Ile Lys Val Phe Gly Glu Thr Val Leu Arg Gly Ser Val
1              5              10              15
Arg Val Ser Gly Ala Lys Asn Ala Thr Thr Lys Leu Leu Val Ala Ser
              20              25              30
Leu Leu Ser Asp Gln Arg Thr Ile Leu Lys Asn Val Pro Asn Ile Glu
              35              40              45
Asp Val Arg Gln Thr Val Asp Leu Cys Arg Val Leu Gly Ala Ile Val
50              55              60
Glu Trp Asp Gln Gln Ala Gln Val Ile Glu Ile His Thr Pro Arg Ile
65              70              75              80

```

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1020:

Trp Arg Ile Gln Leu Arg Asn Asn Arg Cys Arg Ser Tyr Ala Tyr Arg
 1 5 10 15
 Ile Gln Gln Asp Gln Ala Asp Arg Ile Leu Ile Val Thr Asp Ser Gly
 20 25 30
 Gln Ser Leu His Phe Gln Leu Leu Glu Ala Thr Cys Leu Ala Ala Gly
 35 40 45
 Tyr Leu Pro Ser Lys Gly Ile Phe Ser His Val Gly Phe Gly Leu Val
 50 55 60
 Leu Asp Thr Gln Gly Arg Lys Phe Lys Thr Arg Ser Gly Glu Asn Ile
 65 70 75 80
 Lys Leu Arg Glu Leu Leu Asp Thr Ala Val Glu Lys Ala Lys Glu Ser
 85 90 95
 Leu Lys Ala His Arg Pro Asp Ile Ser Glu Glu Glu Leu Ala Tyr Gln
 100 105 110
 Gly Pro Ile Leu Gly Ile Asn Ala Ile Lys Tyr Ala Asp Leu Ser Ser
 115 120 125
 His Arg Ile Asn Asp Tyr Val Phe Ser Phe Glu Lys Met Leu Arg Phe
 130 135 140
 Glu Gly Asn Thr Ala Met Ser Leu Leu Tyr Ala Tyr Val Arg Ile Gln
 145 150 155 160
 Gly Ile Lys Arg Arg Met Gly Leu Glu Ser Leu Pro Gln Glu Gly Pro
 165 170 175
 Leu Ala Ile His Glu Pro Ala Glu Glu Ala Leu Xaa Leu Leu Phe Tyr
 180 185 190
 Val Ser Leu Lys Phe Trp Thr Ser Pro Ser Glu Asn Ser Val Leu Xaa
 195 200 205
 Ser

(2) INFORMATIONS POUR LA SEQ ID NO: 1021:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 337 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(984371..985381)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1021:

Met Thr Thr Leu Leu Ser Phe Leu Thr Ser Leu Cys Ser Ala Ala Ile
 1 5 10 15
 His Gln Ala Phe Pro Glu Leu Glu Glu Leu Thr Leu Asp Ile Thr Pro
 20 25 30
 Ser Thr Lys Glu His Phe Gly His Tyr Gln Cys Asn Asp Ala Met Lys
 35 40 45
 Leu Ala Arg Val Leu Arg Lys Ser Pro Arg Ala Ile Ala Glu Ser Ile
 50 55 60
 Val Ala His Ile Pro Pro Ala Pro Phe Ser Ser Ile Glu Ile Ala Gly
 65 70 75 80
 Ala Gly Phe Ile Asn Phe Thr Phe Ser Lys Glu Phe Leu Ala Ser Gln
 85 90 95
 Leu Gln Thr Phe Ser Lys Glu Leu Ala Asn Gly Phe Arg Ala Ala Ser
 100 105 110

```

Pro Gln Lys Val Ile Ile Asp Phe Ser Ser Pro Asn Ile Ala Lys Asp
      115                      120                      125
Met His Val Gly His Leu Arg Ser Thr Ile Ile Gly Asp Cys Leu Ala
      130                      135                      140
Arg Cys Phe Ser Phe Val Gly His Asp Val Leu Arg Leu Asn His Ile
      145                      150                      155                      160
Gly Asp Trp Gly Thr Ala Phe Gly Met Leu Ile Thr Tyr Leu Gln Glu
      165                      170                      175
Thr Ser Gln Glu Ala Ile His Gln Leu Glu Asp Leu Thr Ala Leu Tyr
      180                      185                      190
Lys Lys Ala His Ala Arg Phe Ala Glu Asp Ser Glu Phe Lys Lys Arg
      195                      200                      205
Ser Gln His Asn Val Val Ala Leu Gln Ser Gly Asp Ala Gln Ala Leu
      210                      215                      220
Ala Leu Trp Ile Gln Ile Cys Ser Val Ser Glu Lys Ser Phe Gln Thr
      225                      230                      235                      240
Ile Tyr Ser Ile Leu Asp Val Glu Leu His Thr Arg Gly Glu Ser Phe
      245                      250                      255
Tyr Asn Pro Phe Leu Ala Glu Val Val Ala Asp Leu Glu Ser Lys Asn
      260                      265                      270
Leu Val Thr Leu Ser Asp Gly Ala Lys Cys Val Phe His Glu Ala Phe
      275                      280                      285
Ser Ile Pro Leu Met Ile Gln Lys Ser Asp Gly Gly Tyr Asn Tyr Ala
      290                      295                      300
Thr Thr Asp Val Ala Ala Met Pro Ile Ala Ser Asn Lys Ile Arg Pro
      305                      310                      315                      320
Ile Glu Phe Leu Ser Leu Gln Thr Gln Asp Asn Pro Tyr Thr Ser Ser
      325                      330                      335
Phe

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1022:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 235 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(985399..986103)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1022:

```

Phe Asp Asn Lys Pro Asn Ser Gly Glu Asn Pro Thr Phe Asp Thr Leu
1      5      10      15
Pro Phe Asn Met Ile Phe Thr Ile Ala Lys Ser Leu Val Arg Leu Leu
      20      25      30
Phe Pro Leu Phe Tyr Arg Arg Lys Ile Leu Arg Ser Lys Ala Ser Ala
      35      40      45
Thr Val Lys Gly Ala Ala Ile Ile Ala Ala Asn His Val Ser Phe Leu
      50      55      60
Asp Pro Ile Ile Ile Pro Leu Ala Phe Pro Gly Lys Leu Tyr Gln Leu
      65      70      75      80
Ala Lys Ser Gly Leu Phe Ser Asn Ser Phe Thr Asn Arg Leu Phe Arg
      85      90      95
Glu Leu Gly Cys Tyr Pro Ile Ser Arg Asn Ala Gly Asn Ala Ala Ala

```

```

          100          105          110
Phe Lys Ala Ala Leu Asn Ile Phe Ser His Gly Gly Arg Leu Ile Ile
          115          120          125
Tyr Pro Glu Gly Thr Arg His Ala Asp Gly Glu Ile His Gln Gly Lys
          130          135          140
Val Gly Val Gly Met Leu Ala Ile Lys Gly Asn Val Pro Val Ile Pro
145          150          155          160
Val Tyr Val Ala Gly Thr Phe Glu Ala Phe Gly Lys Asn Gln Lys Phe
          165          170          175
Pro Lys Leu Trp Arg Thr Leu Thr Thr Val Ile Gly Ser Pro Ile Ser
          180          185          190
Phe Gln Asp Leu Ile Asp Asn Pro Ala Ile Asp Lys Lys Glu Ala Tyr
          195          200          205
Gln Leu Ala Thr Asp Arg Ile Met Thr Lys Ile Thr Glu Leu Arg Thr
          210          215          220
Trp Phe Gln Gln Gly Cys Ile Gly Glu Ile Pro
225          230          235

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1023:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 216 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(986046..986693)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1023:

```

Met Ile Ile Thr Ile Asp Gly Pro Ser Gly Thr Gly Lys Ser Thr Leu
1          5          10          15
Ala Lys Ala Leu Ala Gln Thr Leu Gln Phe Leu Tyr Cys Asn Thr Gly
          20          25          30
Ala Met Tyr Arg Thr Leu Ala Tyr Ala Arg Leu Gln Pro Asp Trp Gln
          35          40          45
Glu Val Pro Leu Glu Asp Phe Leu Ala Ser Pro Pro Phe Ser Phe Ser
          50          55          60
Phe Ser Lys Asp Ser Pro Leu Gln Ala Phe Tyr Gly Asp Arg Leu Leu
65          70          75          80
Thr Ser Glu Leu Ser Ser Gln Glu Val Ala Asn Phe Ala Ser Leu Phe
          85          90          95
Ser Lys Glu Pro Leu Val Arg Ala Tyr Met Gln Thr Leu Gln Lys Gln
          100          105          110
Tyr Ala Thr Val Gly Asn Cys Val Phe Glu Gly Arg Asp Met Gly Ser
          115          120          125
Lys Val Phe Pro His Ala Glu Val Lys Ile Phe Leu Thr Ala Lys Pro
          130          135          140
Glu Ile Arg Ala Glu Arg Leu Lys Asp Leu Pro Gln Gly Ser Leu
145          150          155          160
Pro Lys Glu Ala Leu Met Ala Glu Leu Ile Ala Arg Asp Gln Ala Asp
          165          170          175
Gln Gln Arg Glu Cys Asp Pro Leu Val Ile Pro Gln Asp Ala Ile Val
          180          185          190
Ile Asp Ser Ser Asp Leu Thr Ile Ser Gln Ile Leu Glu Lys Ile Leu
195          200          205

```

[illegible]

(2) INFORMATIONS POUR LA SEQ ID NO: 1025:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 168 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(987616..988119)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1025:

Ile Glu Ile Gly Ser Arg Arg Ile Ile Phe Phe Ile Gln Leu Ala Val
 1 5 10 15
 Ala Gln Xaa Leu Ser Phe Leu His Asp Arg Glu Ile Arg Leu Arg Cys
 20 25 30
 Ile Gly Asp Leu Ser Lys Leu Pro Gln Glu Leu Gln Asn Asn Ile Glu
 35 40 45
 Gln Ala Ser Ser Ala Thr Ala His Tyr Ser Arg Met Glu Leu Ile Phe
 50 55 60
 Ala Ile Asn Tyr Gly Ser Lys Asp Glu Leu Val Arg Ala Phe Lys Glu
 65 70 75 80
 Leu His Gln Asp Leu Ala Ser Lys Lys Ile Ser Val Asn Asp Ile Ser
 85 90 95
 Glu Glu Leu Ile Ser Ser Tyr Leu Asp Thr Ser Gly Leu Pro Asp Pro
 100 105 110
 Asp Leu Leu Ile Arg Thr Gly Gly Glu Met Arg Val Ser Asn Phe Leu
 115 120 125
 Leu Trp Gln Ile Ala Tyr Thr Glu Leu Tyr Val Thr Asp Val Leu Trp
 130 135 140
 Pro Asp Phe Thr Ala Asn Asp Leu Leu Glu Ala Ile Lys Thr Tyr Gln
 145 150 155 160
 Gln Arg Ser Arg Arg Gly Gly Lys
 165

(2) INFORMATIONS POUR LA SEQ ID NO: 1026:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 106 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(987936..988253)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1026:

Thr Ile Leu Ser Glu Thr Cys Tyr Ile Trp Pro Pro Ser Gly Ala Asp
 1 5 10 15
 Ser Ile Pro Gln Ile Val Asp Thr Ala Leu His Leu Gly Val Glu Ala
 20 25 30
 Leu Thr Leu Phe Ala Phe Ser Thr Glu Asn Phe Ser Arg Ser Lys Ser
 35 40 45


```

Glu Val Ala Glu Leu Phe Ser Leu Phe Asn Ser Gln Leu Arg Arg Xaa
  50                      55                      60
Ser Leu Ser Tyr Met Ile Gly Arg Ser Asp Tyr Gly Val Leu Ala Thr
65                      70                      75                      80
Tyr Arg Asn Phe Leu Lys Asn Tyr Lys Thr Thr Leu Ser Lys Pro Pro
                      85                      90                      95
Pro Arg Gln Leu Ile Thr Pro Ala Trp Ser
          100                      105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1027:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 988831..989163

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1027:

```

Asp Met Lys Leu Pro Glu Val Ser Phe Ser Leu Pro Thr Ala Val Trp
1                      5                      10                      15
Ala Ser Ser Thr Lys Arg Leu Ser Gln Glu Lys Glu Phe Ser Ser Leu
20                      25                      30
Asp Arg Val Gln Ser Met Asn Trp Val Gln Arg Ile Val Pro Ser Leu
35                      40                      45
Ile Val Leu Leu Gly Ile Ser Val Leu Gly Cys Ser Val Leu Ala Phe
50                      55                      60
Cys Thr Cys Leu Thr Val Leu Pro Gly Leu Gly Leu Val Ile Leu Gly
65                      70                      75                      80
Ser Leu Leu Leu Tyr Trp Ala Tyr His Gln Ile Ala Asn Met Arg Val
85                      90                      95
Arg Met Ala Leu Ser Phe Glu Ala Ser Ser Glu Ala Pro Ile Gln
          100                      105                      110

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1028:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1250 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 989693..993442

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1028:

```

Xaa Xaa Xaa Trp Thr Arg Gly Ser Gln Asp Tyr Arg Xaa Phe Thr Arg
1                      5                      10                      15
Gln Val Ser Asp Ala Arg Asn Asp Leu Thr Leu Arg Val Ala Lys Ile
20                      25                      30
Leu Ser Thr Leu Lys Leu Arg Gly Asp Ile Lys Xaa His Pro Ser Ile

```

35 40 45
 Pro Gly Ile Val Asn Val His Phe Pro Leu Ala Glu Asp Ala Ala Leu
 50 55 60
 Phe Ile Asp Asn Val Val His Gly Glu Pro Ser Val Pro Val Lys Ser
 65 70 75 80
 Ala Arg Leu Tyr Val Val Gly Ser Ser Glu Phe Thr Gly Glu Thr Val
 85 90 95
 Val Gln Ile Ser Gly Ser Leu Val Thr Ser Leu Thr Glu Glu Asp Leu
 100 105 110
 Ser Phe Val Ser Tyr Glu Asp Lys Asp Val Thr Val Ser Gln Glu Leu
 115 120 125
 Glu Asn Leu Ala Thr Asn Leu Phe Ile Glu Ser Glu Arg Pro Cys Glu
 130 135 140
 Cys Gly Tyr Tyr Ser Leu Trp Asp Ser Met Pro Ile Glu Lys Val Ile
 145 150 155 160
 His Val Thr Arg Asn Ile Cys Ser Gly Leu Arg Leu Leu Pro Thr Arg
 165 170 175
 Lys Thr Gln Val Phe Leu Ser Arg Cys Leu Gly Thr Glu Arg Asp Phe
 180 185 190
 Thr Ala Phe Leu Ala Arg Leu Glu Lys Ala Leu Gln His Glu Glu Val
 195 200 205
 Lys Glu Ala Arg Glu Glu Leu Lys Asp Ala Ser Tyr Leu Leu His Ser
 210 215 220
 Arg Asn Leu Arg Trp Asn Ser Ile Ser Pro Lys Val Val Gly Asn Val
 225 230 235 240
 Val Asp Cys Ser Glu Leu Ser Pro Cys Phe Ser Ser Met Ser Leu Thr
 245 250 255
 Ala Asp Gly Lys Leu Leu Phe His Phe Asp Ala Glu Val Ala Ala Asn
 260 265 270
 Arg Gln Gln Leu Val Gly Asn Glu Arg Leu Asp Leu Glu Arg Leu Phe
 275 280 285
 Ala Met Glu Lys Gln His Ile Ala Thr Arg Leu Asn Arg Ser Val Glu
 290 295 300
 Glu Thr Glu Phe Gly Phe Ala Val Arg Leu Arg Asp Glu Ala Ala Ser
 305 310 315 320
 Gly Lys Ile Val Leu Gln Gly His Arg Val Cys Gln Arg Ile Val Glu
 325 330 335
 His Leu Thr Ala Leu Val Leu Asn Arg Pro Leu Ala Glu Thr Cys Asp
 340 345 350
 Leu Ser Thr Glu Asn Phe Pro Val Tyr Gly Arg Glu Pro Leu Asp Ser
 355 360 365
 Asp Ala Leu Gly Cys Phe Ile Phe Ser Pro Glu Arg Ser Cys Arg His
 370 375 380
 Phe Ser Lys Gly Ser Val Tyr Ile Val Phe Lys Gly Leu Arg Ser Ile
 385 390 395 400
 Val Ala Lys Tyr Glu His Ala Gly Ala Glu Glu Ala Ala Leu Leu Gln
 405 410 415
 His Asp Leu Gln Asn Leu Tyr Ala Cys Phe Ile His Thr Asp Ala Val
 420 425 430
 Ser Trp Ser Leu Gly Glu Asp Arg Val Leu Glu Ile Lys Glu Pro Leu
 435 440 445
 Gln Arg Val Ile Arg Ile Trp Gly Glu Glu Phe Val Gln Ser Phe Gly
 450 455 460
 Lys Ala Ser Leu Glu Val Arg Asp Val Arg Asp Arg Leu Ala Val Val
 465 470 475 480
 Asn Arg Ile Glu Lys Thr Gln His Ala Glu Leu Val Arg Trp Asp Glu
 485 490 495
 Gln Tyr Arg Gln Ala Gln Cys Ser Met Asn Pro Gln Val Arg Leu Arg
 500 505 510

Ala	Ala	Ile	Pro	His	Lys	Asn	Val	Phe	Phe	Glu	Asn	Leu	Lys	Leu	Asn
		515					520					525			
Ile	Arg	Lys	Tyr	Ser	Arg	Gly	Glu	His	Val	Leu	Arg	Phe	Gly	Thr	Asp
	530					535					540				
Phe	Val	Gly	Gly	Lys	Gln	Ile	Arg	Ile	Ala	Phe	Arg	Asp	His	Gln	Gly
545					550					555					560
Asn	Leu	Leu	Thr		Lys	Ala	Gly	Ile	Asp	Lys	Val	Ser	Asp	Glu	Leu
				565					570					575	
Tyr	Ala	Arg	Leu	Asn	Lys	Leu	Gly	Val	Ser	Glu	Val	Gly	Met	Gln	Arg
			580					585					590		
Glu	Gly	Asp	His	Ile	Gln	Val	Ser	Val	Pro	Gly	Ala	Ala	Gly	Ile	Ser
		595					600					605			
Ser	Ala	Asp	Ile	Leu	Gly	Thr	Ser	Lys	Met	Ser	Phe	His	Val	Val	Asn
	610					615					620				
Glu	Gln	Phe	Ser	Ser	Arg	Ser	Pro	Leu	Arg	Tyr	Glu	Val	Gln	Thr	Phe
625					630					635					640
Leu	Asp	Tyr	Leu	Trp	Phe	Thr	Ala	Arg	Ser	Leu	Asp	Glu	Cys	Ser	Pro
				645					650					655	
Gln	Ala	Ile	Asn	Arg	Leu	Ala	Gly	Ala	Leu	Phe	His	Gly	Asp	Asn	Gly
			660					665					670		
Ser	Ala	Pro	Ala	Asn	Val	Arg	Val	Ala	Val	Glu	Lys	Leu	Arg	Glu	Ala
		675					680					685			
Gly	Leu	Ser	Phe	Ser	Lys	Glu	Leu	Glu	Gly	Gly	Ser	Ala	Ser	Leu	Asp
	690					695					700				
Thr	Gln	Tyr	Ser	Met	Ile	Ala	Ile	Glu	Lys	Glu	Ser	Arg	Glu	Gln	Val
705					710					715					720
Asn	Pro	Leu	Met	Ile	Val	Phe	Arg	Asn	His	Ala	Leu	Glu	Gly	Ala	Ser
				725					730					735	
Leu	Lys	Asn	Ile	Arg	Pro	Glu	Phe	Ala	Val	Gly	Glu	Gly	Tyr	Val	Leu
			740					745					750		
Asn	Phe	Gly	Val	Lys	Asp	Lys	Ala	Thr	Phe	Ser	Asp	Gly	Arg	Glu	Thr
		755					760					765			
Pro	Val	Gln	Gln	Phe	His	Ala	Trp	Thr	Ser	Lys	Phe	Cys	Gln	Glu	Gly
		770				775					780				
Val	Ser	Gly	Thr	Lys	Asn	Gly	Leu	Phe	Ser	Gly	Gly	Arg	Gly	Trp	Arg
785					790					795					800
Met	Ala	Val	Val	Leu	Asp	Gly	Tyr	Val	Ile	Ser	Asp	Pro	Val	Leu	Asn
				805					810					815	
Val	Pro	Leu	Lys	Asp	His	Ala	Ser	Val	Ser	Gly	Xaa	Phe	Ser	Tyr	Arg
			820					825					830		
Glu	Val	His	Arg	Leu	Ala	Thr	Asp	Leu	Lys	Ser	Gly	Ala	Met	Ser	Phe
		835					840					845			
Ile	Pro	Glu	Ile	Leu	Ser	Glu	Glu	Val	Val	Ser	Pro	Glu	Leu	Gly	Ser
	850					855					860				
Ser	Gln	Arg	Val	G											

980 985 990
 Gly Phe Ala Leu Thr Leu Ile Ile Gly Ile Phe Ser Ser Met Phe Thr
 995 1000 1005
 Ala Leu Phe Met Thr Lys Phe Phe Phe Val Ile Trp Val Gln Lys Thr
 1010 1015 1020
 Arg Glu Thr Gln Leu His Met Met Asn Lys Phe Ile Gly Ile Lys His
 1025 1030 1035 1040
 Asn Phe Leu Lys Glu Cys Lys Arg Leu Trp Val Val Ser Gly Val Val
 1045 1050 1055
 Leu Val Leu Gly Cys Val Gly Leu Gly Phe Gly Ala Trp Asp Ser Val
 1060 1065 1070
 Phe Gly Met Asp Phe Lys Gly Gly Tyr Ala Leu Thr Leu Asp Ser Asp
 1075 1080 1085
 Val Cys Glu Tyr Asn Pro Glu Gln Met Cys Ser Val Leu Arg Lys Arg
 1090 1095 1100
 Phe Gln Gln Ile Gly Leu Ser Ser Arg Asp Tyr Arg Val Arg Arg Ala
 1105 1110 1115 1120
 Asp Ser Ser Gly Lys Val Lys Ile Tyr Leu Ser Gln Asn Ala Leu Asp
 1125 1130 1135
 Arg Val Glu Gln Ile Glu Gly Ala Gly Ser Glu Gln Lys Gly Ser Asp
 1140 1145 1150
 Tyr His Leu Ala Arg Val Leu Gln Val Leu Ser Asp Ser Gly Ser Ser
 1155 1160 1165
 Thr Thr Ser Met Val Phe Asp Ala Ser Arg Gly Ser Trp Phe Lys Val
 1170 1175 1180
 Ser Gly Gln Leu Ser Asn Lys Met Arg Thr Gln Ala Val Ile Ala Leu
 1185 1190 1195 1200
 Phe Gly Ala Leu Gly Ile Ile Leu Leu Tyr Val Ser Leu Arg Phe Glu
 1205 1210 1215
 Trp Arg Tyr Ala Phe Ser Ala Ile Cys Ala Leu Met His Asp Leu Leu
 1220 1225 1230
 Ala Thr Cys Ala Val Leu Val Ala Leu His Phe Phe Leu Gln Arg Ile
 1235 1240 1245
 Thr Asp
 1250

(2) INFORMATIONS POUR LA SEQ ID NO: 1029:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 126 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 993408..993785

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1029:

Leu Pro Tyr Ile Ser Phe Cys Arg Glu Leu Gln Ile Asp Leu Gln Ala
 1 5 10 15
 Ile Gly Ala Leu Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu
 20 25 30
 Ile Ile Phe Asp Arg Ile Arg Glu Asp Arg Arg Glu Lys Leu Phe Thr
 35 40 45
 Pro Met Pro Ile Leu Ile Asn Asp Ala Leu Gln Lys Thr Leu Gly Arg
 50 55 60

```

Thr Val Met Thr Thr Ala Thr Thr Leu Ser Val Leu Val Ile Leu Leu
65              70              75              80
Phe Val Gly Gly Gly Ser Ile Phe Asn Phe Ala Phe Ile Met Thr Val
              85              90              95
Gly Ile Leu Leu Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu
              100             105             110
Leu Leu Phe Met Val Arg Lys Glu Glu Gln Asn Ser Leu Arg
              115             120             125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1030:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 140 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(993416..993835)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1030:

```

Ser Ser His Asn Phe Arg Ile Thr Tyr Ala Gln Ala Tyr Phe Ile Ile
1              5              10              15
Tyr Arg Arg Glu Phe Cys Ser Ser Leu Arg Thr Met Asn Lys Arg Ser
              20              25              30
Gly Gly Ala Met Tyr Asn Glu Asp Ser Val Pro Asn Lys Ile Pro Thr
              35              40              45
Val Ile Met Asn Ala Lys Leu Lys Ile Glu Pro Pro Pro Thr Asn Asn
              50              55              60
Lys Met Thr Ser Thr Asp Arg Val Val Ala Val Val Ile Thr Val Arg
65              70              75              80
Pro Asn Val Phe Cys Asn Ala Ser Leu Ile Lys Ile Gly Ile Gly Val
              85              90              95
Asn Ser Phe Ser Arg Arg Ser Ser Arg Ile Arg Ser Lys Ile Ile Asn
              100             105             110
Val Leu Phe Lys Glu Tyr Pro Ser Thr Val Ile Asn Ala Pro Ile Ala
              115             120             125
Cys Lys Ser Ile Cys Asn Ser Leu Gln Lys Glu Met
              130             135             140

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1031:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 127 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 993882..994262

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1031:

```

Gln Glu Phe Ser Ser Gly Arg Tyr Met Glu Lys Gly Ser Leu Ser Ser

```

```

1          5          10          15
Leu Gly Gln Lys Trp Asp Tyr Pro Lys His Asn Glu Val Phe Leu Lys
20          25          30
Lys Ile Leu Lys Glu Phe His Leu His Pro Ala Ile Ala Gln Val Leu
35          40          45
Ile Ser Arg Gly Phe Gln Ser Ile Gln Glu Ile Arg Asp Phe Leu Tyr
50          55          60
Pro Gln Leu Ser Ser Leu His Ser Thr Ser Leu Phe Leu Asp Met Glu
65          70          75          80
Lys Ala Val Ala Arg Leu Leu Gln Ala Lys Ala Asn Asn Glu His Val
85          90          95
Met Ile Tyr Gly Asp Gly Asp Val Asp Gly Ile Thr Gly Val Thr Leu
100          105          110
Ile Val Glu Phe Leu Gln Ile Leu Gly Val Lys Thr Ser Tyr Cys
115          120          125

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1032:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 477 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 994226..995656

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1032:

```

Ile Ser Thr Asn Thr Trp Ser Glu Asn Lys Leu Leu Leu Thr Gly Thr
1          5          10          15
Leu Phe Lys Gln His Gly Glu Thr Ala Ser Leu Ile Ser Gln Met Leu
20          25          30
Gln Asp Gly Ile Ser Leu Leu Ile Thr Val Asp Cys Gly Ile Thr Ala
35          40          45
Gly Lys Glu Val Gln Ala Ile Asn Lys Gln Gly Ile Asp Val Ile Val
50          55          60
Thr Asp His His Met Pro Thr Gly Lys Leu Pro His Cys Ile Ala Met
65          70          75          80
Leu Asn Pro Lys Leu Asp Lys Asn Pro Tyr Pro Asn Lys Glu Leu Thr
85          90          95
Gly Val Gly Val Ala Phe Lys Leu Val Cys Ala Thr Tyr Glu Glu Leu
100          105          110
Ile Gln Gln Asp Ala Ser Trp Lys Asp Lys Ile Asp Leu Leu Arg Phe
115          120          125
Leu Asp Leu Val Ser Leu Gly Thr Ile Ala Asp Val Gly Arg Leu Ser
130          135          140
Gly Glu Asn Arg Ile Leu Val Ser Tyr Gly Ile Lys Glu Ile Ala Lys
145          150          155          160
Gly Lys Arg Leu Gly Leu Lys Lys Leu Cys Ser Leu Ser Gly Val Asp
165          170          175
Lys Ser Glu Val Ser Ser Thr Asn Leu Gly Ile Arg Ile Thr Pro Lys
180          185          190
Leu Asn Ser Leu Gly Arg Leu Ala Asp Ser Ser Gln Gly Val Lys Leu
195          200          205
Leu Leu Ser Gln Asp Pro Lys Asn Ile Gly Thr Ile Val Ser Glu Leu
210          215          220

```

```

Ser Ala Val Asn Gln Glu Arg Gln Arg Ile Glu Ala Glu Val Leu Arg
225                230                235                240
Asp Val Glu Arg Ile Leu Ala Ala Asn Pro Lys Leu Thr Ala Gln Ser
                245                250                255
Ala Ile Val Leu Ala Ser Pro Asn Trp His Ser Arg Val Ile Pro Ile
                260                265                270
Ile Ser Ala Arg Leu Ala Arg Thr Tyr Asn Lys Pro Val Ala Ile Ile
                275                280                285
Ala Leu Gln Asp Gly Ile Gly Lys Gly Ser Leu Arg Thr Ile Gly Ser
                290                295                300
Phe Pro Leu Leu Gly Val Leu Arg Lys Cys Glu Ser Phe Phe Leu Ser
305                310                315                320
Tyr Gly Gly His Asp Phe Ala Ala Gly Leu Met Ile Lys Glu Asp Gln
                325                330                335
Val Glu Gly Phe Arg Lys Lys Phe Ile His Leu Val Ser Ser Ser Leu
                340                345                350
Arg Lys Asp Asp Ala Met Arg Thr Leu Ser Leu Asp Val Gly Met Asp
                355                360                365
Phe Ser Arg Ile Asn Arg Asp Leu Ile Ala Ser Met Glu Leu Leu Glu
                370                375                380
Pro Phe Gly Lys Gly Asn Val Ser Pro Val Phe Tyr Thr Lys Ala Ile
385                390                395                400
Gln Val Arg Tyr Pro Lys Leu Leu Ala Gly Asn His Val Lys Leu Tyr
                405                410                415
Leu Asn Ser Gly Glu Arg Asn Leu Glu Gly Thr Ala Phe Gly Gln Gly
                420                425                430
Asp Lys Ile Ser Leu Leu Lys Ala Asn Trp Asn Ile Pro Leu Asp Ile
                435                440                445
Ala Tyr Thr Leu Arg Ile Met Arg Arg Ser Ala Arg Gly Ala Ile Arg
                450                455                460
Leu Leu Ile Gln Asp Phe Arg Ile Gln Ile Pro Arg Leu
465                470                475

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1033:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 183 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 996063..996611

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1033:

```

Met Glu Cys Leu Gln Gln Asp Thr Gly Val Glu Ala Glu Gln Val Gln
1                5                10                15
Val Gln Gln Gln Glu Glu Asn Ala Val Pro Val Thr Ser Gln Arg Val
                20                25                30
Ser Ile Thr Gln Ala Ala Lys Leu His Asn Val Thr Arg Gln Ala Ile
                35                40                45
Tyr Val Ala Ile Lys Gln Lys Lys Leu Lys Ala Ser Lys Thr Thr Arg
                50                55                60
Trp Glu Ile Asp Leu Gln Asp Leu Glu Asp Tyr Arg Arg Asn Arg Tyr
65                70                75                80
Ser Arg Ala Lys Ser Thr Tyr Gln Gly Glu Leu Leu Phe Asp Asn Glu

```

```

      85      90      95
Lys Gly Phe Tyr Ser Val Gly Gln Val Ala Ser Met Leu Asp Val Pro
      100      105      110
Glu Gln Lys Ile Tyr Tyr Ala Thr Arg Ile Gly Ala Met Lys Gly Glu
      115      120      125
Arg Arg Gly Ser Ala Trp Val Ile His Val Ser Glu Val Asp Arg Tyr
      130      135      140
Arg Asn Asp Tyr Leu Lys Lys Glu Ala Glu Arg Lys Gly Lys Ser Leu
      145      150      155      160
Ala Ala Met Arg Glu Gly Phe Glu Ala Leu Gly Ala Asp Leu Leu Ala
      165      170      175
Asp Ala Glu Asn Phe Ile Ser
      180

```

(2) INFORMATION POUR LA SEQ ID NO: 1034:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 461 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 996885..998267

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1034:

```

Met Thr Val Gln Asn Val Arg Val Arg Val Ala Pro Ser Pro Thr Gly
1      5      10      15
Asp Pro His Val Gly Thr Ala Tyr Met Ala Gln Phe Asn Glu Val Phe
      20      25      30
Ala Arg Lys Tyr Asn Gly Gln Met Ile Leu Arg Ile Glu Asp Thr Asp
      35      40      45
Gln Thr Arg Ser Arg Asp Asp Tyr Glu Ala Asn Ile Phe Leu Ala Leu
      50      55      60
Lys Trp Cys Gly Ile Arg Trp Asp Glu Gly Pro Asp Val Gly Gly Ala
      65      70      75      80
Tyr Gly Pro Tyr Arg Gln Ser Glu Arg Thr Glu Ile Tyr Lys Lys Tyr
      85      90      95
Ala Glu Ile Leu Leu Gln Thr Asp Cys Ala Tyr Lys Cys Phe Ala Thr
      100      105      110
Pro Gln Glu Leu Gln Glu Met Arg Ala Val Ala Ser Thr Leu Gly Tyr
      115      120      125
Arg Gly Gly Tyr Asp Arg Arg Tyr Arg Tyr Leu Ser Pro Glu Glu Val
      130      135      140
Arg Gln Arg Glu Glu Gln Gly Gln Pro Tyr Thr Ile Arg Leu Lys Val
      145      150      155      160
Pro Leu Thr Gly Glu Ser Val Phe Glu Asp Gln Cys Lys Gly Arg Val
      165      170      175
Val Phe Pro Trp Ala Asp Val Asp Asp Gln Val Leu Val Lys Ser Asp
      180      185      190
Gly Phe Pro Thr Tyr His Phe Ala Asn Val Val Asp Asp His Leu Met
      195      200      205
Gly Ile Thr His Val Leu Arg Gly Glu Glu Trp Leu Ser Ser Thr Pro
      210      215      220
Lys His Leu Leu Leu Tyr Lys Ala Phe Gly Trp Glu Pro Pro Gln Phe
      225      230      235      240

```



```

Phe His Met Pro Leu Leu Leu Asn Pro Asp Gly Ser Lys Leu Ser Lys
                245                      250                255
Arg Lys Asn Pro Thr Ser Ile Phe Tyr Tyr Arg Asp Ala Gly Tyr Lys
                260                      265                270
Lys Glu Ala Phe Met Asn Phe Leu Thr Leu Met Gly Tyr Ser Met Glu
                275                      280                285
Gly Asp Glu Glu Ile Tyr Ser Met Gln Arg Leu Ile Glu Ala Phe Asp
                290                      295                300
Pro Lys Arg Ile Gly Arg Ser Gly Ala Val Phe Asp Ile Arg Lys Leu
305                      310                      315                320
Asp Trp Met Asn Lys His Tyr Leu Asn His Glu Gly Ser Pro Glu Ser
                325                      330                335
Leu Leu Gln Glu Leu Lys Gly Trp Leu Trp Asn Asp Glu Phe Leu Leu
                340                      345                350
Lys Ile Leu Pro Leu Cys Gln Ser Arg Ile Thr Thr Leu Ala Asp Phe
                355                      360                365
Val Gly Leu Thr Ser Phe Phe Thr Ala Ile Pro Gln Tyr Ser Lys
                370                      375                380
Glu Glu Leu Leu Pro Ser Ser Leu Lys Gln Glu Gln Ala Ala Val Met
385                      390                      395                400
Leu Tyr Ser Leu Val Lys Tyr Leu Glu Lys Lys Asp Leu Trp Glu Lys
                405                      410                415
Asp Phe Phe Tyr Gln Gly Ser Lys Trp Leu Ala Glu Ala Phe Gln Val
                420                      425                430
His His Lys Lys Ala Val Ile Leu Cys Tyr Met Trp Leu Leu Leu Val
                435                      440                445
Gln Asn Arg Asp Phe Leu Phe Leu Ile Arg Trp Asn Tyr
                450                      455                460

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1035:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 88 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 998962..999225

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1035:

```

Met Lys Lys Thr Ala Leu Leu Ala Ala Leu Cys Ser Val Val Ser Leu
1          5          10          15
Ser Ser Cys Cys Arg Ile Val Asp Cys Cys Phe Glu Asp Pro Cys Ala
                20          25          30
Pro Ile Gln Cys Ser Pro Cys Glu Ser Lys Lys Lys Asp Val Asp Gly
                35          40          45
Gly Cys Asn Ser Cys Asn Gly Tyr Val Pro Ala Cys Lys Pro Cys Gly
50          55          60
Gly Asp Thr His Gln Asp Ala Glu His Gly Pro Gln Ala Arg Glu Ile
65          70          75          80
Pro Val Asp Gly Lys Cys Arg Gln
                85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1036:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 547 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 999393..1001033

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1036:

Met	Asn	Lys	Leu	Ile	Arg	Arg	Ala	Val	Thr	Ile	Phe	Ala	Val	Thr	Ser	1	5	10	15
Val	Ala	Ser	Leu	Phe	Ala	Ser	Gly	Val	Leu	Glu	Thr	Ser	Met	Ala	Glu	20	25	30	
Phe	Ile	Ser	Thr	Asn	Val	Ile	Ser	Leu	Ala	Asp	Thr	Lys	Ala	Lys	Asp	35	40	45	
Asn	Thr	Ser	His	Lys	Ser	Lys	Lys	Ala	Arg	Lys	Asn	His	Ser	Lys	Glu	50	55	60	
Thr	Pro	Val	Asn	Arg	Lys	Lys	Val	Ala	Pro	Val	His	Glu	Ser	Lys	Ala	65	70	75	80
Thr	Gly	Pro	Lys	Gln	Asp	Ser	Cys	Phe	Gly	Arg	Met	Tyr	Thr	Val	Lys	85	90	95	
Val	Asn	Asp	Asp	Arg	Asn	Val	Glu	Ile	Thr	Gln	Ala	Val	Pro	Lys	Tyr	100	105	110	
Ala	Thr	Val	Gly	Ser	Pro	Tyr	Pro	Val	Glu	Ile	Thr	Ala	Thr	Gly	Lys	115	120	125	
Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln	Gln	Leu	Pro	Cys	Glu	Ala	130	135	140	
Glu	Phe	Val	Arg	Ser	Asp	Pro	Ala	Thr	Thr	Pro	Thr	Ala	Asp	Gly	Lys	145	150	155	160
Leu	Val	Trp	Lys	Ile	Asp	Arg	Leu	Gly	Gln	Gly	Glu	Lys	Ser	Lys	Ile	165	170	175	
Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	Cys	Cys	Phe	Thr	Ala	Ala	180	185	190	
Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg	Ser	Val	Thr	Lys	Cys	Gly	Gln	195	200	205	
Pro	Ala	Ile	Cys	Val	Lys	Gln	Glu	Gly	Pro	Glu	Asn	Ala	Cys	Leu	Arg	210	215	220	
Cys	Pro	Val	Val	Tyr	Lys	Ile	Asn	Val	Val	Asn	Gln	Gly	Thr	Ala	Thr	225	230	235	240
Ala	Arg	Asn	Val	Val	Val	Glu	Asn	Pro	Val	Pro	Asp	Ser	Tyr	Ala	His	245	250	255	
Ser	Ser	Gly	Gln	Arg	Val	Leu	Thr	Phe	Thr	Leu	Gly	Asp	Met	Gln	Pro	260	265	270	
Gly	Glu	His	Arg	Thr	Ile	Thr	Val	Glu	Phe	Cys	Pro	Leu	Lys	Arg	Gly	275	280	285	
Arg	Ala	Thr	Asn	Ile	Ala	Met	Val	Ser	Tyr	Cys	Gly	Gly	His	Lys	Asn	290	295	300	
Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn	Glu	Pro	Cys	Val	Gln	Val	Ser	305	310	315	320
Ile	Ala	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys	Lys	Pro	Val	Glu	Tyr	Val	325	330	335	
Ile	Ser	Val	Ser	Asn	Pro	Gly	Asp	Leu	Val	Leu	Arg	Asp	Val	Val	Val	340	345	350	
Lys	Asp	Thr	Leu	Ser	Pro	Gly	Val	Thr	Val	Leu	Glu	Ala	Ala	Gly	Ala	355	360	365	

```

Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu Asn Pro
  370                      375                      380
Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr Pro Gly
385                      390                      395                      400
Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys Gly Thr
                      405                      410                      415
Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val Ala Ala
                      420                      425                      430
Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val Gly Glu
                      435                      440                      445
Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp
450                      455                      460
Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln Pro Val
465                      470                      475                      480
Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr Val Val
                      485                      490                      495
Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu Phe Ser
                      500                      505                      510
Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu Ala Ile
                      515                      520                      525
Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu Asn Thr
530                      535                      540
His Ile Tyr
545

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1037:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 101 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1001214..1001516

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1037:

```

Met Ser Thr Val Pro Val Val Gln Gly Ala Gly Ser Ser Asn Ser Ala
  1                      5                      10                      15
Gln Asp Ile Ser Thr Ser Ser Ala Pro Leu Thr Leu Lys Gly Arg Ile
                      20                      25                      30
Ser Asn Leu Leu Ser Ser Thr Ala Phe Lys Val Gly Leu Val Val Ile
                      35                      40                      45
Gly Leu Leu Leu Val Met Ala Thr Ile Phe Leu Val Ser Ala Ser Phe
50                      55                      60
Val Cys Lys Ser His Leu Ser Ser Tyr Ser Cys Tyr Cys Gly Met Arg
65                      70                      75                      80
Glu Tyr Leu Arg Arg Asn Phe Ile His Gly Arg Ile Leu Phe Ser Gly
                      85                      90                      95
Glu Met Glu Leu Met
                      100

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1038:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 91 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1001392..1001664

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1038:

Phe	Arg	Pro	Ala	Ser	Phe	Val	Asn	Pro	Ile	Tyr	Leu	Ala	Ile	Pro	Ala
1				5					10					15	
Ile	Val	Gly	Cys	Val	Asn	Ile	Cys	Val	Gly	Ile	Leu	Ser	Met	Glu	Gly
			20					25					30		
Tyr	Cys	Ser	Pro	Glu	Arg	Trp	Ser	Leu	Cys	Lys	Lys	Ile	Leu	Lys	Ala
		35					40					45			
Ser	Glu	Asp	Ile	Ile	Asp	Asp	Gly	Gln	Ile	Asn	Asn	Ser	Asn	Lys	Val
	50				55					60					
Phe	Thr	Asp	Glu	Arg	Leu	Asn	Ala	Ile	Asp	Gly	Val	Val	Val	Ser	Leu
65					70					75					80
Ser	Arg	Arg	Asn	Ser	Leu	Val	Asp	Gln	Thr	Gln					
				85					90						

(2) INFORMATIONS POUR LA SEQ ID NO: 1039:

(i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 625 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1001823..1003697)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1039:

Leu	Leu	Val	Leu	Thr	Leu	Phe	Pro	Gln	Leu	Ala	Phe	Ser	Ala	Glu	Pro
1				5					10					15	
Leu	Arg	Arg	Gln	Asp	Val	Arg	Lys	Thr	Val	Asp	Lys	Leu	Val	Glu	His
			20					25					30		
His	Ile	Asp	Thr	Gln	Gln	Ile	Ser	Pro	Tyr	Ile	Leu	Ser	Arg	Ser	Leu
		35					40					45			
Glu	Asp	Tyr	Val	Arg	Ser	Phe	Asp	Ser	His	Lys	Ala	Tyr	Leu	Thr	Gln
	50					55					60				
Asp	Glu	Val	Phe	Ser	His	Ala	Phe	Ser	Glu	Glu	Ala	Thr	His	Pro	Leu
65					70					75					80
Phe	Lys	Gln	Tyr	Gln	Glu	Asp	Asn	Phe	Ser	Ser	Phe	Lys	Glu	Leu	Asp
				85					90				95		
Thr	Cys	Ile	Gln	Gln	Ser	Ile	Ser	Arg	Ala	Arg	Glu	Trp	Arg	Ser	Ser
			100					105					110		
Trp	Leu	Thr	Asp	Ser	Ile	Arg	Val	Ile	Gln	Asp	Ala	Met	Ser	His	Thr
		115					120					125			
Ile	Glu	Lys	Lys	Pro	Ser	Ala	Trp	Ala	Ser	Ser	Ile	Glu	Glu	Val	Lys
	130					135					140				
Gln	Arg	Gln	Tyr	Asp	Leu	Leu	Leu	Ser	Tyr	Ala	Ser	Ile	Tyr	Leu	Glu
					145					155					160

Asp Ala Ala Lys Asn Arg Tyr Gln Gly Lys Glu His Gly Leu Val Lys
 165 170 175
 Leu Cys Ile Arg Gln Ile Glu Asn His Glu Asn Pro Tyr Ile Gly Ile
 180 185 190
 Asn Asp His Gly Tyr Arg Met Ser Pro Glu Glu Glu Ala Asn Ser Phe
 195 200 205
 His Val Arg Ile Ile Lys Ser Ile Ala His Ser Leu Asp Ala His Thr
 210 215 220
 Ala Tyr Phe Ser Gln Glu Glu Ala Leu Ser Met Arg Ala Gln Leu Glu
 225 230 235 240
 Lys Gly Met Cys Gly Ile Gly Val Val Leu Lys Glu Asp Ile Asp Gly
 245 250 255
 Val Val Val Lys Glu Val Leu Ala Gly Gly Pro Ala Asp Lys Thr Gly
 260 265 270
 Ser Leu Arg Val Gly Asp Ile Ile Tyr Arg Val Asn Gly Lys Asn Ile
 275 280 285
 Glu Asn Thr Pro Phe Pro Gly Val Leu Asp Ser Leu Arg Gly Ser Pro
 290 295 300
 Gly Ser Ser Val Thr Leu Asp Ile His Arg Gln Asn Asn Asp His Val
 305 310 315 320
 Ile Gln Leu Arg Arg Glu Lys Ile Leu Leu Asp Ser Arg Arg Val Asp
 325 330 335
 Val Ser Tyr Glu Pro Tyr Gly Asn Gly Ile Ile Gly Lys Ile Thr Leu
 340 345 350
 His Ser Phe Tyr Glu Gly Glu Asn Gln Val Ser Ser Glu Gln Asp Leu
 355 360 365
 Arg Lys Ala Ile Arg Glu Leu Gln Glu Lys Asn Leu Leu Gly Leu Val
 370 375 380
 Leu Asp Ile Arg Glu Asn Thr Gly Gly Phe Leu Ser Gln Ala Ile Lys
 385 390 395 400
 Val Ser Gly Leu Phe Leu Thr Asn Gly Val Val Val Val Ser Arg Tyr
 405 410 415
 Ala Asp Gly Ser Val Lys Arg Tyr Arg Thr Ile Ser Pro Gln Lys Phe
 420 425 430
 Tyr Asp Gly Pro Leu Ala Val Leu Val Ser Lys Ser Ser Ala Ser Ala
 435 440 445
 Ala Glu Ile Val Ala Gln Thr Leu Gln Asp Tyr Gly Val Ala Leu Ile
 450 455 460
 Val Gly Asp Gln Gln Thr Tyr Gly Lys Gly Thr Ile Gln His Gln Thr
 465 470 475 480
 Ile Thr Gly Ser Asn Ser Gln Glu Asp Phe Phe Lys Val Thr Val Gly
 485 490 495
 Arg Tyr Tyr Ser Pro Ser Gly Lys Ser Thr Gln Leu Glu Gly Val Lys
 500 505 510
 Ser Asp Ile Val Ile Pro Ser Arg Tyr Ala Glu Asp Lys Leu Gly Glu
 515 520 525
 Arg Phe Leu Glu Tyr Ala Leu Pro Ala Asp Gln Tyr Asp Asn Val Ile
 530 535 540
 Asn Asp Asn Leu Gly Asp Leu Asp Ile Asn Ile Arg Pro Trp Phe Gln
 545 550 555 560
 Lys Tyr Tyr Ser Pro His Leu Gln Lys Pro Glu Leu Val Trp Arg Glu
 565 570 575
 Met Leu Pro Gln Leu Ala His Asn Ser Gln Glu Arg Leu Glu Lys Asn
 580 585 590
 Lys Asn Phe Glu Ile Phe Val Gln His Leu Lys Lys Thr Asn Lys Gln
 595 600 605
 Asp Arg Ser Phe Gly Ser Asn Asp Leu Gln Met Glu Glu Cys Glu His
 610 615 620
 Arg

(2) INFORMATION POUR LA SEQ ID NO: 1040:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1004477..1004845

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1040:

Met	Pro	Thr	Ile	Asn	Gln	Leu	Ile	Arg	Lys	Lys	Arg	Gln	Ser	Gly	Ala
1				5					10					15	
Thr	Arg	Lys	Lys	Ser	Pro	Ala	Leu	Gln	Lys	Ser	Pro	Gln	Lys	Arg	Gly
			20					25					30		
Val	Cys	Leu	Gln	Val	Lys	Thr	Lys	Thr	Pro	Lys	Lys	Pro	Asn	Ser	Ala
		35					40					45			
Leu	Arg	Lys	Val	Ala	Trp	Val	Arg	Leu	Ser	Asn	Gly	Gln	Glu	Val	Ile
	50					55					60				
Ala	Tyr	Ile	Gly	Gly	Glu	Gly	His	Asn	Leu	Gln	Glu	His	Ser	Ile	Val
65					70					75					80
Leu	Val	Gln	Gly	Gly	Arg	Xaa	Lys	Asp	Leu	Pro	Gly	Val	Arg	Tyr	His
				85					90					95	
Ile	Val	Arg	Gly	Ala	Leu	Xaa	Cys	Ala	Ala	Val	Lys	Asn	Arg	Lys	Gln
			100					105					110		
Ser	Arg	Ser	Arg	Tyr	Gly	Ala	Lys	Arg	Pro	Lys					
		115					120								

(2) INFORMATION POUR LA SEQ ID NO: 1041:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 131 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1004990..1005382

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1041:

Leu 1	Leu	His	Gly 5	Lys	Lys	Ser	Ile	Ala	Arg 10	Lys	Ile	Val	Tyr	Gly 15	Ala
Leu	Glu	Arg	Phe 20	Ala	Lys	Arg	Leu	Gly 25	Leu	Glu	Asn	Pro	Leu 30	Glu	Gly
Phe	Glu	Glu	Ala 35	Leu	Glu	Asn	Ala 40	Lys	Pro	Ile	Leu	Glu 45	Val	Arg	Ser
Arg	Arg 50	Val	Gly	Gly	Ala	Thr 55	Tyr	Gln	Val	Pro	Val 60	Glu	Val	Ala	Pro
Asp 65	Arg	Arg	Ser	Cys	Leu 70	Ala	Met	Gln	Trp	Ile 75	Ile	Lys	His	Ala	Arg 80

Ser Lys Pro Gly Lys Cys Met Glu Val Gly Leu Ala Asn Glu Leu Ile
 85 90 95
 Asp Cys Phe Asn Lys Gln Gly Ala Thr Ile Lys Lys Arg Glu Asp Thr
 100 105 110
 His Arg Met Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Lys Trp Xaa
 115 120 125
 Xaa Asn Val
 130

(2) INFORMATIONS POUR LA SEQ ID NO: 1042:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 694 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1005415..1007496

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1042:

Met Ser Asp Gln Glu Phe Gly Leu Asp Ala Ile Arg Asn Ile Gly Ile
 1 5 10 15
 Met Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu
 20 25 30
 Phe Tyr Ala Gly Arg Thr His Lys Ile Gly Glu Val His Glu Gly Gly
 35 40 45
 Ala Thr Met Asp Trp Met Glu Gln Glu Gln Glu Arg Gly Ile Thr Ile
 50 55 60
 Thr Ser Ala Ala Thr Thr Val Phe Trp Leu Gly Ala Lys Ile Asn Ile
 65 70 75 80
 Ile Asp Thr Pro Gly His Val Asp Phe Thr Ile Glu Val Glu Arg Ser
 85 90 95
 Leu Arg Val Leu Asp Gly Ala Val Ala Val Phe Asp Ala Val Ser Gly
 100 105 110
 Val Glu Pro Gln Ser Glu Thr Val Trp Arg Gln Ala Asn Lys Tyr Gly
 115 120 125
 Val Pro Arg Ile Ala Phe Val Asn Lys Met Asp Arg Met Gly Ala Asn
 130 135 140
 Tyr Xaa Gly Ala Val Glu Ser Met Arg Glu Lys Leu Gly Ala Asn Ala
 145 150 155 160
 Xaa Pro Val His Cys Pro Ile Gly Ser Glu Ser Gln Phe Val Gly Met
 165 170 175
 Val Asp Leu Ile Ser Gln Lys Ala Leu Tyr Phe Leu Glu Glu Thr Leu
 180 185 190
 Gly Ala Lys Trp Glu Glu Arg Lys Ile Pro Glu Asp Leu Gln Glu Gln
 195 200 205
 Cys Ala Thr Leu Arg Met Gln Leu Leu Glu Glu Leu Ala Thr Val Asp
 210 215 220
 Glu Ser Asn Glu Ala Phe Met Glu Lys Val Leu Glu Asn Pro Asp Ser
 225 230 235 240
 Ile Thr Glu Glu Glu Ile His Thr Val Met Arg Lys Gly Val Ile Glu
 245 250 255
 Gly Lys Ile Asn Pro Val Leu Cys Gly Ser Ala Phe Lys Asn Lys Gly
 260 265 270
 Val Gln Gln Leu Leu Asp Val Ile Val Lys Trp Leu Pro Ser Pro Leu

275 280 285
 Asp Arg Gly Asn Val Arg Gly Ile Asn Leu Lys Thr Gly Glu Glu Val
 290 295 300
 Ser Leu Lys Pro Ser Lys Asp Gly Pro Leu Ala Ala Leu Ala Phe Lys
 305 310 315 320
 Ile Met Thr Asp Pro Tyr Val Gly Arg Ile Thr Phe Ile Arg Ile Tyr
 325 330 335
 Ser Gly Thr Leu Lys Lys Gly Ser Ala Ile Leu Asn Ser Thr Lys Asp
 340 345 350
 Lys Lys Glu Arg Ile Ser Arg Leu Leu Glu Met His Ala Asn Glu Arg
 355 360 365
 Thr Asp Arg Asp Glu Phe Thr Val Gly Asp Ile Gly Ala Cys Val Gly
 370 375 380
 Leu Lys Phe Ser Val Thr Gly Asp Thr Leu Cys Asp Glu Asn Gln Glu
 385 390 395 400
 Ile Val Leu Glu Arg Ile Glu Ala Pro Glu Pro Val Ile Asp Met Ala
 405 410 415
 Ile Glu Pro Lys Ser Lys Gly Asp Arg Glu Lys Leu Ala Gln Ala Leu
 420 425 430
 Ser Ala Leu Ser Glu Glu Asp Pro Thr Phe Arg Val Ser Thr Asn Glu
 435 440 445
 Glu Thr Gly Gln Thr Ile Ile Ser Gly Met Gly Glu Leu His Leu Asp
 450 455 460
 Ile Leu Arg Asp Arg Met Ile Arg Glu Phe Arg Val Glu Ala Asn Val
 465 470 475 480
 Gly Lys Pro Gln Val Ser Tyr Lys Glu Thr Ile Thr Lys Thr Ser Asn
 485 490 495
 Ser Glu Thr Lys Tyr Val Lys Gln Ser Gly Gly Arg Gly Gln Tyr Ala
 500 505 510
 His Val Cys Leu Glu Ile Glu Pro Asn Glu Pro Gly Lys Gly Asn Glu
 515 520 525
 Val Val Ser Lys Ile Val Gly Gly Val Ile Pro Lys Glu Tyr Ile Pro
 530 535 540
 Ala Val Ile Lys Gly Val Glu Glu Gly Leu Asn Ser Gly Val Leu Ala
 545 550 555 560
 Gly Tyr Gly Leu Val Asp Val Lys Val Ser Ile Val Phe Gly Ser Tyr
 565 570 575
 His Glu Val Asp Ser Ser Glu Met Ala Phe Lys Ile Cys Gly Ser Met
 580 585 590
 Ala Val Lys Glu Ala Cys Arg Lys Ala Leu Pro Val Ile Leu Glu Pro
 595 600 605
 Ile Met Lys Val Thr Val Ile Thr Pro Glu Asp His Leu Gly Asp Val
 610 615 620
 Ile Gly Asp Leu Asn Arg Arg Gly Lys Ile Leu Gly Gln Glu Ser
 625 630 635 640
 Ser Arg Asn Met Ala Gln Val Ser Ala Glu Val Pro Leu Ser Glu Met
 645 650 655
 Phe Gly Tyr Met Thr Ser Leu Arg Ser Leu Thr Ser Gly Arg Ala Thr
 660 665 670
 Ser Thr Met Glu Pro Ala Phe Phe Ala Lys Val Pro Gln Lys Ile Gln
 675 680 685
 Glu Glu Ile Val Lys Lys
 690

(2) INFORMATIONS POUR LA SEQ ID NO: 1043:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé
(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1007507..1007821

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1043:

Met	Lys	Gln	Gln	Lys	Gln	Arg	Ile	Arg	Ile	Arg	Leu	Lys	Gly	Phe	Asp
1				5				10						15	
Gln	Gly	Gln	Leu	Asp	Gln	Ser	Thr	Ala	Asn	Ile	Val	Glu	Thr	Ala	Lys
		20						25					30		
Arg	Thr	Gly	Ala	Arg	Val	Val	Gly	Pro	Ile	Pro	Leu	Pro	Thr	Lys	Arg
		35					40					45			
Glu	Val	Tyr	Thr	Val	Leu	Arg	Ser	Pro	His	Val	Asp	Lys	Lys	Ser	Arg
	50					55				60					
Glu	Gln	Phe	Glu	Ile	Arg	Thr	His	Lys	Arg	Leu	Ile	Asp	Ile	Leu	Asp
65				70					75					80	
Pro	Thr	Gly	Lys	Thr	Ile	Asp	Ala	Leu	Lys	Met	Leu	Ser	Leu	Pro	Ala
			85					90					95		
Gly	Val	Asp	Ile	Lys	Ile	Lys	Ala	Ala							
			100					105							

(2) INFORMATIONS POUR LA SEQ ID NO: 1044:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 299 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1007802..1008698

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1044:

Ile	Leu	Arg	Ser	Arg	Leu	Pro	Asn	Ser	Phe	Asp	Leu	Lys	Met	Ser	Leu
1				5				10						15	
Phe	Ser	Lys	Phe	Lys	Ala	Gln	Trp	Met	Phe	Leu	His	Ser	Arg	Glu	Leu
		20						25					30		
Cys	Ser	Ser	Thr	Ser	Asp	Ile	Gly	Asn	Thr	Cys	Ser	Asp	Pro	Val	Phe
		35					40					45			
Gln	Ile	Leu	Cys	Asn	Pro	Val	Arg	Ser	Glu	Ile	Ser	Tyr	Lys	Val	Gly
	50					55				60					
Asp	Ser	Leu	Gly	Val	Phe	Pro	Thr	Asn	Pro	Ser	Thr	Leu	Val	Asp	Ser
65				70					75					80	
Val	Leu	Asp	Ala	Leu	Gln	Tyr	Gly	Pro	Arg	Ser	Pro	Val	Val	Ser	Arg
			85					90					95		
His	Ala	Asp	Ser	Val	Leu	Pro	Leu	His	Glu	Phe	Leu	Thr	Ser	Tyr	Val
			100					105					110		
Asp	Leu	Asp	Lys	Ile	Pro	Lys	Ser	Leu	Arg	Pro	Phe	Phe	Pro	Gly	Asp
		115					120					125			
Leu	Asp	Asp	Thr	Trp	Ser	Leu	Ala	Glu	Ala	Ile	Leu	Val	Tyr	Gln	Pro
	130					135					140				
Arg	Ile	Pro	Phe	Glu	Glu	Phe	Ile	Arg	Ser	Ala	Met	Pro	Leu	Leu	Pro

```

145                               150                               155                               160
Arg Phe Tyr Ser Ile Ala Ser Ser Pro Thr Cys Ser His Gly Lys Leu
                               165                               170                               175
Glu Leu Leu Val Arg Cys Val Ser Phe Gln Gly Lys Thr Gln Leu Arg
                               180                               185                               190
Tyr Gly Leu Cys Ser Ala Phe Leu Cys Lys Asp Leu Gln Glu Gly Glu
                               195                               200                               205
Ser Phe Arg Gly Phe Ile Gln Pro Thr Arg His Phe Thr Leu Glu Gln
                               210                               215                               220
Lys Asn Phe Gly Lys Pro Leu Ile Met Ile Gly Ala Gly Thr Gly Ile
225                               230                               235                               240
Ala Pro Tyr Lys Gly Phe Leu Gln His Arg Ile Tyr His Gln Asp Val
                               245                               250                               255
Gly Ser Asn Ile Leu Phe Phe Gly Glu Arg Phe Glu Lys Ser Asn Phe
                               260                               265                               270
Tyr Tyr Arg Ala Phe Ser Pro Gly Ala Asp Arg Phe Arg Lys Thr Pro
                               275                               280                               285
Val Ile His Ser Leu Phe Gln Arg Phe Arg Val
                               290                               295

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1045:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 87 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1009121..1009381)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1045:

```

Ile Tyr Arg Val Gly Ile Gly Gln Asp Ser His Arg Phe Leu Pro Asp
1                               5                               10                               15
Glu Asp Pro Lys Pro Cys Ile Leu Gly Gly Ile Ile Phe Glu Asn Thr
                               20                               25                               30
Pro Gly Phe Glu Ala Asn Ser Asp Gly Asp Val Val Phe His Ala Ile
                               35                               40                               45
Cys Asn Ala Phe Ser Ser Val Thr His Lys Gly Ile Leu Gly Gly Leu
                               50                               55                               60
Ala Asp Glu Leu Leu Lys Thr Lys Gly Ile Thr Asp Ser Val Val Tyr
65                               70                               75                               80
Leu Gln Glu Leu Ser Pro Leu
                               85

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1046:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 469 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1010648..1012054

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1046:

Leu	Asp	His	Leu	Leu	His	Ala	Phe	Pro	Ser	Ile	Gly	Gln	Ser	Ile	Val
1				5					10					15	
Gln	Glu	Leu	Lys	Ser	Gln	Arg	Ser	Arg	Leu	Lys	Met	Ile	Ala	Ser	Glu
			20					25					30		
Asn	Phe	Ser	Ser	Leu	Ser	Val	Gln	Leu	Ala	Met	Gly	Asn	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Tyr	Cys	Glu	Gly	Ser	Pro	Phe	Lys	Arg	Phe	Tyr	Ser	Cys	Cys
	50					55					60				
Glu	Asn	Val	Asp	Ala	Ile	Glu	Trp	Glu	Cys	Ala	Glu	Thr	Ala	Lys	Glu
65					70					75					80
Leu	Phe	Gly	Ala	Glu	Ser	Ala	Phe	Val	Gln	Pro	His	Ser	Gly	Ala	Asp
				85					90					95	
Ala	Asn	Leu	Leu	Ala	Ile	Met	Ser	Ile	Ile	Thr	Gln	Lys	Ile	Gln	Ser
			100					105					110		
Pro	Ala	Val	Gln	Gln	Leu	Gly	Tyr	Lys	Thr	Ile	Asn	Asp	Leu	Pro	Glu
		115					120					125			
Gln	Glu	Tyr	Glu	Ala	Leu	Lys	Ala	Glu	Met	Ala	Gln	His	Lys	Cys	Leu
	130					135					140				
Gly	Pro	Ser	Leu	Asn	Ser	Gly	Gly	His	Leu	Thr	His	Gly	Thr	Val	Arg
145					150					155					160
Met	Asn	Ile	Met	Ser	Lys	Leu	Met	His	Cys	Leu	Pro	Tyr	Glu	Val	Asn
				165					170					175	
Leu	Asp	Thr	Glu	Leu	Phe	Asp	Tyr	Asp	Glu	Ile	Ala	Lys	Xaa	Ala	Lys
			180					185					190		
Glu	His	Lys	Pro	Thr	Val	Leu	Ile	Ala	Gly	Tyr	Ser	Ser	Tyr	Ser	Arg
		195					200					205			
Arg	Phe	Asn	Phe	Ala	Thr	Leu	Lys	Gln	Ile	Ala	Glu	Asp	Cys	Gly	Ala
	210					215					220				
Val	Leu	Trp	Val	Asp	Met	Ala	His	Phe	Ala	Gly	Leu	Val	Ala	Gly	Gly
225					230					235					240
Val	Phe	Val	Gly	Glu	Asn	Pro	Met	Pro	Tyr	Ala	Asp	Ile	Val	Thr	
				245				250					255		
Thr	Thr	Thr	His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Leu	Val	Leu
			260					265					270		
Ala	Lys	Xaa	Glu	Tyr	Ala	Asn	Thr	Leu	Asn	Lys	Ala	Cys	Leu	Xaa	Met
		275					280					285			
Met	Gly	Gly	Pro	Leu	Pro	His	Val	Ile	Ala	Ala	Lys	Ala	Ile	Ala	Leu
	290					295					300				
Lys	Glu	Ala	Met	Thr	Ile	Asn	Phe	Arg	Lys	Tyr	Ala	His	Lys	Val	Val
305					310					315					320
Glu	Asn	Ala	Gln	Thr	Leu	Ala	Glu	Val	Phe	Gln	Arg	Asn	Gly	Leu	Arg
				325					330					335	
Leu	Leu	Thr	Gly	Gly	Thr	Asp	Asn	His	Met	Leu	Ile	Ile	Asp	Leu	Thr
			340					345					350		
Ser	Leu	Gly	Val	Pro	Gly	Arg	Ile	Ala	Glu	Asp	Met	Leu	Thr	Ser	Val
		355					360					365			
Gly	Ile	Ala	Val	Asn	Arg	Asn	Thr	Ile	Pro	Ser	Asp	Ala	Ser	Gly	Gln
	370					375					380				
Trp	Lys	Thr	Ser	Gly	Ile	Arg	Leu	Gly	Thr	Pro	Ala	Leu	Thr	Thr	Leu
385					390					395					400
Gly	Met	Gly	Ser	Ala	Glu	Met	Glu	Glu	Val	Ala	Asn	Ile	Ile	Val	Lys
				405					410					415	
Val	Leu	Arg	Asn	Ile	Thr	Val	Arg	Ser	Asn	Ala	Glu	Ser	Gly	Ser	Ser
			420					425				430			
Lys	Ser	Glu	Gly	Glu	Leu	Ser	Glu	Gly	Ile	Ala	Gln	Glu	Ala	Arg	Gln

(2) INFORMATION POUR LA SEQ ID NO: 1047:

(A) LONGUEUR: 152 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1011942..1012397)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1047:

(2) INFORMATION POUR LA SEQ ID NO: 1048:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 198 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1012042..1012635

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1048:

Gly Asn Ala Ser Leu Val Gly Asp Ser Met Pro Glu Gly Glu Met Met
1 5 10 15

```

His Lys Leu Gln Asp Val Ile Asp Arg Lys Leu Leu Asp Ser Arg Arg
      20      25      30
Ile Phe Phe Ser Glu Pro Val Thr Glu Lys Ser Ala Ala Glu Ala Ile
      35      40      45
Lys Lys Leu Trp Tyr Leu Glu Leu Thr Asn Pro Gly Gln Pro Ile Val
      50      55      60
Phe Val Ile Asn Ser Pro Gly Gly Ser Val Asp Ala Ser Phe Ala Val
      65      70      75      80
Trp Asp Gln Ile Lys Met Ile Ser Ser Pro Leu Thr Thr Val Val Thr
      85      90      95
Gly Leu Ala Ala Ser Thr Gly Ser Val Leu Ser Leu Cys Ala Val Pro
      100      105      110
Gly Arg Arg Phe Ala Thr Pro His Ala Arg Ile Met Ile Thr Lys Pro
      115      120      125
Ser Ile Gly Gly Thr Ile Thr Gly Gln Ala Thr Asp Leu Asp Ile His
      130      135      140
Ala Arg Glu Xaa Leu Lys Thr Lys Ala Arg Ile Ile Asp Val Tyr Val
      145      150      155      160
Glu Ala Thr Gly Gln Ser Pro Glu Val Ile Glu Lys Ala Ile Asp Arg
      165      170      175
Asp Met Trp Met Ser Ala Asn Glu Ala Met Glu Phe Gly Leu Leu Asp
      180      185      190
Gly Ile Ser Leu Leu Phe
      195

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1049:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 90 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1012593..1012862

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1049:

```

Ser Asn Gly Val Trp Thr Val Arg Trp Asp Phe Ser Ser Leu Leu Thr
1      5      10
Thr Cys Arg Tyr Leu Leu Tyr Ser Gly Ala Gly Asn Ser Phe Ile Leu
      20      25      30
Gly Glu Ser Met Pro Ser Leu Glu Asp Val Leu Phe Leu Cys Gln Glu
      35      40      45
Glu Met Val Asp Gly Phe Leu Cys Val Glu Ser Ser Glu Ile Ala Asp
      50      55      60
Ala Lys Leu Thr Val Phe Asn Ser Asp Gly Ser Ile Ala Ser Met Cys
      65      70      75      80
Gly Asn Gly Leu Gln Ser Gln Trp Arg Thr
      85      90

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1050:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 210 acides aminés
- (B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1012811..1013440

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1050:

```

Trp Ile Tyr Arg Val Tyr Val Arg Glu Trp Val Ala Val Ala Met Ala
1      5      10      15
His Val Ala Gln Cys Phe Gly Leu Glu Asp Val Ser Ile Glu Thr Glu
20      25      30
Arg Gly Val Tyr Gln Gly Lys Phe Phe Ser Met Asn Arg Val Leu Val
35      40      45
Asp Met Thr Leu Pro Asp Trp Lys Lys Ala Glu Arg Lys Leu Thr His
50      55      60
Val Leu Pro Gly Met Pro Glu Gln Val Phe Phe Ile Asp Thr Gly Val
65      70      75      80
Pro His Val Val Val Phe Val Ser Asp Leu Ser Lys Val Pro Val Gln
85      90      95
Glu Trp Gly Ser Phe Leu Arg Tyr His Glu Asp Phe Ala Pro Glu Gly
100      105      110
Val Asn Val Asp Phe Val Gln Arg Lys Lys Asp Asp Leu Leu Val
115      120      125
Tyr Thr Tyr Glu Arg Gly Cys Glu Arg Glu Thr Leu Ser Cys Gly Thr
130      135      140
Gly Met Leu Ala Ser Ala Leu Val Ala Ala Asp Ile Phe Ser Leu Gly
145      150      155      160
Gln Asp Phe Ser Ile Ala Val Cys Ser Arg Ser Arg Asn Leu Ile Lys
165      170      175
Ile Phe Ser Glu Lys Gly Lys Val Phe Leu Glu Gly Pro Val Ser Leu
180      185      190
Leu Asn Arg Ser Glu Asn Phe Gly Trp Leu Glu Pro Lys Ser Arg Arg
195      200      205
Phe Gly
210

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1051:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 200 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1013456..1014055

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1051:

```

His Lys Arg Glu Leu Leu Ser Asn Arg Ala Ser Pro Ile Leu Glu Pro
1      5      10      15
Met Thr Thr Tyr Pro Val Pro Gln Asn Pro Leu Leu Leu Arg Val Leu
20      25      30
Arg Leu Met Asp Ala Phe Ser Lys Ser Asp Asp Glu Arg Asp Phe Tyr
35      40      45

```

Leu	Asp	Arg	Val	Xaa	Gly	Phe	Ile	Leu	Tyr	Ile	Asp	Leu	Asp	Lys	Asp
50						55					60				
Gln	Glu	Asp	Leu	Asp	Lys	Ile	Tyr	Gln	Glu	Leu	Glu	Glu	Asn	Ala	Asp
65					70					75					80
Arg	Tyr	Cys	Leu	Ile	Pro	Lys	Leu	Thr	Phe	Tyr	Glu	Ile	Lys	Lys	Ile
				85					90					95	
Met	Glu	Thr	Phe	Val	Asn	Glu	Lys	Ile	Tyr	Asp	Ile	Asp	Thr	Lys	Glu
			100					105					110		
Lys	Phe	Leu	Glu	Ile	Val	Gln	Ser	Lys	Asn	Ala	Arg	Glu	Gln	Phe	Gln
		115					120					125			
Glu	Phe	Leu	Tyr	Asp	His	Glu	Thr	Glu	Gln	Glu	Lys	Trp	Gln	Gln	Phe
	130					135					140				
Tyr	Val	Glu	Arg	Ser	Arg	Ile	Arg	Ile	Ile	Glu	Trp	Leu	Arg	Asn	Asn
145					150					155					160
Gln	Phe	Gln	Phe	Val	Phe	Glu	Glu	Asp	Leu	Asp	Phe	Ser	Lys	His	Ile
				165					170					175	
Leu	Glu	Gln	Leu	Lys	Val	His	Leu	Phe	Asp	Ala	Lys	Val	Ser	Lys	Glu
			180					185					190		
Leu	Thr	Gln	Ala	Arg	His	Phe	Phe								
			195				200								

(2) INFORMATIONS POUR LA SEQ ID NO: 1052:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 171 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1013977..1014489

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1052:

Ala	His	Phe	Arg	Thr	Thr	Glu	Gly	Thr	Ser	Ile	Arg	Cys	Gln	Gly	Ile
1				5					10					15	
Glu	Arg	Val	Asn	Thr	Gly	Ala	Ser	Leu	Leu	Leu	Asn	Lys	Ser	Lys	Val
			20					25					30		
Tyr	Tyr	Ser	Asn	Glu	Ala	Leu	Asn	Pro	Arg	Pro	Lys	Arg	Gly	Arg	Pro
		35				40						45			
Pro	Lys	Gln	Ser	Ala	Lys	Val	Glu	Ala	Glu	Thr	Thr	Ile	Ser	Asn	Asp
	50					55					60				
Ile	Tyr	Thr	Lys	Val	Pro	Ser	Ala	Ala	Arg	Arg	Phe	Leu	Phe	Leu	Pro
65				70					75						80
Glu	Ile	Thr	Ser	Pro	Ser	Ser	Leu	Thr	Phe	Ser	Glu	Lys	Phe	Asp	Thr
			85						90					95	
Glu	Glu	Glu	Phe	Leu	Ala	His	Leu	Arg	Gly	Gly	Gly	Arg	Leu	Glu	Asp
			100					105					110		
Gln	Leu	Asn	Leu	Ala	Lys	Phe	Ser	Glu	Arg	Phe	Asp	Ser	Leu	Arg	Glu
		115						120					125		
Leu	Ser	Ala	Lys	Leu	Gly	Tyr	Asp	Ser	Asp	Gly	Glu	Thr	Gly	Asp	Phe
	130					135					140				
Phe	Asn	Glu	Glu	Tyr	Asp	Asp	Glu	Glu	Glu	Glu	Ile	Lys	Pro	Lys	Lys
145					150					155					160
Thr	Thr	Lys	Arg	Gly	Arg	Lys	Lys	Ser	Arg	Ser					
				165						170					

(2) INFORMATIONS POUR LA SEQ ID NO: 1053:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 232 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1014529..1015224)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1053:

Asn	Ser	Leu	Glu	Thr	Ile	Met	Thr	Asp	Phe	His	Asp	Lys	Pro	Asn	Ile
1				5					10					15	
Gln	Ile	Met	Phe	Asp	Ser	Leu	Ala	Pro	Thr	Tyr	Asp	Lys	Ile	Asn	Gly
			20					25					30		
Ile	Leu	Ser	Leu	Gly	Leu	His	Ile	Ala	Trp	Asn	Asn	Ala	Leu	Val	Ser
			35				40					45			
Leu	Leu	Gly	Glu	Thr	Asn	His	Leu	Leu	Asp	Leu	Cys	Ala	Gly	Thr	Gly
	50					55				60					
Arg	Val	Ala	Leu	Ser	Tyr	Val	Gln	Asn	Tyr	Pro	Arg	Ala	Ser	Ala	Thr
65					70				75					80	
Leu	Val	Asp	Phe	Ser	Thr	Lys	Met	Leu	Glu	Asn	Val	Gln	Lys	Arg	His
				85				90					95		
Pro	Ser	Ala	Pro	Phe	Ser	Tyr	Ile	Thr	Ser	Asp	Val	Thr	His	Leu	Pro
			100					105					110		
Leu	Pro	Asp	Asn	Thr	Phe	Arg	Leu	Ala	Ser	Met	Ala	Tyr	Gly	Leu	Arg
			115				120					125			
Asn	Leu	Ser	Tyr	Pro	Leu	Glu	Ala	Leu	Arg	Glu	Val	Tyr	Arg	Val	Leu
			130			135					140				
Gln	Pro	Gly	Gly	His	Leu	Gly	Ile	Leu	Glu	Leu	Thr	Arg	Pro	Ala	Thr
145					150				155					160	
Tyr	Asn	Pro	Val	Tyr	Leu	Leu	His	Lys	Leu	Tyr	Leu	Asn	Leu	Val	Val
				165				170					175		
Pro	Ser	Val	Gly	Arg	Phe	Tyr	Ser	Gly	Asn	Ser	Tyr	Ala	Tyr	Ser	Tyr
			180					185					190		
Leu	Lys	Glu	Ser	Ile	Arg	Asp	Leu	Pro	Arg	Met	Pro	Leu	Ser	Lys	Gln
		195					200					205			
Ser	Phe	Met	Gln	Arg	Ile	Tyr	Ala	Leu	Ser	Gly	Asn	Ala	Asn	Tyr	Phe
	210					215					220				
Leu	Ala	Gln	Gln	Pro	Phe	Gly	Phe								
225						230									

(2) INFORMATIONS POUR LA SEQ ID NO: 1054:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 286 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1015145..1016002)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1054:

```

Arg Asp Val Pro Ser His Asn Thr Thr Trp Ser Tyr Pro Met Leu Ser
1          5          10          15
Gln Phe Gln Asp Arg Leu Asn Ile Gly Cys Val Arg Tyr Val Asn Ala
20          25          30
Leu Pro Phe Ser Ser Gly Leu Ser Gln Ala Pro Gly Val Ser Leu Leu
35          40          45
Met Asp Thr Pro Thr Asn Leu Val Pro Lys Leu Leu Ser Arg Glu Ile
50          55          60
Asp Tyr Ala Leu Thr Ser Val Ala Ala Thr Phe Ser Ser Ser Leu His
65          70          75          80
Arg Val Ser Ser Phe Gly Ile Ala Ala Tyr Lys Lys Ile Leu Ser Val
85          90          95
Asn Leu His Ala Thr Ser Gln Phe Phe Ala Lys Glu Ala Pro His Ile
100         105         110
Ala Ala Thr Lys Glu Ser Leu Ser Ile Leu Leu Leu Arg Val Leu
115         120         125
Cys Glu Asn Leu Trp Asn Ile Pro Phe Pro Ser Val Thr Leu Leu Ser
130         135         140
Ser Asp Ser Ile Leu Thr Gln Ala Glu His Tyr Asp Ala Leu Leu Leu
145         150         155         160
Ile Gly Asp Thr Ala Leu Arg His Pro Ile Ile Pro Gly Phe His Thr
165         170         175
Tyr Asp Leu Ala Ala Ser Trp Tyr Asp Leu Thr Ala Lys Pro Phe Val
180         185         190
Phe Ala Gly Ile Leu Ser Leu Ser Thr Ile Ser Phe Gln Leu Gln
195         200         205
Gln Glu Phe Ser Ser Thr Leu Asn Tyr Phe Gln Asn His Lys Glu Asp
210         215         220
Ile Thr Ser Lys Ala Ala Ala Leu Leu Lys Leu Pro Glu Ser Leu Met
225         230         235         240
Gln Glu Tyr Tyr Thr Leu Cys Arg Tyr Glu Leu Ser Glu Glu Asp Phe
245         250         255
Ala Gly Leu Glu Gln Phe Arg Asp Tyr Tyr Asp Arg Leu Pro Arg Gln
260         265         270
Ala Lys Tyr Pro Asn His Val Arg Phe Ser Cys Ala Tyr Leu
275         280         285

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1055:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 352 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1015939..1016994)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1055:

```

Leu Phe Asp Asp Tyr Leu Ser Gly Ala Arg Leu Ser Glu Lys Gln Ala
1          5          10          15
Leu Gln Leu Leu Leu Val Asp Ala Glu Asp Gln Gln Ala Leu Trp Ser
20          25          30
Phe Ala Asp Leu Ile Arg Ala Asn Arg Val Gly Asp Thr Val Phe Tyr

```

```

          35          40          45
Ser Ser Thr Leu Tyr Leu Tyr Pro Thr Asn Phe Cys Gln Phe Asn Cys
50          55          60
Thr Phe Cys Ser Phe Tyr Ala Lys Pro Gly Asn Pro Thr Gly Trp Phe
65          70          75          80
Phe Thr Pro Asp Gln Leu Val Gln Ser Ile Lys Glu Asn Pro Ser Pro
85          90          95
Ile Thr Glu Thr His Ile Val Ala Gly Cys Tyr Pro Ser Cys Asn Leu
100          105          110
Ala Tyr Tyr Glu Glu Leu Phe Ser Lys Ile Lys Gln Asn Phe Pro Asp
115          120          125
Leu His Ile Lys Ala Leu Ser Ala Ile Glu Tyr Asp Tyr Leu Ser Lys
130          135          140
Leu Asp Asn Leu Pro Val Lys Glu Val Met Gln Arg Leu Arg Ile Ala
145          150          155          160
Gly Leu Asp Ser Ile Pro Gly Gly Gly Ala Glu Ile Leu Val Asp Glu
165          170          175
Val Arg Glu Thr Leu Ser Arg Gly Arg Leu Ser Ser Gln Gly Phe Leu
180          185          190
Glu Ile His Glu Thr Ala His Ser Leu Gly Ile Pro Ser Asn Ala Thr
195          200          205
Met Leu Cys Tyr His Arg Glu Thr Pro Ala Asp Ile Met Thr His Met
210          215          220
Ser Lys Leu Arg Ala Leu Gln Asp Lys Thr Ser Gly Phe Lys Asn Phe
225          230          235          240
Ile Leu Leu Lys Phe Ala Ser Glu Asn Asn Ala Leu Gly Lys Arg Leu
245          250          255
His Lys Met Thr Ser Arg His Ser Ile Pro Pro Ala Thr Ile Ile Ala
260          265          270
Val Ala Arg Leu Phe Leu Asp Asn Ile Pro Asn Ile Lys Ala Leu Trp
275          280          285
Asn Tyr Leu Gly Leu Asp Val Ala Leu His Leu Leu Ser Cys Gly Xaa
290          295          300
Asn Asp Leu Ser Ser Thr His Gln Gly Glu Lys Val Phe Arg Met Ala
305          310          315          320
Ser Ser Gln Glu Pro Ile Arg Met Asp Ile Glu Gly Met Ser His Leu
325          330          335
Ile Ile Gln His Gly Arg Ile Pro Cys Leu Val Asn Ser Lys Thr Val
340          345          350

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1056:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 174 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1017245..1017766)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1056:

```

Arg Glu Thr Cys Val Phe Gly Phe Val Ala Gly Gly Leu Asp Asp Arg
1          5          10          15
Asn Leu Tyr Asn His Phe Phe Asp Ser Asp Gln Gln Gln Tyr Ser Pro
20          25          30

```

```

Gly Leu Thr Ala Val Ile Cys Asn Lys Tyr Ser Arg Asp Ser Leu Leu
      35              40              45
Glu Ala Leu Tyr Gln Arg Gln Cys Tyr Ala Thr Thr Gly Gln Arg Ile
      50              55              60
Ile Val Asn Phe Gln Ile Thr Ser Ala Pro Met Gly Ser Glu Leu Ser
65      70              75              80
Thr Ala Ile Lys Pro Gly Leu Val Ile Asn Arg His Ile Ser Gly Tyr
      85              90              95
Val Ala Gly Thr Ala Lys Ile Ala Ser Ile Glu Ile Ile Arg Asn Gly
      100             105             110
Asp Ile Leu His Pro Phe His Pro Asp Gly Asn Asn Phe Glu Tyr Glu
      115             120             125
Tyr Asp Asp Leu Ser Pro Phe Ala Gln Val Thr Leu Lys Asp Pro Gln
      130             135             140
Asn Gly Ala Pro Phe Ala Phe Tyr Tyr Leu Arg Val Thr Gln Glu Asn
145      150             155             160
Gly Ala Met Ala Leu Ser Ser Pro Xaa Trp Ile Asp Leu Asn
      165             170

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1057:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 332 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1017916..1018911)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1057:

```

Lys Arg Leu Pro Arg Ile Leu Trp Leu Gln Lys Leu Cys Met Leu Pro
1      5              10              15
Glu Ala Ile Ser Leu Leu Ser Asn Leu Leu Ser Leu Val Met Trp Lys
      20              25              30
Leu Gly Thr Leu Ser Leu Leu Phe Leu Ala Pro Leu Pro Thr Ser Leu
      35              40              45
Lys Arg Thr Leu Gln Val Met Val Leu Asn Tyr Leu Leu Asn Ala Val
50      55              60
Asn Leu Ser Leu Phe Met Leu Thr His Gln Gly Lys Asp Leu Leu Lys
65      70              75              80
Asp Pro Asp Ile Phe Thr Met Asp Ile Arg Gly Asn Val Leu Lys Asn
      85              90              95
Ile Arg Ile Phe Ala Pro Ser Tyr Val Ile Lys Asn Lys Arg Phe Asp
      100             105             110
Ile Thr Val Arg Phe Glu Asp Glu Phe Gly Asn Leu Thr Asn Phe Ser
      115             120             125
Pro Glu Glu Thr His Ile Glu Leu Ser Tyr Glu His Leu Arg Glu Asn
      130             135             140
Leu Asn Trp Gln Leu Phe Ile Pro Glu Thr Gly Phe Val Ile Leu Pro
145      150             155             160
Asn Leu Tyr Phe Asn Glu Pro Gly Ile Tyr Arg Ile Gln Leu Arg Asn
      165             170             175
Gln Ala Thr Lys Glu Val Phe Thr Ser Ala Pro Ile Lys Cys Phe Ala
      180             185             190
Glu Thr Ser Ser His Leu Leu Trp Gly Leu Leu His Gly Glu Ser Asp

```

```

                195                200                205
Arg Val Asp Ser Glu Gly Asn Ile Glu Ser Cys Leu Arg Tyr Phe Arg
210                215                220
Asp Asp Cys Ala Leu Asn Phe Phe Ala Thr Ser Ser Phe Glu Ile Gln
225                230                235                240
Asp Gly Leu Thr Pro Glu Thr Ile Lys Thr Ile Asn Gln Thr Val Ala
245                250                255
Asp Phe Asn Glu Glu Asp Arg Phe Ile Ala Leu Ser Gly Ala Gln Tyr
260                265                270
Leu Ser Glu Glu Pro Gly Glu Gly Ile Arg Glu Val Leu Leu Met Lys
275                280                285
Glu Pro Lys Ser Pro Gly Lys His Lys Glu Cys Lys Leu Phe Pro Leu
290                295                300
Ser Lys Leu Tyr Lys Gln Ser Thr Ser His Glu Leu Ile Ser Ile Pro
305                310                315                320
Gln Leu His Cys Phe Lys Glu Ile Trp Ile Gln Phe
325                330

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1058:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 204 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1018580..1019191)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1058:

```

Arg Ser Ser Val Lys His Ala Lys Ala Lys Phe Leu Gln Ile Lys Asp
1      5      10      15
Phe Leu Val Thr Arg Thr Tyr Ile Leu Val Ala Met Arg Arg Ser Val
20     25     30
Cys Tyr Val Thr Pro Ser Val Ala Arg Ala Gly Gln Ile Ser Thr Trp
35     40     45
Arg Phe Glu Tyr Ser Ser Ala Asn Phe Leu Pro Glu Gly Thr Leu Leu
50     55     60
Lys Phe Asp Leu Gly Ile Asp Gly Arg Pro Ile Asp Trp Glu Ile Pro
65     70     75     80
Ser Ile Asp Leu Ser Gln Pro Cys Asn Thr Ile Tyr Leu Glu Thr Pro
85     90     95
Ser Glu Asp Ile Val Ala Ala Lys Ala Val Tyr Ala Pro Gly Gly Tyr
100    105    110
Ile Pro Thr Phe Glu Phe Thr Leu Pro Cys Asp Val Glu Ala Gly Asp
115    120    125
Thr Phe Ser Ile Ile Leu Gly Ser Ser Pro Asn Phe Pro Gln Glu Asp
130    135    140
Ser Ser Gly Asn Gly Ala Gln Leu Phe Thr Gln Arg Arg Lys Pro Phe
145    150    155    160
Ser Leu Tyr Val Asp Pro Ser Gly Lys Gly Ser Phe Glu Arg Ser Arg
165    170    175
Tyr Leu His Asn Gly Tyr Gln Arg Lys Cys Ile Lys Lys Tyr Pro Asp
180    185    190
Phe Cys Ser Phe Leu Cys Asp Gln Lys Gln Thr Leu
195    200

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1059:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 123 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1019831..1020199)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1059:

Arg	Leu	Ser	Leu	Met	Asn	Thr	Asp	Leu	Gln	Lys	Ala	Phe	Val	Ser	Met	1	5	10	15
Glu	Asp	Ile	Val	Glu	Glu	Ile	Phe	Gly	Glu	Ile	Ala	Asp	Glu	Tyr	Asp	20	25	30	
Asp	Gln	Glu	Asp	Val	His	Tyr	Lys	Xaa	Ile	Gly	Asn	Ala	Trp	Ile	Val	35	40	45	
Asp	Gly	Arg	Met	Asn	Ile	Ser	Asp	Ala	Glu	Glu	Cys	Phe	Gly	Leu	His	50	55	60	
Ile	Glu	His	Glu	Ser	Ser	Tyr	Asp	Thr	Leu	Gly	Gly	Tyr	Val	Phe	His	65	70	75	80
Lys	Leu	Gly	Ala	Val	Pro	Glu	Lys	Gly	Met	Lys	Ile	Tyr	Tyr	Glu	Asp	85	90	95	
Phe	Ala	Ile	Asp	Ile	Leu	Ser	Cys	Ser	Asp	Arg	Ser	Val	Glu	Lys	Met	100	105	110	
Lys	Ile	Thr	Pro	Arg	Arg	Arg	Lys	Pro	Leu	Ser						115	120		

(2) INFORMATIONS POUR LA SEQ ID NO: 1060:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 298 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1020114..1021007)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1060:

Ala	Ser	Ser	Leu	Phe	Val	Asp	Ser	Pro	Asn	Asn	Phe	Phe	Tyr	Arg	Ser	1	5	10	15
Trp	Leu	Phe	Ser	Pro	Leu	Ile	Met	Leu	Tyr	Ile	Leu	Leu	Ala	Ile	Ile	20	25	30	
Val	Leu	Phe	Leu	Phe	Leu	Gly	Ser	Ala	Thr	His	Arg	Arg	Ala	Ser	Ile	35	40	45	
Ser	Ala	Tyr	Gly	Gly	Glu	Gly	Leu	Pro	Pro	Phe	Ser	Ser	Cys	Pro	Lys	50	55	60	
Val	Leu	Pro	Leu	Leu	Cys	Leu	Ile	Tyr	Gly	Met	Leu	Gly	Ala	Pro	Val	65	70	75	80
Tyr	Gln	Tyr	Ile	His	Asn	Phe	Phe	Ser	Leu	Ser	Pro	Ser	Ile	Phe	Trp				

```

      85      90      95
Leu Ile Phe Leu Ser Leu Ala Leu Val Ile Tyr Lys Phe Leu Pro Leu
      100      105      110
Cys Pro Gly Tyr Ser Asp Asp Ser Phe Ser Tyr Lys Val Ser Ser Ser
      115      120      125
Thr Val Lys Thr Leu Glu Asn Cys Leu Ala Gly Phe Lys Thr Pro Ser
      130      135      140
Ile Thr Ala Met Gln Gln Thr Pro Pro Pro Glu Pro Pro Asn Glu Leu
145      150      155      160
Ser Thr Asn Ile Ser Cys Leu Asn His Met Ile Ala Arg Glu Ile Met
      165      170      175
Thr Pro Lys Ala Asp Ile Phe Ala Leu Gln Gly Asp Thr Pro Ile Ser
      180      185      190
Gln Ala Phe Pro Leu Ile Ile Asp Glu Gly Tyr Ser Arg Ile Pro Leu
      195      200      205
Phe Thr Lys Ser Ile Asp Asp Ile Thr Gly Met Val Leu Val Lys Asp
210      215      220
Leu Ser Pro Val Tyr Tyr Lys Asp Pro His Thr Ser Gln Pro Leu Ser
225      230      235      240
Ser Ile Ala Tyr Pro Pro Leu Tyr Thr Pro Glu Ile Arg Arg Ala Ser
      245      250      255
Leu Leu Leu Gln Glu Phe Xaa Gln Lys Arg Cys His Leu Ala Ile Val
      260      265      270
Val Asn Glu Tyr Gly Phe Thr Glu Gly Leu Cys Leu Tyr Gly Arg Tyr
      275      280      285
Arg Arg Arg Asn Leu Trp Arg Asn Cys Arg
290      295

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1061:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
 (A) LONGUEUR: 165 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1021075..1021569)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1061:

```

Val Ile Phe Phe Leu Leu Ile Leu Asp Arg Ser Ser Pro Gln Ile Phe
1      5      10      15
Ile Ser Asn Glu Gln Gln Asp Val Ser Ile Asp Leu Gln Ser Ala Gln
      20      25      30
Arg Leu Val Val Leu Phe Leu Glu Leu Gln Lys Val Ser Thr Asp Gln
      35      40      45
Val Tyr Val Tyr Phe Leu Asp Asp Thr Ala Leu Ala Gln Leu His Asp
      50      55      60
Glu Gln Phe Ser Asp Pro Ser Leu Thr Asp Thr Ile Thr Leu Pro Ile
65      70      75      80
Asp Lys Pro Gly Ile Ala Ser Phe Pro His Val Leu Gly Glu Ala Phe
      85      90      95
Val Ser Pro Lys Ala Ala Met Arg Phe Leu Glu Gln Tyr Thr Glu Asp
      100      105      110
Gln Leu Tyr His Glu Ile Ser Arg Tyr Val Val His Ser Leu Leu His
      115      120      125

```

Met Leu Gly Tyr Asp Asp Gln Thr Asp Glu Asp Lys Arg Ile Met Gln
 130 135 140
 Glu Gln Glu Asp Val Ser Leu Ser Phe Leu Ala Glu His Gln Ala Leu
 145 150 155 160
 Leu Arg Pro Ala Val
 165

(2) INFORMATIONS POUR LA SEQ ID NO: 1062:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 105 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1022097..1022411)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1062:

Gln Gln Ser Leu Gly Leu Asn Gln Asp Pro Leu Asn Lys Val Val Met
 1 5 10 15
 Val Pro Phe Pro Asn Arg Glu Val Leu Cys Ile Gly Leu Val Ala Gly
 20 25 30
 Glu Ala Pro Thr Thr Cys Ser Gln Asp Ala Asp Asp Pro Met Ile Thr
 35 40 45
 Val Phe Ile Pro Thr Thr Pro Asn Pro Thr Ser Gly Phe Leu Thr Leu
 50 55 60
 Phe Lys Lys Ser Asp Ile Thr Phe Leu Asp Met Lys Ile Glu Asp Ala
 65 70 75 80
 Phe Lys Tyr Val Ile Ser Cys Gly Val Leu Asn Ser Asp Pro Cys Ala
 85 90 95
 Thr Ser Pro Phe Ile His Pro Gln Phe
 100 105

(2) INFORMATIONS POUR LA SEQ ID NO: 1063:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 107 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1023347..1023667

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1063:

Met Glu Pro Tyr Ala Val Ile Gln Thr Gly Asn Lys Gln Tyr Gln Val
 1 5 10 15
 Arg Lys Gly Asp Val Ile Asp Val Glu Leu Leu Asp Gly Ile Ser Glu
 20 25 30
 Glu Asn Lys Glu Val Leu Phe Gln Asp Val Leu Phe Thr Phe Asp Gly
 35 40 45
 Glu Lys Ala Ser Val Gly Ala Pro Thr Val Gly Asn Ala Val Val Lys

```

          50          55          60
Gly Glu Leu Val Ser Phe Val Arg Gly Glu Lys Val Val Ala Tyr Lys
65          70          75          80
Tyr Lys Lys Arg Lys Asn Tyr His Lys Lys Ile Gly His Arg Gln Asn
          85          90          95
Tyr Leu Arg Val Lys Ile Ser Asp Leu Val Met
          100          105

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1064:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 83 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1023701..1023949

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1064:

```

Met Ala His Lys Lys Gly Gln Gly Ala Ser Arg Asn Gly Arg Asp Ser
1          5          10          15
Glu Ser Lys Arg Leu Gly Leu Lys Val Gly Ala Gly Gln Arg Val Ser
          20          25          30
Thr Gly Ser Ile Leu Val Arg Gln Arg Gly Thr Lys Trp His Pro Ala
          35          40          45
Val Asn Val Gly Arg Gly Lys Asp Asp Thr Leu Phe Ala Leu Ala Asp
          50          55          60
Gly Ile Val Val Met Lys Lys Thr Asp Arg Thr Tyr Val Ser Val Ile
65          70          75          80
Pro Gln Ala

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1065:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
- (A) LONGUEUR: 245 acides aminés
- (B) TYPE: acide aminé
- (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1024042..1024776

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1065:

```

Met Phe Val Asp Gln Ile Thr Leu Glu Leu Arg Ala Gly Lys Gly Gly
1          5          10          15
Asn Gly Val Val Ala Trp Arg Lys Glu Lys Tyr Leu Pro Lys Gly Gly
          20          25          30
Pro Tyr Gly Gly Asn Gly Gly Asn Gly Gly Ser Ile Leu Ile Glu Thr
          35          40          45
Val Thr Asn Met Tyr Ser Phe Glu Glu Tyr Arg Asn Leu Arg Phe Leu
50          55          60

```



```

Lys Ala Asp Asp Gly Gln Ala Gly Ala Ser Asn Asn Arg Thr Gly Arg
65          70          75          80
Asn Gly Lys Asp Leu Val Leu Lys Val Pro Glu Gly Thr Leu Leu Arg
          85          90          95
Asp Ala Ala Thr Gly Glu Leu Ile His Asp Phe Thr Lys Asp Gly Glu
          100         105         110
Arg Ile Val Val Cys Gln Gly Gly Arg Gly Gly Lys Gly Asn Val Phe
          115         120         125
Phe Lys Thr Ser Thr Asn Arg Ala Pro Thr Lys Ala Thr Pro Gly Lys
          130         135         140
Pro Gly Glu Ile Arg Leu Val Glu Leu Glu Leu Lys Leu Ile Ala Asp
145          150         155         160
Ile Gly Leu Val Gly Phe Pro Asn Ala Gly Lys Ser Thr Leu Phe Asn
          165         170         175
Thr Leu Ala Arg Thr Glu Val Lys Val Gly Ala Tyr Pro Phe Thr Thr
          180         185         190
Leu His Pro Ser Leu Gly Leu Val His Gln Glu Gly Met Leu Tyr Gln
          195         200         205
Lys Thr Trp Ile Met Ala Asp Ile Pro Gly Ile Ile Glu Gly Ala Ser
          210         215         220
Gln Asn Arg Gly Leu Gly Leu Asp Phe Phe Gly Ile Leu Asn Val Arg
225          230         235         240
Asp Tyr Cys Tyr Ser
          245

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1066:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 114 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1024704..1025045

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1066:

```

Arg Ser Val Ala Lys Pro Gly Ile Gly Ile Gly Phe Leu Arg His Ile
1          5          10          15
Glu Arg Thr Arg Leu Leu Leu Phe Val Ile Asp Ile Ser Gly Ile Glu
          20          25          30
Arg His Ser Pro Glu Gln Asp Leu Lys Ile Leu Met Gly Glu Leu Leu
          35          40          45
Ala Tyr Lys Glu Glu Leu Lys Asp Lys Asp Met Val Ile Ala Leu Asn
          50          55          60
Lys Ile Asp Gln Leu Leu Pro Asp Glu Arg Glu Glu Arg Val Ala Leu
65          70          75          80
Leu Lys Gln Gln Phe Pro Asp Gln Glu Phe Ile Leu Leu Ser Gly Leu
          85          90          95
Thr Gly Glu Gly Val Asp Ala Leu Tyr Asp Leu Phe Lys Ser Lys Leu
          100         105         110
Ser Glu

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1067:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 305 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1024967...1025881)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1067:

```

Asn Phe Arg Lys Ile Leu Leu Gln His Phe Trp Glu Met Pro Met Ile
1      5      10      15
Ser Ile Leu Cys Ser Leu Phe Pro Pro Leu Leu Phe Pro Ser Leu Leu
20      25      30
Ala Ala Phe Gly Ala Ser Ile Ala Ala Gly Ile Val Gly Ser Tyr Ile
35      40      45
Val Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile Ala His Ser Ile
50      55      60
Leu Gly Gly Val Gly Ile Ala Leu Trp Leu Gln Tyr Gln Phe Asn Leu
65      70      75      80
Pro Ile Ser Pro Leu His Gly Ala Ile Ala Ser Ala Ile Phe Val Ala
85      90      95
Ile Cys Ile Gly Asn Val His Leu Lys Tyr His Glu Arg Glu Asp Ser
100      105      110
Ile Ile Ser Met Ile Trp Ser Ile Gly Met Ala Ile Gly Ile Ile Cys
115      120      125
Ile Ser Lys Leu Pro Ser Phe Asn Ser Glu Leu Ser Asp Phe Leu Phe
130      135      140
Gly Asn Ile Leu Trp Val Thr Pro Gln Asp Leu Tyr Phe Leu Gly Ile
145      150      155      160
Leu Asp Leu Phe Ile Val Ala Thr Val Ser Ile Cys His Thr Arg Phe
165      170      175
Leu Ala Leu Cys Phe Asp Glu Lys Tyr Met Ala Leu Asn His Tyr Ser
180      185      190
Ile Lys Thr Trp Tyr Leu Leu Leu Leu Ile Leu Thr Ala Ile Thr Thr
195      200      205
Val Val Leu Met Tyr Val Met Gly Val Ile Leu Met Leu Ser Met Leu
210      215      220
Val Leu Pro Val Ser Ile Ala Cys Arg Phe Ser Tyr Lys Met Ser His
225      230      235      240
Ile Ile Tyr Ile Ala Ser Ile Leu Asn Ile Val Cys Ser Phe Leu Gly
245      250      255
Ile Met Leu Ala Tyr Leu Leu Asp Leu Pro Val Gly Pro Val Ile Ala
260      265      270
Ile Leu Met Gly Gly Ala Tyr Ser Leu Ser Leu Leu Leu Asn Arg Ser
275      280      285
Tyr Asn Ala Ser Thr Pro Ser Pro Val Ser Pro Glu Ser Lys Ile Asn
290      295      300
Ser
305

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1068:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 236 acides aminés

(iii) HYPOTHETIQUE: oui

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1068:

(2) INFORMATIONN POUR LA SEQ ID NO: 1069:

(A) LONGUEUR: 278 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1026546..1027379)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1069:

Asp Asn Met Arg Leu Leu Phe Leu Leu Leu Phe Ser Leu Gly Ile Thr
 1 5 10 15
 Cys Ser Tyr Gly Asp Glu Val Ser Thr Arg Lys Gln Ile Leu Val Ser

```

                20                25                30
Ile Val Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Gly Asp Thr Cys
                35                40                45
Gln Val Phe Ser Ile Val Met Asp Asn His Asp Pro His Asn Tyr Glu
                50                55                60
Leu Ser Pro Lys Tyr Ile Glu Lys Ile Arg Gln Val Glu Leu Trp Phe
65                70                75                80
Arg Ile Gly Glu Gly Phe Glu Lys Thr Cys Glu Arg Ile Ile Ser Cys
                85                90                95
Lys Gln Val Asp Leu Ala Ala Asn Ile Asp Lys Ile Thr Asn Gly Ala
                100                105                110
Cys Cys Gln Arg Phe Leu Ser Phe Asp Thr His Thr Trp Leu Ser Pro
                115                120                125
Lys Asn Leu Lys Ile Gln Ile Gln Ala Ile Thr Glu Ala Leu Val Glu
130                135                140
Thr Ala Pro Glu His Glu Thr Leu Tyr Arg Lys Asn Cys Ser Leu Leu
145                150                155                160
Gln Ser Gln Leu Asp Leu Leu Asp Gln Lys Ile Ser Ser Ile Val Ser
                165                170                175
Ser Thr Ser Gln Arg Asn Val Leu Val Thr His Gly Ala Phe Ala Tyr
                180                185                190
Phe Cys Arg Asp Tyr Gly Phe Ile Gln His Thr Ile Glu Arg Ala Asn
                195                200                205
His Ser Glu Leu Ser Pro Lys Asp Val Val Arg Val Glu Arg Thr Ile
210                215                220
Arg Asp His Asn Leu His Ser Val Ile Leu Leu Lys His Ala Gly Lys
225                230                235                240
Arg Ser Ser Ala Ala Leu Val Arg Lys Phe Asn Met Thr Pro Ile Leu
                245                250                255
Leu Asp Pro Tyr Ala Glu Asp Val Phe Asn Asn Leu Leu Ala Ile Ala
260                265                270
Thr Ala Phe Ala Asn Leu
275

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1070:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 892 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1027929..1030604)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1070:

```

Arg Asp Ser Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser
1                5                10                15
Gln Ser Thr Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr
                20                25                30
Val Thr Ile Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn
35                40                45
Asn Ala Asn Asn Ala Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly
50                55                60
Ala Ile Gly Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe
65                70                75                80

```

Leu Glu Asn Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Asp
 85 90 95
 Thr Gln Asn Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe
 100 105 110
 Glu Lys Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val
 115 120 125
 Ser Ile Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu
 130 135 140
 Glu Gly Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu
 145 150 155 160
 Gly Ser Val Leu Phe Thr Gly Asn Leu Val Thr Pro Thr Leu Ser Thr
 165 170 175
 Thr Thr Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr
 180 185 190
 Gly Ala Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr
 195 200 205
 Asp Asn Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly Asn Ile Cys Phe
 210 215 220
 Arg Asn Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr Gly Thr Ser Thr
 225 230 235 240
 Phe Cys Ser Ile Ala Gly Asp Val Lys Leu Thr Met Gln Ala Ala Lys
 245 250 255
 Gly Lys Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr Ser Thr Lys Lys
 260 265 270
 Thr Gly Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp Ile Asn Lys Ser
 275 280 285
 Glu Asp Ser Glu Thr Val Asn Ser Ala Phe Thr Gly Thr Ile Leu Phe
 290 295 300
 Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Val Val
 305 310 315 320
 Leu His Ser Gly Ser Leu Val Leu Lys Pro Asn Thr Glu Leu His Val
 325 330 335
 Ile Ser Phe Glu Gln Lys Glu Gly Ser Ser Leu Val Met Thr Pro Gly
 340 345 350
 Ser Val Leu Ser Asn Gln Thr Val Ala Asp Gly Ala Leu Val Ile Asn
 355 360 365
 Asn Met Thr Ile Asp Leu Ser Ser Val Glu Lys Asn Gly Ile Ala Glu
 370 375 380
 Gly Asn Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile Asp Thr Thr Thr
 385 390 395 400
 Ser Gly Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu Ser Asn Gln Asn
 405 410 415
 Ser Asp Asp Thr Lys Glu Gln Asn Asn Asn Asp Ala Ser Asn Gln Gly
 420 425 430
 Glu Ser Ala Asn Gly Ser Ser Ser Pro Ala Val Ala Ala Ala His Thr
 435 440 445
 Ser Arg Thr Arg Asn Phe Ala Ala Ala Thr Ala Thr Pro Thr Thr
 450 455 460
 Thr Pro Thr Ala Thr Thr Thr Ser Asn Gln Val Ile Leu Gly Gly
 465 470 475 480
 Glu Ile Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe Gln Asn Pro Ala
 485 490 495
 Leu Arg Ser Asp Gln Gln Ile Ser Leu Leu Val Leu Pro Thr Asp Ser
 500 505 510
 Ser Lys Met Gln Ala Gln Lys Ile Val Leu Thr Gly Asp Ile Ala Pro
 515 520 525
 Gln Lys Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro Asp Gln Leu Gln
 530 535 540
 Asn Gly Thr Ile Ser Ala Leu Trp Lys Phe Asp Ser Tyr Arg Gln Trp

Met	Lys	Phe	Leu	Ser	Ala	Thr	Ala	Val	Phe	Ala	Ala	Val	Leu	Ser	Ser
1				5					10				15		
Val	Thr	Glu	Ala	Ser	Ser	Ile	Gln	Asp	Gln	Ile	Lys	Asn	Thr	Asp	Cys
		20					25					30			
Asn	Val	Ser	Lys	Val	Gly	Tyr	Ser	Thr	Ser	Gln	Ala	Phe	Thr	Asp	Met
	35					40						45			
Met	Leu	Ala	Asp	Asn	Thr	Glu	Tyr	Arg	Ala	Ala	Asp	Ser	Val	Ser	Phe
	50					55					60				
Tyr	Asp	Phe	Ser	Thr	Ser	Ser	Gly	Leu	Pro	Arg	Lys	His	Leu	Ser	Ser
65					70					75				80	
Ser	Ser	Glu	Ala	Ser	Pro	Thr	Thr	Glu	Gly	Val	Ser	Ser	Ser	Ser	Ser
			85					90						95	
Gly	Glu	Asn	Thr	Glu	Asn	Ser	Gln	Asp	Ser	Ala	Pro	Ser	Ser	Gly	Glu
		100					105						110		
Thr	Asp	Lys	Lys	Thr	Glu	Glu	Glu	Leu	Asp	Asn	Gly	Gly	Ile	Ile	Tyr
	115						120					125			
Ala	Arg	Glu	Lys	Leu	Thr	Ile	Ser	Glu	Ser	Gln	Asp	Ser	Leu	Ser	Asn
	130					135					140				
Pro	Ser	Ile	Glu	Leu	His	Asp	Asn	Ser	Phe	Phe	Phe	Gly	Glu	Gly	Glu
145					150					155					160
Val	Ile	Phe	Asp	His	Arg	Val	Ala	Leu	Lys	Asn	Gly	Gly	Ala	Ile	Tyr
			165					170						175	
Gly	Glu	Lys	Glu	Val	Val	Phe	Glu	Asn	Ile	Lys	Ser	Leu	Leu	Val	Glu
		180					185						190		
Val	Asn	Ile	Xaa	Xaa	Glu	Lys	Gly	Ser	Val	Tyr	Ala	Lys	Glu	Arg	
	195					200					205				
Val	Ser	Leu	Glu	Asn	Val	Thr	Glu	Ala	Thr	Phe	Ser	Ser	Asn	Gly	Gly
	210					215					220				
Glu	Gln	Gly	Gly	Gly	Gly	Ile	Tyr	Ser	Glu	Gln	Asp	Met	Leu	Ile	Ser
225					230					235					240
Asp	Cys	Asn	Asn	Val	His	Phe	Gln	Gly	Asn	Ala	Ala	Gly	Ala	Thr	Ala
			245					250						255	
Val	Lys	Gln	Cys	Leu	Asp	Glu	Glu	Met	Ile	Val	Leu	Leu	Thr	Glu	Cys
		260					265						270		
Val	Asp	Ser	Leu	Ser	Glu	Asp	Thr	Leu	Asp	Ser	Thr	Pro	Glu	Thr	Glu
	275					280						285			
Gln	Thr	Lys	Ser	Asn	Gly	Asn	Gln	Asp	Gly	Ser	Ser	Glu	Thr	Lys	Asp
	290					295					300				
Thr	Gln	Val	Ser	Glu	Ser	Pro	Glu	Ser	Thr	Pro	Ser	Pro	Asp	Asp	Val
305					310					315					320
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Tyr	Thr	Glu	Lys	Ser	Leu	Thr	Ile	Thr
			325					330						335	
Gly	Ile	Thr	Gly	Thr	Ile	Asp	Phe	Val	Ser	Asn	Ile	Ala	Thr	Asp	Ser
		340						345					350		
Gly	Ala	Gly	Val	Phe	Thr	Lys	Glu	Asn	Leu	Ser	Cys	Thr	Asn	Thr	Asn
	355						360					365			
Ser	Leu	Gln	Phe	Leu	Lys	Asn	Ser	Ala	Gly	Gln	His	Gly	Gly	Gly	Ala
	370					375					380				
Tyr	Val	Thr	Gln	Thr	Met	Ser	Val	Thr	Asn	Thr	Ser	Glu	Ser	Ile	
385					390					395				400	
Thr	Thr	Pro	Pro	Leu	Val	Gly	Glu	Val	Ile	Phe	Ser	Glu	Asn	Thr	Ala
			405					410						415	
Lys	Gly	His	Gly	Gly	Gly	Ile	Cys	Thr	Asn	Lys	Leu	Ser	Leu	Ser	Asn
		420						425				430			
Leu	Lys	Thr	Val	Thr	Leu	Thr	Lys	Asn	Ser	Ala	Lys	Glu	Ser	Gly	Gly
	435					440						445			
Ala	Ile	Phe	Thr	Asp	Leu	Ala	Ser	Ile	Pro	Thr	Thr	Asp	Thr	Pro	Glu
	450					455					460				
Ser	Ser	Thr	Pro	Ser	Ser	Ser	Ser	Pro	Ala	Ser	Thr	Xaa	Glu	Val	Val

465 470 475 480
 Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu Pro Ala
 485 490 495
 Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln Thr Glu
 500 505 510
 Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn Ile Leu
 515 520 525
 Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly Ala Ile
 530 535 540
 Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu Leu Ser
 545 550 555 560
 Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr Glu Ser
 565 570 575
 Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn Ser Ala
 580 585 590
 Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu Ser Asn
 595 600 605
 Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala Ile Val
 610 615 620
 Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu Gly Glu
 625 630 635 640
 Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly Ser Ser
 645 650 655
 Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp Thr Gly
 660 665 670
 Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr Gly Asn
 675 680 685
 Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn Glu Glu
 690 695 700
 Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn Thr Asp
 705 710 715 720
 Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser Val Ser
 725 730 735
 Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly Ala Ala
 740 745 750
 Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn Ala Cys
 755 760 765
 Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val Ser Asn
 770 775 780
 Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser
 785 790 795 800
 Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly Pro Thr Glu Pro Glu
 805 810 815
 Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile Gly Gly Gly Ala Ile
 820 825 830
 Tyr Gly Glu Thr Val Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe
 835 840 845
 Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys
 850 855 860
 Ser Asn Val Leu Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu
 865 870 875 880
 Asp Ser Gly Thr Leu Asp Glu Leu Ser Pro Ser Pro Gly Ile Leu Ser
 885 890 895
 Leu Leu Asn Leu Gln Gln Val Arg Leu Leu Glu Glu Leu Ser Thr Leu
 900 905 910
 Leu Leu

(2) INFORMATIONS POUR LA SEQ ID NO: 1072:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 118 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1031733..1032086

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1072:

```

Ser Asp Ser Ala Ser Val Arg Glu Gly Ala Ala Gly Ser Ala Val Glu
1          5          10          15
Ala Lys Asn Arg Phe Ile Leu Ala Glu Ala Thr Thr Ser Xaa Val Leu
          20          25          30
Ala Gly Glu Glu Glu Glu Gly Val Glu Asp Ser Gly Val Ser Val Val
          35          40          45
Gly Ile Asp Ala Arg Ser Val Lys Ile Ala Pro Pro Asp Ser Phe Ala
          50          55          60
Glu Phe Leu Val Arg Val Thr Val Phe Lys Leu Asp Lys Glu Ser Leu
65          70          75          80
Leu Val Gln Ile Pro Pro Cys Pro Leu Ala Val Phe Ser Glu Lys
          85          90          95
Ile Thr Ser Pro Thr Arg Gly Gly Val Val Ile Leu Ser Leu Val Val
          100          105          110
Leu Val Thr Asp Met Val
          115

```

(2) INFORMATIONS POUR LA SEQ ID NO: 1073:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 1194 acides aminés
 (B) TYPE: acide aminé
 (D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1033456..1037037)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1073:

```

Leu Ile Thr His Gln Lys Asn Met Val Val Glu Pro Leu Leu Pro Lys
1          5          10          15
Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
          20          25          30
Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
          35          40          45
Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
          50          55          60
Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
65          70          75          80
Ala Tyr Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
          85          90          95
Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Asp Pro Val

```

100 105 110
 Ala Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu
 115 120 125
 Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Glu
 130 135 140
 Lys Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val
 145 150 155 160
 Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile
 165 170 175
 Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser
 180 185 190
 Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Lys Ser
 195 200 205
 Leu Lys Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu Val
 210 215 220
 Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser Asn
 225 230 235 240
 Leu Lys Ser Gly Phe Ser Phe Ser Asn Lys Ala Asn Ser Ser Ser
 245 250 255
 Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala Ser
 260 265 270
 Leu Gln Ala Ala Ala Ala Ala Ala Pro Ser Ser Pro Ala Thr Pro Thr
 275 280 285
 Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Gln Phe Thr Phe
 290 295 300
 Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile Asp
 305 310 315 320
 Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile Tyr
 325 330 335
 Ala Lys Thr Ser Leu Ser Ile Arg Ser Ser Asp Ala Gly Thr Ser Tyr
 340 345 350
 Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr Gly
 355 360 365
 Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn Cys
 370 375 380
 Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Met Ala Thr Pro Lys Thr
 385 390 395 400
 Ser Ser Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile Gly Gly Ala Ile
 405 410 415
 Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg Phe Ser Gly Asn
 420 425 430
 Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala Asn Ala Asn Thr
 435 440 445
 Pro Arg Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr Glu Lys Ile Thr
 450 455 460
 Leu Lys Asn Ser Ser Phe Ile Phe Glu Arg Asn Gln Ala Asn Lys Arg
 465 470 475 480
 Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly Asn Asn Ile Thr
 485 490 495
 Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala Ile Tyr Phe Thr
 500 505 510
 Lys Asp Ala Lys Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn
 515 520 525
 Lys Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser Gly Gln Asn Thr
 530 535 540
 Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp Pro Gly Thr Thr
 545 550 555 560
 Gln Ser Pro Gln Thr Asp Ala Ile Leu Thr Leu Leu Ala Ser Ser Gly
 565 570 575

Asn	Ile	Thr	Phe	Ser	Asn	Asn	Ser	Leu	Gln	Asn	Asn	Gln	Gly	Gly	Thr		
			580					585					590				
Pro	Ala	Ser	Lys	Phe	Cys	Ser	Ile	Ala	Gly	Tyr	Val	Lys	Leu	Ser	Leu		
			595				600					605					
Gln	Ala	Thr	Lys	Gly	Lys	Thr	Ile	Ser	Phe	Phe	Asp	Cys	Val	His	Thr		
	610					615					620						
Ser	Thr	Lys	Lys	Thr	Gly	Ser	Thr	Gln	Asn	Val	Tyr	Glu	Thr	Leu	Asp		
625					630					635					640		
Ile	Asn	Lys	Lys	Glu	Asn	Ser	Lys	Pro	Tyr	Thr	Gly	Thr	Ile	Val	Phe		
				645					650					655			
Ser	Ser	Glu	Leu	His	Glu	Asn	Lys	Ser	Tyr	Ile	Pro	Gln	Asn	Ala	Ile		
			660					665					670				
Leu	His	Asn	Gly	Thr	Leu	Val	Leu	Lys	Glu	Lys	Thr	Glu	Leu	His	Val		
	675					680						685					
Val	Ser	Phe	Glu	Gln	Lys	Glu	Gly	Ser	Lys	Leu	Ile	Met	Glu	Pro	Gly		
	690					695					700						
Ala	Val	Leu	Ser	Asn	Gln	Asn	Ile	Ala	Asn	Gly	Ala	Leu	Ala	Ile	Asn		
705					710					715					720		
Gly	Leu	Thr	Ile	Asp	Leu	Ser	Ser	Met	Gly	Thr	Pro	Gln	Ala	Gly	Glu		
				725					730					735			
Ile	Phe	Ser	Pro	Pro	Glu	Leu	Arg	Ile	Val	Ala	Thr	Thr	Ser	Ser	Ala		
			740					745					750				
Ser	Gly	Arg	Ser	Gly	Val	Ser	Arg	Ser	Ile	Pro	Thr	Asn	Pro	Lys	Gly		
	755						760					765					
Ile	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Ser	Ala	Ala	Thr	Thr	Pro	Thr	Met		
	770					775					780						
Ser	Glu	Asn	Lys	Val	Phe	Leu	Thr	Gly	Asp	Leu	Thr	Leu	Ile	Asp	Pro		
785					790				795						800		
Asn	Gly	Asn	Phe	Tyr	Gln	Asn	Pro	Met	Leu	Gly	Ser	Asp	Leu	Asp	Val		
			805					810					815				
Pro	Leu	Ile	Lys	Leu	Pro	Thr	Asn	Thr	Ser	Asp	Val	Gln	Val	Tyr	Asp		
			820					825					830				
Leu	Thr	Leu	Ser	Gly	Asp	Leu	Phe	Pro	Gln	Lys	Gly	Tyr	Met	Gly	Thr		
	835					840						845					
Trp	Thr	Leu	Asn	Ser	Asn	Pro	Gln	Thr	Gly	Lys	Leu	Gln	Ala	Arg	Trp		
	850				855						860						
Thr	Phe	Asp	Thr	Tyr	Arg	Arg	Trp	Val	Tyr	Ile	Pro	Arg	Asp	Asn	His		
865					870					875					880		
Phe	Tyr	Ala	Asn	Ser	Ile	Leu	Gly	Ser	Gln	Asn	Ser	Met	Ile	Val	Val		
			885					890					895				
Lys	Gln	Gly	Leu	Ile	Asn	Asn	Met	Leu	Asn	Asn	Ala	Arg	Phe	Asp	Asp		
		900					905						910				
Ile	Ala	Tyr	Asn	Asn	Phe	Trp	Val	Ser	Gly	Val	Gly	Thr	Phe	Leu	Ala		
	915					920						925					
Gln	Gln	Gly	Thr	Pro	Leu	Ser	Glu	Glu	Phe	Ser	Tyr	Tyr	Ser	Arg	Gly		
	930				935						940						
Thr	Ser	Val	Ala	Ile	Asp	Ala	Lys	Pro	Arg	Gln	Asp	Phe	Ile	Leu	Gly		
945					950					955					960		
Ala	Ala	Phe	Ser	Lys	Met	Val	Gly	Lys	Thr	Lys	Ala	Ile	Lys	Lys	Met		
			965					970					975				
His	Asn	Tyr	Phe	His	Lys	Gly	Ser	Glu	Tyr	Ser	Tyr	Gln	Ala	Ser	Val		
		980					985					990					
Tyr	Gly	Gly	Lys	Phe	Leu	Tyr	Phe	Leu	Leu	Asn	Lys	Gln	His	Gly	Trp		
	995					1000						1005					
Ala	Leu	Pro	Phe	Leu	Ile	Gln	Gly	Val	Val	Ser	Tyr	Gly	His	Ile	Lys		
	1010				1015						1020						
His	Asp	Thr	Thr	Ile	Leu	Tyr	Pro	Ser	Ile	His	Glu	Arg	Asn	Lys	Gly		
1025					1030					1035					1040		
Asp	Trp	Glu	Asp	Leu	Gly	Trp	Leu	Ala	Asp	Leu	Arg	Ile	Ser	Met	Asp		

1045 1050 1055
 Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile Thr Val Tyr Gly
 1060 1065 1070
 Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Ile Asp
 1075 1080 1085
 Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg Asn Leu Ser Leu
 1090 1095 1100
 Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn Cys Asn Ile Leu
 1105 1110 1115 1120
 Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser Ile Tyr Arg Asn
 1125 1130 1135
 Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn Glu Ala Gly Gln
 1140 1145 1150
 Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg Ala Glu Tyr Ser
 1155 1160 1165
 Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr Gly Asn Tyr Thr
 1170 1175 1180
 Ile Asp Val Gly Met Tyr Thr Tyr Arg Lys
 1185 1190

(2) INFORMATIONS POUR LA SEQ ID NO: 1074:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 79 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1035674..1035910

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1074:

Asp Pro Leu Val Ala Leu Gly Val Phe Ala Leu Ala Arg Val Pro Ile
 1 5 10 15
 Ala Ala Pro Lys Ser Ala Val Phe Pro Glu Asn Arg Glu Thr Pro Asp
 20 25 30
 Arg Val Met Ala Val Pro Ala Met Ala Pro Pro Met Val Ser Leu Ile
 35 40 45
 Glu Phe Pro Glu Asp Glu Glu Val Phe Gly Val Ala Ile Glu Ala Val
 50 55 60
 Leu Leu Glu Asn Val Ala Gly Gln Phe Asn Val Thr Val Gly Glu
 65 70 75

(2) INFORMATIONS POUR LA SEQ ID NO: 1075:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 111 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: 1036175..1036507

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1075:

Val	Gly	Val	Ala	Gly	Asp	Asp	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Cys	Arg
1				5					10					15	
Glu	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Glu	Ala	Val	Val	Ala	Thr	Pro	Val
			20					25					30		
Asp	Glu	Glu	Phe	Ala	Leu	Leu	Phe	Glu	Lys	Glu	Lys	Pro	Asp	Phe	Arg
		35					40					45			
Leu	Glu	Ile	Phe	Thr	Val	Leu	Ala	Cys	Lys	Pro	Pro	Pro	Ser	Phe	Pro
	50					55					60				
Thr	Arg	Phe	Ser	Val	Thr	Asp	Lys	Glu	Thr	Arg	Ala	Ser	Ser	Phe	Lys
65					70					75					80
Asp	Phe	Leu	Gln	Gln	Ile	Pro	Pro	Pro	Ile	Ser	Val	Ala	Glu	Phe	Ser
			85						90					95	
Glu	Ile	Phe	Ser	Trp	Ser	Met	Arg	Asp	Ile	Leu	Ala	Phe	Leu	Ala	
			100					105					110		

(2) INFORMATIONS POUR LA SEQ ID NO: 1076:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 542 acides aminés

(B) TYPE: acide aminé

(D) CONFIGURATION: linéaire

(iii) HYPOTHETIQUE: oui

(viii) POSITION DANS LE GENOME: complement(1036967..1038592)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1076:

Leu	Asn	Phe	Ser	Arg	Val	Gly	Thr	Ser	Ser	Ser	Thr	Thr	Phe	Thr	Glu
1				5					10					15	
Thr	Val	Gly	Glu	Ala	Gly	Ala	Glu	Tyr	Ile	Val	Ser	Ser	Asn	Ala	Ser
			20					25					30		
Phe	Thr	Lys	Phe	Thr	Asn	Ile	Pro	Thr	Thr	Asn	Thr	Thr	Thr	Pro	Thr
		35					40					45			
Asn	Ser	Asn	Ser	Ser	Ser	Ser	Asn	Arg	Glu	Thr	Ala	Ser	Val	Ser	Lys
	50					55					60				
Asp	Ser	Asp	Ser	Thr	Thr	Thr	Thr	Pro	Asp	Pro	Lys	Gly	Gly	Gly	Xaa
65				70						75					80
Phe	Tyr	Asn	Ala	His	Ser	Gly	Val	Leu	Ser	Phe	Met	Thr	Arg	Ser	Gly
			85					90						95	
Thr	Glu	Gly	Ser	Leu	Thr	Leu	Ser	Glu	Ile	Lys	Met	Thr	Gly	Glu	Gly
			100					105					110		
Gly	Ala	Ile	Phe	Ser	Gln	Gly	Glu	Leu	Leu	Phe	Thr	Asp	Leu	Thr	Gly
		115					120					125			
Leu	Thr	Ile	Gln	Asn	Asn	Leu	Ser	Gln	Leu	Ser	Gly	Gly	Ala	Ile	Phe
	130					135					140				
Gly	Gly	Ser	Thr	Ile	Ser	Leu	Ser	Gly	Ile	Thr	Lys	Ala	Thr	Phe	Ser
145				150						155					160
Ser	Asn	Ser	Ala	Glu	Val	Pro	Ala	Pro	Val	Lys	Lys	Pro	Thr	Lys	Pro
			165						170					175	
Glu	Ala	Gln	Thr	Ala	Gly	Glu	Thr	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Gly
			180					185					190		
Asn	Asp	Ser	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Ala	Glu	Pro	Ala	Ala
			195				200						205		

Ala Asn Leu Gln Ser His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala
 210 215 220
 Gln Thr Asp Thr Glu Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly
 225 230 235 240
 Gly Ala Ile Tyr Ala Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Lys
 245 250 255
 Val Leu Phe Ser Ile Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe
 260 265 270
 Ala Glu Lys Asp Val Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln
 275 280 285
 Thr Asn Gly Ala Glu Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp
 290 295 300
 Leu Ser Ile Gln Ser Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser
 305 310 315 320
 Lys Gln Gly Gly Gly Ala Leu Tyr Val Glu Gly Asn Ile Asn Phe Gln
 325 330 335
 Asp Leu Glu Glu Ile Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Lys
 340 345 350
 Thr Lys Lys Ile Thr Leu Pro Ser Lys Ala Gln Ala Ser Ala Gly Asn
 355 360 365
 Ala Asp Ala Trp Ala Ser Ser Ser Pro Gln Ser Ser Ser Gly Ala Thr
 370 375 380
 Thr Val Ser Asp Ser Gly Asp Ser Ser Ser Gly Ser Asn Ser Asp Thr
 385 390 395 400
 Ser Lys Thr Val Pro Val Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp
 405 410 415
 Lys Asn Leu Ser Ile Thr Asn Ile Thr Gly Ile Ile Glu Ile Ala Ile
 420 425 430
 Asn Lys Ala Thr Asp Val Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu
 435 440 445
 Thr Cys Lys Asn Ser His Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp
 450 455 460
 Lys Gln Gly Gly Gly Ile Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn
 465 470 475 480
 Leu Thr Gly Lys Thr Leu Phe Gln Glu Asn Thr Ala Lys Lys Glu Gly
 485 490 495
 Gly Gly Leu Phe Ile Lys Gly Thr Asp Lys Ala Leu Thr Met Thr Gly
 500 505 510
 Leu Asp Ser Phe Cys Leu Ile Asn Asn Thr Ser Glu Lys His Gly Gly
 515 520 525
 Gly Ala Phe Val Thr Gln Arg Asn Leu Ser Asp Leu His Leu
 530 535 540

REVENDICATIONS

1. Séquence nucléotidique de séquence SEQ ID N° 1 du génome de *Chlamydia trachomatis* LGV2.

5

2. Séquence nucléotidique de *Chlamydia trachomatis*, caractérisée en ce qu'elle est choisie parmi :

a) une séquence nucléotidique comportant au moins 99,9 % d'identité avec la séquence SEQ ID N° 1 ;

10 b) une séquence nucléotidique homologue à la séquence SEQ ID N° 1 ;

c) une séquence nucléotidique complémentaire de la séquence SEQ ID N° 1 ou complémentaire d'une séquence nucléotidique telle que définie en a), ou b), et une séquence

15 nucléotidique de leur ARN correspondant ;

d) une séquence nucléotidique de fragment représentatif de la séquence SEQ ID N° 1, ou de fragment représentatif de séquence nucléotidique telle que définie en a), b) ou c) ;

20 e) une séquence nucléotidique comprenant une séquence telle que définie en a), b), c) ou d) ;

f) une séquence nucléotidique susceptible d'être obtenue à partir d'une séquence nucléotidique telle que définie en a), b), c), d) ou e) ; et

25 g) une séquence nucléotidique modifiée d'une séquence nucléotidique telle que définie en a), b), c), d), e) ou f).

3. Séquence nucléotidique selon la revendication 2, caractérisée en ce qu'elle est choisie parmi les séquences
30 ORF2 à ORF1076.

4. Séquence nucléotidique caractérisée en ce qu'elle comprend une séquence nucléotidique choisie parmi :

a) une séquence nucléotidique selon la revendication 3 ;

35 b) une séquence nucléotidique homologue comportant au moins 80 % d'identité avec une séquence nucléotidique selon la revendication 3 ou telle que définie en a) ;

- c) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence selon la revendication 3 ou telle que définie en a) ou b) ;
- d) une séquence nucléotidique de fragment représentatif d'une séquence selon la revendication 3 ou d'une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique susceptible d'être obtenue à partir d'une séquence selon la revendication 3 ou telle que définie en a), b), c) ou d) ; et
- f) une séquence nucléotidique modifiée d'une séquence selon la revendication 3 ou telle que définie en a), b), c), d) ou e).

5. Polypeptide codé par une séquence nucléotidique selon l'une des revendications 2 à 4.

6. Polypeptide selon la revendication 5, caractérisé en ce qu'il est codé par un fragment représentatif correspondant à une séquence ORF d'une séquence nucléotidique selon l'une des revendications 1 à 4.

7. Polypeptide de *Chlamydia trachomatis*, caractérisé en ce qu'il est choisi parmi les séquences SEQ ID N°2 à SEQ ID N°1076.

8. Polypeptide caractérisé en ce qu'il comprend un polypeptide choisi parmi :
- a) un polypeptide selon l'une des revendications 5 à 7 ;
 - b) un polypeptide homologue à un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a) ;
 - c) un fragment d'au moins 5 acides aminés d'un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a) ou b) ;
 - a) un fragment biologiquement actif d'un polypeptide selon l'une des revendications 5 à 7, ou tel que défini en a), b) ou c) ; et

b) un polypeptide modifié d'un polypeptide selon l'une des revendications 5 à 7 ou tel que défini en a), b), c) ou d).

9. Séquence nucléotidique codant pour un polypeptide
5 selon la revendication 8.

10. Séquence nucléotidique selon l'une des revendications
2 à 4, et 9, caractérisée en ce qu'elle code pour un
polypeptide d'enveloppe cellulaire de *Chlamydia trachomatis*
10 ou un de ses fragments.

11. Séquence nucléotidique selon la revendication 10,
caractérisée en ce qu'elle code pour un polypeptide
d'enveloppe cellulaire externe de *Chlamydia trachomatis* ou
15 un de ses fragments.

12. Séquence nucléotidique selon l'une des revendications
10 et 11, caractérisée en ce qu'elle est choisie parmi les
séquences suivantes :
20 ORF3; ORF19; ORF51; ORF189; ORF212; ORF213; ORF324; ORF477;
ORF478; ORF479; ORF481; ORF482; ORF483; ORF484; ORF486;
ORF488; ORF489; ORF490; ORF572; ORF573; ORF742; ORF817;
ORF818; ORF820; ORF1035; ORF1036; ORF1037; ORF1038;
ORF1070; ORF1071; ORF1073 et un de leurs fragments
25 représentatifs.

13. Séquence nucléotidique selon l'une des revendications 2
à 4, et 9, caractérisée en ce qu'elle code pour un
polypeptide transmembranaire de *Chlamydia trachomatis* ou un
30 de ses fragments, présentant entre 1 et 3 domaines
transmembranaires, et en ce qu'elle comprend une séquence
nucléotidique choisie parmi les séquences suivantes :
ORF2; ORF3; ORF5; ORF8; ORF9; ORF10; ORF11; ORF12; ORF17;
ORF21; ORF26; ORF27; ORF28; ORF29; ORF30; ORF31; ORF33;
35 ORF35; ORF37; ORF39; ORF40; ORF41; ORF42; ORF43; ORF44;
ORF45; ORF46; ORF47; ORF48; ORF49; ORF52; ORF53; ORF55;
ORF56; ORF58; ORF65; ORF66; ORF68; ORF70; ORF74; ORF75;

ORF76; ORF78; ORF79; ORF81; ORF82; ORF83; ORF86; ORF91;
 ORF92; ORF94; ORF97; ORF100; ORF102; ORF103; ORF105;
 ORF106; ORF107; ORF109; ORF110; ORF111; ORF112; ORF113;
 ORF114; ORF115; ORF116; ORF117; ORF120; ORF122; ORF123;
 5 ORF130; ORF134; ORF135; ORF137; ORF140; ORF141; ORF143;
 ORF144; ORF145; ORF147; ORF148; ORF149; ORF150; ORF151;
 ORF155; ORF156; ORF162; ORF163; ORF164; ORF165; ORF166;
 ORF167; ORF168; ORF169; ORF170; ORF171; ORF173; ORF175;
 ORF176; ORF177; ORF181; ORF183; ORF184; ORF186; ORF187;
 10 ORF188; ORF190; ORF191; ORF192; ORF194; ORF195; ORF196;
 ORF197; ORF198; ORF199; ORF201; ORF202; ORF204; ORF206;
 ORF207; ORF209; ORF212; ORF213; ORF217; ORF219; ORF220;
 ORF221; ORF222; ORF223; ORF224; ORF225; ORF227; ORF228;
 ORF231; ORF232; ORF234; ORF236; ORF237; ORF243; ORF244;
 15 ORF245; ORF247; ORF248; ORF249; ORF252; ORF254; ORF257;
 ORF260; ORF261; ORF263; ORF265; ORF266; ORF267; ORF270;
 ORF271; ORF272; ORF274; ORF276; ORF277; ORF278; ORF279;
 ORF282; ORF283; ORF284; ORF285; ORF287; ORF289; ORF290;
 ORF291; ORF294; ORF298; ORF305; ORF306; ORF310; ORF311;
 20 ORF313; ORF315; ORF316; ORF319; ORF320; ORF322; ORF323;
 ORF325; ORF326; ORF327; ORF328; ORF330; ORF331; ORF332;
 ORF333; ORF334; ORF335; ORF336; ORF338; ORF339; ORF340;
 ORF341; ORF344; ORF345; ORF348; ORF349; ORF350; ORF351;
 ORF352; ORF353; ORF356; ORF357; ORF358; ORF361; ORF362;
 25 ORF366; ORF367; ORF368; ORF370; ORF372; ORF373; ORF375;
 ORF377; ORF378; ORF379; ORF380; ORF382; ORF383; ORF384;
 ORF385; ORF387; ORF389; ORF390; ORF391; ORF393; ORF396;
 ORF398; ORF399; ORF403; ORF404; ORF406; ORF407; ORF413;
 ORF414; ORF417; ORF418; ORF420; ORF421; ORF424; ORF426;
 30 ORF427; ORF428; ORF430; ORF433; ORF434; ORF435; ORF436;
 ORF437; ORF440; ORF443; ORF446; ORF448; ORF450; ORF451;
 ORF454; ORF455; ORF457; ORF458; ORF459; ORF463; ORF464;
 ORF466; ORF467; ORF468; ORF469; ORF470; ORF473; ORF474;
 ORF475; ORF476; ORF477; ORF479; ORF480; ORF481; ORF483;
 35 ORF484; ORF485; ORF486; ORF487; ORF488; ORF491; ORF493;
 ORF496; ORF497; ORF498; ORF500; ORF501; ORF503; ORF504;
 ORF508; ORF512; ORF513; ORF514; ORF519; ORF521; ORF523;

	ORF524;	ORF526;	ORF527;	ORF529;	ORF530;	ORF531;	ORF532;
	ORF534;	ORF536;	ORF537;	ORF538;	ORF540;	ORF541;	ORF542;
	ORF543;	ORF544;	ORF545;	ORF546;	ORF547;	ORF551;	ORF552;
	ORF553;	ORF555;	ORF558;	ORF559;	ORF560;	ORF561;	ORF562;
5	ORF566;	ORF567;	ORF568;	ORF569;	ORF571;	ORF572;	ORF574;
	ORF575;	ORF576;	ORF580;	ORF582;	ORF585;	ORF587;	ORF589;
	ORF592;	ORF593;	ORF595;	ORF596;	ORF597;	ORF599;	ORF601;
	ORF602;	ORF603;	ORF604;	ORF608;	ORF609;	ORF610;	ORF611;
	ORF615;	ORF616;	ORF617;	ORF618;	ORF621;	ORF622;	ORF623;
10	ORF624;	ORF625;	ORF628;	ORF632;	ORF633;	ORF634;	ORF635;
	ORF637;	ORF638;	ORF640;	ORF641;	ORF643;	ORF646;	ORF648;
	ORF649;	ORF651;	ORF652;	ORF653;	ORF654;	ORF655;	ORF658;
	ORF664;	ORF665;	ORF666;	ORF668;	ORF669;	ORF670;	ORF671;
	ORF672;	ORF673;	ORF674;	ORF676;	ORF677;	ORF678;	ORF680;
15	ORF682;	ORF683;	ORF684;	ORF686;	ORF688;	ORF689;	ORF690;
	ORF691;	ORF692;	ORF693;	ORF695;	ORF696;	ORF698;	ORF701;
	ORF703;	ORF704;	ORF705;	ORF706;	ORF707;	ORF709;	ORF710;
	ORF711;	ORF712;	ORF713;	ORF714;	ORF715;	ORF717;	ORF718;
	ORF720;	ORF721;	ORF722;	ORF724;	ORF726;	ORF728;	ORF729;
20	ORF730;	ORF731;	ORF732;	ORF733;	ORF734;	ORF737;	ORF738;
	ORF739;	ORF740;	ORF742;	ORF743;	ORF744;	ORF745;	ORF746;
	ORF748;	ORF750;	ORF751;	ORF752;	ORF753;	ORF754;	ORF755;
	ORF757;	ORF758;	ORF759;	ORF760;	ORF764;	ORF766;	ORF768;
	ORF769;	ORF771;	ORF772;	ORF773;	ORF774;	ORF775;	ORF776;
25	ORF777;	ORF778;	ORF779;	ORF780;	ORF781;	ORF782;	ORF783;
	ORF786;	ORF787;	ORF788;	ORF789;	ORF790;	ORF793;	ORF798;
	ORF800;	ORF802;	ORF803;	ORF806;	ORF808;	ORF809;	ORF810;
	ORF811;	ORF813;	ORF814;	ORF817;	ORF820;	ORF822;	ORF824;
	ORF825;	ORF827;	ORF828;	ORF829;	ORF830;	ORF833;	ORF834;
30	ORF835;	ORF837;	ORF838;	ORF839;	ORF840;	ORF841;	ORF842;
	ORF843;	ORF845;	ORF848;	ORF849;	ORF850;	ORF851;	ORF852;
	ORF854;	ORF855;	ORF856;	ORF857;	ORF859;	ORF860;	ORF862;
	ORF863;	ORF864;	ORF866;	ORF869;	ORF872;	ORF873;	ORF874;
	ORF878;	ORF879;	ORF880;	ORF881;	ORF883;	ORF884;	ORF885;
35	ORF886;	ORF887;	ORF892;	ORF893;	ORF894;	ORF895;	ORF897;
	ORF899;	ORF900;	ORF901;	ORF904;	ORF906;	ORF909;	ORF910;
	ORF912;	ORF914;	ORF917;	ORF920;	ORF921;	ORF922;	ORF923;

ORF924; ORF925; ORF926; ORF927; ORF930; ORF933; ORF934;
 ORF935; ORF936; ORF937; ORF940; ORF941; ORF942; ORF943;
 ORF944; ORF945; ORF947; ORF948; ORF951; ORF952; ORF953;
 ORF954; ORF955; ORF956; ORF957; ORF958; ORF960; ORF961;
 5 ORF962; ORF963; ORF964; ORF966; ORF967; ORF969; ORF970;
 ORF971; ORF973; ORF974; ORF979; ORF980; ORF981; ORF982;
 ORF984; ORF988; ORF989; ORF990; ORF991; ORF995; ORF996;
 ORF999; ORF1001; ORF1003; ORF1004; ORF1005; ORF1006;
 ORF1007; ORF1009; ORF1010; ORF1011; ORF1012; ORF1013;
 10 ORF1014; ORF1016; ORF1017; ORF1018; ORF1020; ORF1021;
 ORF1025; ORF1026; ORF1027; ORF1029; ORF1030; ORF1031;
 ORF1035; ORF1036; ORF1037; ORF1038; ORF1039; ORF1040;
 ORF1044; ORF1045; ORF1047; ORF1048; ORF1050; ORF1051;
 ORF1052; ORF1053; ORF1055; ORF1056; ORF1057; ORF1058;
 15 ORF1061; ORF1062; ORF1063; ORF1064; ORF1065; ORF1066;
 ORF1068; ORF1069; ORF1072; ORF1074; ORF1076 et un de leurs
 fragments représentatifs.

14. Séquence nucléotidique selon l'une des revendications 2
 20 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide transmembranaire de *Chlamydia trachomatis* ou un
 de ses fragments, présentant entre 4 et 6 domaines
 transmembranaires et en ce qu'elle comprend une séquence
 nucléotidique choisie parmi les séquences suivantes :
 25 ORF7; ORF14; ORF16; ORF32; ORF34; ORF36; ORF38; ORF50;
 ORF57; ORF59; ORF61; ORF62; ORF63; ORF64; ORF67; ORF69;
 ORF72; ORF77; ORF80; ORF84; ORF87; ORF93; ORF95; ORF99;
 ORF108; ORF119; ORF125; ORF126; ORF129; ORF131; ORF136;
 ORF139; ORF146; ORF152; ORF154; ORF160; ORF161; ORF172;
 30 ORF179; ORF182; ORF185; ORF200; ORF203; ORF205; ORF239;
 ORF242; ORF250; ORF253; ORF256; ORF259; ORF262; ORF268;
 ORF275; ORF281; ORF286; ORF288; ORF292; ORF295; ORF296;
 ORF297; ORF299; ORF300; ORF308; ORF314; ORF317; ORF318;
 ORF324; ORF342; ORF343; ORF355; ORF360; ORF374; ORF376;
 35 ORF386; ORF388; ORF392; ORF394; ORF395; ORF402; ORF405;
 ORF411; ORF415; ORF416; ORF422; ORF423; ORF429; ORF432;
 ORF441; ORF442; ORF444; ORF449; ORF452; ORF456; ORF460;

ORF461; ORF465; ORF471; ORF472; ORF482; ORF489; ORF492;
 ORF494; ORF495; ORF502; ORF505; ORF506; ORF509; ORF516;
 ORF517; ORF520; ORF525; ORF533; ORF539; ORF549; ORF554;
 ORF557; ORF563; ORF570; ORF573; ORF581; ORF590; ORF591;
 5 ORF600; ORF607; ORF612; ORF613; ORF620; ORF626; ORF629;
 ORF630; ORF639; ORF644; ORF647; ORF656; ORF659; ORF661;
 ORF685; ORF687; ORF699; ORF700; ORF708; ORF716; ORF719;
 ORF725; ORF747; ORF749; ORF756; ORF765; ORF767; ORF794;
 ORF796; ORF797; ORF799; ORF801; ORF807; ORF821; ORF823;
 10 ORF826; ORF847; ORF853; ORF861; ORF870; ORF871; ORF875;
 ORF882; ORF888; ORF889; ORF898; ORF902; ORF903; ORF911;
 ORF916; ORF931; ORF939; ORF975; ORF976; ORF978; ORF983;
 ORF986; ORF987; ORF992; ORF993; ORF1000; ORF1002; ORF1008;
 ORF1019; ORF1022; ORF1032; ORF1034; ORF1046; ORF1054;
 15 ORF1060; ORF1071 et un de leurs fragments représentatifs.

15. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide transmembranaire de *Chlamydia trachomatis* ou un
 20 de ses fragments, présentant au moins 7 domaines
 transmembranaires et en ce qu'elle comprend une séquence
 nucléotidique choisie parmi les séquences suivantes :
 ORF4; ORF6; ORF13; ORF20; ORF51; ORF71; ORF88; ORF118;
 ORF128; ORF132; ORF133; ORF158; ORF159; ORF174; ORF180;
 25 ORF189; ORF210; ORF211; ORF214; ORF215; ORF226; ORF229;
 ORF233; ORF235; ORF240; ORF246; ORF251; ORF255; ORF273;
 ORF354; ORF364; ORF369; ORF371; ORF397; ORF401; ORF409;
 ORF412; ORF419; ORF439; ORF453; ORF462; ORF490; ORF510;
 ORF511; ORF518; ORF535; ORF548; ORF550; ORF564; ORF565;
 30 ORF578; ORF579; ORF614; ORF631; ORF636; ORF650; ORF662;
 ORF667; ORF679; ORF681; ORF702; ORF727; ORF741; ORF763;
 ORF791; ORF792; ORF815; ORF816; ORF832; ORF846; ORF858;
 ORF865; ORF867; ORF868; ORF877; ORF891; ORF896; ORF907;
 ORF908; ORF918; ORF919; ORF932; ORF959; ORF977; ORF994;
 35 ORF998; ORF1024; ORF1028; ORF1042; ORF1067; ORF1070;
 ORF1073 et un de leurs fragments représentatifs.

16. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme intermédiaire, notamment dans le métabolisme des sucres et/ou des cofacteurs et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF10; ORF44; ORF45; ORF46; ORF47; ORF93; ORF101; ORF102; ORF103; ORF106; ORF107; ORF120; ORF121; ORF130; ORF135; ORF140; ORF143; ORF144; ORF145; ORF158; ORF159; ORF160; ORF161; ORF192; ORF193; ORF196; ORF196; ORF197; ORF198; ORF199; ORF227; ORF229; ORF236; ORF236; ORF239; ORF243; ORF245; ORF264; ORF265; ORF297; ORF331; ORF333; ORF359; ORF360; ORF374; ORF404; ORF405; ORF405; ORF410; ORF415; ORF415; ORF416; ORF417; ORF432; ORF460; ORF461; ORF462; ORF495; ORF513; ORF515; ORF566; ORF566; ORF566; ORF589; ORF613; ORF645; ORF646; ORF647; ORF652; ORF653; ORF654; ORF672; ORF673; ORF674; ORF682; ORF684; ORF692; ORF700; ORF725; ORF801; ORF802; ORF835; ORF836; ORF837; ORF860; ORF861; ORF862; ORF863; ORF869; ORF869; ORF925; ORF964; ORF983 et un de leurs fragments représentatifs.

17. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des nucléotides, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF142; ORF142; ORF169; ORF256; ORF268; ORF325; ORF352; ORF366; ORF435; ORF444; ORF528; ORF529; ORF530; ORF548; ORF549; ORF601; ORF602; ORF617; ORF619; ORF644; ORF745; ORF971; ORF972; ORF1023 et un de leurs fragments représentatifs.

18. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments

impliqué dans le métabolisme des acides nucléiques, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF5; ORF12; ORF82; ORF96; ORF97; ORF98; ORF99; ORF100;
5 ORF105; ORF118; ORF136; ORF137; ORF163; ORF190; ORF204;
ORF259; ORF260; ORF262; ORF290; ORF300; ORF301; ORF302;
ORF387; ORF427; ORF434; ORF441; ORF444; ORF471; ORF595;
ORF596; ORF597; ORF599; ORF600; ORF605; ORF612; ORF624;
ORF625; ORF650; ORF657; ORF658; ORF702; ORF703; ORF704;
10 ORF708; ORF719; ORF766; ORF767; ORF775; ORF779; ORF787;
ORF788; ORF794; ORF841; ORF842; ORF883; ORF884; ORF907;
ORF918; ORF924; ORF928; ORF929; ORF962; ORF962; ORF963;
ORF969; ORF970; ORF975; ORF979; ORF995; ORF1031; ORF1032 et
un de leurs fragments représentatifs.

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19. Séquence nucléotidique selon l'une des revendications 2 à 5, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des acides aminés, et en ce
20 qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF27; ORF41; ORF55; ORF56; ORF57; ORF59; ORF62; ORF63;
ORF64; ORF65; ORF119; ORF132; ORF240; ORF241; ORF277;
ORF278; ORF279; ORF382; ORF406; ORF428; ORF442; ORF446;
25 ORF447; ORF453; ORF454; ORF541; ORF542; ORF591; ORF608;
ORF609; ORF610; ORF618; ORF648; ORF649; ORF660; ORF661;
ORF677; ORF717; ORF765; ORF797; ORF871; ORF875; ORF920;
ORF922; ORF937; ORF998; ORF1020; ORF1021; ORF1034; ORF1044;
ORF1046; ORF1049 et un de leurs fragments représentatifs.

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20. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des polypeptides, et en ce
35 qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF21; ORF21; ORF22; ORF23; ORF24; ORF25; ORF26; ORF75;
 ORF84; ORF84; ORF86; ORF92; ORF133; ORF151; ORF152; ORF157;
 ORF179; ORF209; ORF307; ORF326; ORF343; ORF344; ORF345;
 ORF371; ORF429; ORF519; ORF557; ORF586; ORF587; ORF630;
 5 ORF656; ORF706; ORF707; ORF730; ORF751; ORF752; ORF786;
 ORF847; ORF885; ORF923; ORF978; ORF1039; ORF1048 et un de
 leurs fragments représentatifs.

21. Séquence nucléotidique selon l'une des revendications 2
 10 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide de *Chlamydia trachomatis* ou un de ses fragments
 impliqué dans le métabolisme des acides gras, et en ce
 qu'elle comprend une séquence nucléotidique choisie parmi
 les séquences suivantes :

15 ORF4; ORF15; ORF16; ORF141; ORF173; ORF205; ORF205; ORF206;
 ORF207; ORF208; ORF312; ORF355; ORF415; ORF550; ORF558;
 ORF560; ORF561; ORF574; ORF574; ORF577; ORF578; ORF590;
 ORF614; ORF772; ORF808; ORF809; ORF904; ORF905; ORF905;
 ORF933; ORF934; ORF934; ORF936 et un de leurs fragments
 20 représentatifs.

22. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide de *Chlamydia trachomatis* ou un de ses fragments
 25 impliqué dans la synthèse de la paroi, et en ce qu'elle
 comprend une séquence nucléotidique choisie parmi les
 séquences suivantes :

ORF87; ORF196; ORF242; ORF269; ORF628; ORF629; ORF634;
 ORF635; ORF637; ORF638; ORF1019 et un de leurs fragments
 30 représentatifs.

23. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide de *Chlamydia trachomatis* ou un de ses fragments
 35 impliqué dans le processus de transcription, traduction
 et/ou maturation, et en ce qu'elle comprend une séquence
 nucléotidique choisie parmi les séquences suivantes :

ORF112; ORF113; ORF332; ORF212; ORF213; ORF350; ORF362;
 ORF363; ORF364; ORF407; ORF451; ORF546; ORF643; ORF744;
 ORF746; ORF833; ORF868; ORF981; ORF982; ORF1003; ORF1011;
 ORF1042 et un de leurs fragments représentatifs.

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24. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide ribosomal de *Chlamydia trachomatis* ou un de ses
 fragments, et en ce qu'elle comprend une séquence
 nucléotidique choisie parmi les séquences suivantes :

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ORF114; ORF115; ORF116; ORF328; ORF361; ORF375; ORF445;
 ORF543; ORF584; ORF585; ORF743; ORF813; ORF941; ORF942;
 ORF944; ORF946; ORF947; ORF948; ORF950; ORF951; ORF952;
 ORF953; ORF954; ORF955; ORF955; ORF957; ORF958; ORF960;

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ORF961; ORF1040; ORF1041; ORF1043; ORF1063; ORF1064 et un
 de leurs fragments représentatifs.

25. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide de transport de *Chlamydia trachomatis* ou un de
 ses fragments, et en ce qu'elle comprend une séquence
 nucléotidique choisie parmi les séquences suivantes :

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ORF6; ORF50; ORF51; ORF80; ORF125; ORF126; ORF128; ORF129;
 ORF215; ORF246; ORF248; ORF249; ORF251; ORF252; ORF253;
 ORF255; ORF271; ORF275; ORF293; ORF309; ORF323; ORF324;
 ORF398; ORF401; ORF449; ORF511; ORF512; ORF564; ORF565;
 ORF667; ORF679; ORF680; ORF711; ORF712; ORF713; ORF714;
 ORF715; ORF730; ORF731; ORF736; ORF737; ORF738; ORF870;
 ORF908; ORF919; ORF977; ORF987; ORF988; ORF992; ORF993;

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ORF994; ORF1028; ORF1029 et un de leurs fragments
 représentatifs.

26. Séquence nucléotidique selon l'une des revendications 2
 à 4, et 9, caractérisée en ce qu'elle code pour un
 polypeptide de *Chlamydia trachomatis* ou un de ses fragments
 impliqué dans le processus de virulence, et en ce qu'elle

35

comprend une séquence nucléotidique choisie parmi les séquences suivantes :

ORF20; ORF815; ORF816; ORF898; ORF1059; ORF1060 et un de leurs fragments représentatifs.

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27. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le système de sécrétion et/ou sécrété, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

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ORF758; ORF888; ORF889; ORF890; ORF891; ORF896; ORF897; ORF898 et un de leurs fragments représentatifs.

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28. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide spécifique des *Chlamydiae* ou un de ses fragments, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

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ORF22; ORF29; ORF31; ORF32; ORF34; ORF35; ORF39; ORF40;
ORF43; ORF48; ORF49; ORF50; ORF52; ORF53; ORF54; ORF72;
ORF77; ORF78; ORF87; ORF90; ORF95; ORF108; ORF110; ORF111;
ORF122; ORF123; ORF124; ORF127; ORF138; ORF144; ORF146;
ORF153; ORF155; ORF164; ORF166; ORF175; ORF182; ORF184;
25 ORF186; ORF187; ORF188; ORF202; ORF210; ORF247; ORF258;
ORF266; ORF267; ORF270; ORF273; ORF274; ORF295; ORF296;
ORF305; ORF306; ORF309; ORF318; ORF319; ORF322; ORF326;
ORF342; ORF357; ORF376; ORF379; ORF380; ORF388; ORF390;
ORF400; ORF431; ORF433; ORF438; ORF443; ORF456; ORF457;
30 ORF458; ORF464; ORF468; ORF470; ORF473; ORF486; ORF489;
ORF497; ORF501; ORF503; ORF504; ORF508; ORF512; ORF521;
ORF522; ORF523; ORF524; ORF533; ORF535; ORF536; ORF537;
ORF538; ORF539; ORF540; ORF554; ORF563; ORF572; ORF579;
ORF595; ORF603; ORF604; ORF606; ORF607; ORF615; ORF616;
35 ORF622; ORF641; ORF642; ORF659; ORF668; ORF670; ORF693;
ORF695; ORF696; ORF699; ORF703; ORF704; ORF716; ORF726;
ORF728; ORF739; ORF742; ORF747; ORF750; ORF751; ORF755;

ORF757; ORF759; ORF761; ORF762; ORF763; ORF764; ORF773;
 ORF780; ORF781; ORF789; ORF800; ORF803; ORF804; ORF818;
 ORF820; ORF822; ORF823; ORF824; ORF827; ORF828; ORF839;
 ORF849; ORF850; ORF851; ORF852; ORF855; ORF856; ORF857;
 5 ORF858; ORF859; ORF860; ORF861; ORF862; ORF863; ORF865;
 ORF868; ORF869; ORF870; ORF871; ORF872; ORF873; ORF874;
 ORF875; ORF877; ORF878; ORF880; ORF882; ORF884; ORF886;
 ORF893; ORF901; ORF906; ORF910; ORF912; ORF915; ORF916;
 ORF917; ORF926; ORF929; ORF933; ORF965; ORF967; ORF968;
 10 ORF984; ORF986; ORF989; ORF990; ORF996; ORF997; ORF1001;
 ORF1002; ORF1013; ORF1016; ORF1031; ORF1033; ORF1035;
 ORF1049; ORF1051; ORF1052; ORF1054; ORF1056; ORF1057;
 ORF1058; ORF1062; ORF1070; ORF1071; ORF1073 et un de leurs
 fragments représentatifs.

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29. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide d'enveloppe cellulaire de *Chlamydia trachomatis* ou un de ses fragments.

20 30. Polypeptide selon la revendication 29, caractérisé en ce qu'il s'agit d'un polypeptide d'enveloppe cellulaire externe de *Chlamydia trachomatis* ou un de ses fragments.

31. Polypeptide selon l'une des revendications 29 et 30,
 25 caractérisé en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°3; SEQ ID N°19; SEQ ID N°51; SEQ ID N°189; SEQ ID
 N°212; SEQ ID N°213; SEQ ID N°324; SEQ ID N°477; SEQ ID
 N°478; SEQ ID N°479; SEQ ID N°481; SEQ ID N°482; SEQ ID
 30 N°483; SEQ ID N°484; SEQ ID N°486; SEQ ID N°488; SEQ ID
 N°489; SEQ ID N°490; SEQ ID N°572; SEQ ID N°573; SEQ ID
 N°742; SEQ ID N°817; SEQ ID N°818; SEQ ID N°820; SEQ ID
 N°1035; SEQ ID N°1036; SEQ ID N°1037; SEQ ID N°1038; SEQ ID
 N°1070; SEQ ID N°1071; SEQ ID N°1073 et un de leurs
 35 fragments.

32. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide transmembranaire de *Chlamydia trachomatis* ou un de ses fragments, présentant entre 1 et 3 domaines transmembranaires, et en ce qu'il est choisi parmi les

5 polypeptides de séquences suivantes :

SEQ ID N°2; SEQ ID N°3; SEQ ID N°5; SEQ ID N°8; SEQ ID N°9; SEQ ID N°10; SEQ ID N°11; SEQ ID N°12; SEQ ID N°17; SEQ ID N°21; SEQ ID N°26; SEQ ID N°27; SEQ ID N°28; SEQ ID N°29;

10 SEQ ID N°30; SEQ ID N°31; SEQ ID N°33; SEQ ID N°35; SEQ ID N°37; SEQ ID N°39; SEQ ID N°40; SEQ ID N°41; SEQ ID N°42; SEQ ID N°43; SEQ ID N°44; SEQ ID N°45; SEQ ID N°46; SEQ ID N°47; SEQ ID N°48; SEQ ID N°49; SEQ ID N°52; SEQ ID N°53; SEQ ID N°55; SEQ ID N°56; SEQ ID N°58; SEQ ID N°65; SEQ ID

15 N°66; SEQ ID N°68; SEQ ID N°70; SEQ ID N°74; SEQ ID N°75; SEQ ID N°76; SEQ ID N°78; SEQ ID N°79; SEQ ID N°81; SEQ ID N°82; SEQ ID N°83; SEQ ID N°86; SEQ ID N°91; SEQ ID N°92; SEQ ID N°94; SEQ ID N°97; SEQ ID N°100; SEQ ID N°102; SEQ ID N°103; SEQ ID N°105; SEQ ID N°106; SEQ ID N°107; SEQ ID

20 N°109; SEQ ID N°110; SEQ ID N°111; SEQ ID N°112; SEQ ID N°113; SEQ ID N°114; SEQ ID N°115; SEQ ID N°116; SEQ ID N°117; SEQ ID N°120; SEQ ID N°122; SEQ ID N°123; SEQ ID N°130; SEQ ID N°134; SEQ ID N°135; SEQ ID N°137; SEQ ID N°140; SEQ ID N°141; SEQ ID N°143; SEQ ID N°144; SEQ ID

25 N°145; SEQ ID N°147; SEQ ID N°148; SEQ ID N°149; SEQ ID N°150; SEQ ID N°151; SEQ ID N°155; SEQ ID N°156; SEQ ID N°162; SEQ ID N°163; SEQ ID N°164; SEQ ID N°165; SEQ ID N°166; SEQ ID N°167; SEQ ID N°168; SEQ ID N°169; SEQ ID N°170; SEQ ID N°171; SEQ ID N°173; SEQ ID N°175; SEQ ID

30 N°176; SEQ ID N°177; SEQ ID N°181; SEQ ID N°183; SEQ ID N°184; SEQ ID N°186; SEQ ID N°187; SEQ ID N°188; SEQ ID N°190; SEQ ID N°191; SEQ ID N°192; SEQ ID N°194; SEQ ID N°195; SEQ ID N°196; SEQ ID N°197; SEQ ID N°198; SEQ ID N°199; SEQ ID N°201; SEQ ID N°202; SEQ ID N°204; SEQ ID

35 N°206; SEQ ID N°207; SEQ ID N°209; SEQ ID N°212; SEQ ID N°213; SEQ ID N°217; SEQ ID N°219; SEQ ID N°220; SEQ ID N°221; SEQ ID N°222; SEQ ID N°223; SEQ ID N°224; SEQ ID

	Nº225;	SEQ	ID	Nº227;	SEQ	ID	Nº228;	SEQ	ID	Nº231;	SEQ	ID
	Nº232;	SEQ	ID	Nº234;	SEQ	ID	Nº236;	SEQ	ID	Nº237;	SEQ	ID
	Nº243;	SEQ	ID	Nº244;	SEQ	ID	Nº245;	SEQ	ID	Nº247;	SEQ	ID
	Nº248;	SEQ	ID	Nº249;	SEQ	ID	Nº252;	SEQ	ID	Nº254;	SEQ	ID
5	Nº257;	SEQ	ID	Nº260;	SEQ	ID	Nº261;	SEQ	ID	Nº263;	SEQ	ID
	Nº265;	SEQ	ID	Nº266;	SEQ	ID	Nº267;	SEQ	ID	Nº270;	SEQ	ID
	Nº271;	SEQ	ID	Nº272;	SEQ	ID	Nº274;	SEQ	ID	Nº276;	SEQ	ID
	Nº277;	SEQ	ID	Nº278;	SEQ	ID	Nº279;	SEQ	ID	Nº282;	SEQ	ID
	Nº283;	SEQ	ID	Nº284;	SEQ	ID	Nº285;	SEQ	ID	Nº287;	SEQ	ID
10	Nº289;	SEQ	ID	Nº290;	SEQ	ID	Nº291;	SEQ	ID	Nº294;	SEQ	ID
	Nº298;	SEQ	ID	Nº305;	SEQ	ID	Nº306;	SEQ	ID	Nº310;	SEQ	ID
	Nº311;	SEQ	ID	Nº313;	SEQ	ID	Nº315;	SEQ	ID	Nº316;	SEQ	ID
	Nº319;	SEQ	ID	Nº320;	SEQ	ID	Nº322;	SEQ	ID	Nº323;	SEQ	ID
	Nº325;	SEQ	ID	Nº326;	SEQ	ID	Nº327;	SEQ	ID	Nº328;	SEQ	ID
15	Nº330;	SEQ	ID	Nº331;	SEQ	ID	Nº332;	SEQ	ID	Nº333;	SEQ	ID
	Nº334;	SEQ	ID	Nº335;	SEQ	ID	Nº336;	SEQ	ID	Nº338;	SEQ	ID
	Nº339;	SEQ	ID	Nº340;	SEQ	ID	Nº341;	SEQ	ID	Nº344;	SEQ	ID
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25	Nº389;	SEQ	ID	Nº390;	SEQ	ID	Nº391;	SEQ	ID	Nº393;	SEQ	ID
	Nº396;	SEQ	ID	Nº398;	SEQ	ID	Nº399;	SEQ	ID	Nº403;	SEQ	ID
	Nº404;	SEQ	ID	Nº406;	SEQ	ID	Nº407;	SEQ	ID	Nº413;	SEQ	ID
	Nº414;	SEQ	ID	Nº417;	SEQ	ID	Nº418;	SEQ	ID	Nº420;	SEQ	ID
	Nº421;	SEQ	ID	Nº424;	SEQ	ID	Nº426;	SEQ	ID	Nº427;	SEQ	ID
30	Nº428;	SEQ	ID	Nº430;	SEQ	ID	Nº433;	SEQ	ID	Nº434;	SEQ	ID
	Nº435;	SEQ	ID	Nº436;	SEQ	ID	Nº437;	SEQ	ID	Nº440;	SEQ	ID
	Nº443;	SEQ	ID	Nº446;	SEQ	ID	Nº448;	SEQ	ID	Nº450;	SEQ	ID
	Nº451;	SEQ	ID	Nº454;	SEQ	ID	Nº455;	SEQ	ID	Nº457;	SEQ	ID
	Nº458;	SEQ	ID	Nº459;	SEQ	ID	Nº463;	SEQ	ID	Nº464;	SEQ	ID
35	Nº466;	SEQ	ID	Nº467;	SEQ	ID	Nº468;	SEQ	ID	Nº469;	SEQ	ID
	Nº470;	SEQ	ID	Nº473;	SEQ	ID	Nº474;	SEQ	ID	Nº475;	SEQ	ID
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	N°724; SEQ ID N°726; SEQ ID N°728; SEQ ID N°729; SEQ ID
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	N°734; SEQ ID N°737; SEQ ID N°738; SEQ ID N°739; SEQ ID
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	N°788; SEQ ID N°789; SEQ ID N°790; SEQ ID N°793; SEQ ID
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	N°811; SEQ ID N°813; SEQ ID N°814; SEQ ID N°817; SEQ ID
	N°820; SEQ ID N°822; SEQ ID N°824; SEQ ID N°825; SEQ ID
	N°827; SEQ ID N°828; SEQ ID N°829; SEQ ID N°830; SEQ ID
20	N°833; SEQ ID N°834; SEQ ID N°835; SEQ ID N°837; SEQ ID
	N°838; SEQ ID N°839; SEQ ID N°840; SEQ ID N°841; SEQ ID
	N°842; SEQ ID N°843; SEQ ID N°845; SEQ ID N°848; SEQ ID
	N°849; SEQ ID N°850; SEQ ID N°851; SEQ ID N°852; SEQ ID
	N°854; SEQ ID N°855; SEQ ID N°856; SEQ ID N°857; SEQ ID
25	N°859; SEQ ID N°860; SEQ ID N°862; SEQ ID N°863; SEQ ID
	N°864; SEQ ID N°866; SEQ ID N°869; SEQ ID N°872; SEQ ID
	N°873; SEQ ID N°874; SEQ ID N°878; SEQ ID N°879; SEQ ID
	N°880; SEQ ID N°881; SEQ ID N°883; SEQ ID N°884; SEQ ID
	N°885; SEQ ID N°886; SEQ ID N°887; SEQ ID N°892; SEQ ID
30	N°893; SEQ ID N°894; SEQ ID N°895; SEQ ID N°897; SEQ ID
	N°899; SEQ ID N°900; SEQ ID N°901; SEQ ID N°904; SEQ ID
	N°906; SEQ ID N°909; SEQ ID N°910; SEQ ID N°912; SEQ ID
	N°914; SEQ ID N°917; SEQ ID N°920; SEQ ID N°921; SEQ ID
	N°922; SEQ ID N°923; SEQ ID N°924; SEQ ID N°925; SEQ ID
35	N°926; SEQ ID N°927; SEQ ID N°930; SEQ ID N°933; SEQ ID
	N°934; SEQ ID N°935; SEQ ID N°936; SEQ ID N°937; SEQ ID
	N°940; SEQ ID N°941; SEQ ID N°942; SEQ ID N°943; SEQ ID

N°944; SEQ ID N°945; SEQ ID N°947; SEQ ID N°948; SEQ ID
 N°951; SEQ ID N°952; SEQ ID N°953; SEQ ID N°954; SEQ ID
 N°955; SEQ ID N°956; SEQ ID N°957; SEQ ID N°958; SEQ ID
 N°960; SEQ ID N°961; SEQ ID N°962; SEQ ID N°963; SEQ ID
 5 N°964; SEQ ID N°966; SEQ ID N°967; SEQ ID N°969; SEQ ID
 N°970; SEQ ID N°971; SEQ ID N°973; SEQ ID N°974; SEQ ID
 N°979; SEQ ID N°980; SEQ ID N°981; SEQ ID N°982; SEQ ID
 N°984; SEQ ID N°988; SEQ ID N°989; SEQ ID N°990; SEQ ID
 N°991; SEQ ID N°995; SEQ ID N°996; SEQ ID N°999; SEQ ID
 10 N°1001; SEQ ID N°1003; SEQ ID N°1004; SEQ ID N°1005; SEQ ID
 N°1006; SEQ ID N°1007; SEQ ID N°1009; SEQ ID N°1010; SEQ ID
 N°1011; SEQ ID N°1012; SEQ ID N°1013; SEQ ID N°1014; SEQ ID
 N°1016; SEQ ID N°1017; SEQ ID N°1018; SEQ ID N°1020; SEQ ID
 N°1021; SEQ ID N°1025; SEQ ID N°1026; SEQ ID N°1027; SEQ ID
 15 N°1029; SEQ ID N°1030; SEQ ID N°1031; SEQ ID N°1035; SEQ ID
 N°1036; SEQ ID N°1037; SEQ ID N°1038; SEQ ID N°1039; SEQ ID
 N°1040; SEQ ID N°1044; SEQ ID N°1045; SEQ ID N°1047; SEQ ID
 N°1048; SEQ ID N°1050; SEQ ID N°1051; SEQ ID N°1052; SEQ ID
 N°1053; SEQ ID N°1055; SEQ ID N°1056; SEQ ID N°1057; SEQ ID
 20 N°1058; SEQ ID N°1061; SEQ ID N°1062; SEQ ID N°1063; SEQ ID
 N°1064; SEQ ID N°1065; SEQ ID N°1066; SEQ ID N°1068; SEQ ID
 N°1069; SEQ ID N°1072; SEQ ID N°1074; SEQ ID N°1076 et un
 de leurs fragments.

25 33. Polypeptide selon l'une des revendications 5 à 8,
 caractérisé en ce qu'il s'agit d'un polypeptide
 transmembranaire de *Chlamydia trachomatis* ou un de ses
 fragments, présentant entre 4 et 6 domaines
 transmembranaires, et en ce qu'il est choisi parmi les
 30 polypeptides de séquences suivantes :
 SEQ ID N°7; SEQ ID N°14; SEQ ID N°16; SEQ ID N°32; SEQ ID
 N°34; SEQ ID N°36; SEQ ID N°38; SEQ ID N°50; SEQ ID N°57;
 SEQ ID N°59; SEQ ID N°61; SEQ ID N°62; SEQ ID N°63; SEQ ID
 N°64; SEQ ID N°67; SEQ ID N°69; SEQ ID N°72; SEQ ID N°77;
 35 SEQ ID N°80; SEQ ID N°84; SEQ ID N°87; SEQ ID N°93; SEQ ID
 N°95; SEQ ID N°99; SEQ ID N°108; SEQ ID N°119; SEQ ID
 N°125; SEQ ID N°126; SEQ ID N°129; SEQ ID N°131; SEQ ID

	N°136; SEQ ID N°139; SEQ ID N°146; SEQ ID N°152; SEQ ID
	N°154; SEQ ID N°160; SEQ ID N°161; SEQ ID N°172; SEQ ID
	N°179; SEQ ID N°182; SEQ ID N°185; SEQ ID N°200; SEQ ID
	N°203; SEQ ID N°205; SEQ ID N°239; SEQ ID N°242; SEQ ID
5	N°250; SEQ ID N°253; SEQ ID N°256; SEQ ID N°259; SEQ ID
	N°262; SEQ ID N°268; SEQ ID N°275; SEQ ID N°281; SEQ ID
	N°286; SEQ ID N°288; SEQ ID N°292; SEQ ID N°295; SEQ ID
	N°296; SEQ ID N°297; SEQ ID N°299; SEQ ID N°300; SEQ ID
	N°308; SEQ ID N°314; SEQ ID N°317; SEQ ID N°318; SEQ ID
10	N°324; SEQ ID N°342; SEQ ID N°343; SEQ ID N°355; SEQ ID
	N°360; SEQ ID N°374; SEQ ID N°376; SEQ ID N°386; SEQ ID
	N°388; SEQ ID N°392; SEQ ID N°394; SEQ ID N°395; SEQ ID
	N°402; SEQ ID N°405; SEQ ID N°411; SEQ ID N°415; SEQ ID
	N°416; SEQ ID N°422; SEQ ID N°423; SEQ ID N°429; SEQ ID
15	N°432; SEQ ID N°441; SEQ ID N°442; SEQ ID N°444; SEQ ID
	N°449; SEQ ID N°452; SEQ ID N°456; SEQ ID N°460; SEQ ID
	N°461; SEQ ID N°465; SEQ ID N°471; SEQ ID N°472; SEQ ID
	N°482; SEQ ID N°489; SEQ ID N°492; SEQ ID N°494; SEQ ID
	N°495; SEQ ID N°502; SEQ ID N°505; SEQ ID N°506; SEQ ID
20	N°509; SEQ ID N°516; SEQ ID N°517; SEQ ID N°520; SEQ ID
	N°525; SEQ ID N°533; SEQ ID N°539; SEQ ID N°549; SEQ ID
	N°554; SEQ ID N°557; SEQ ID N°563; SEQ ID N°570; SEQ ID
	N°573; SEQ ID N°581; SEQ ID N°590; SEQ ID N°591; SEQ ID
	N°600; SEQ ID N°607; SEQ ID N°612; SEQ ID N°613; SEQ ID
25	N°620; SEQ ID N°626; SEQ ID N°629; SEQ ID N°630; SEQ ID
	N°639; SEQ ID N°644; SEQ ID N°647; SEQ ID N°656; SEQ ID
	N°659; SEQ ID N°661; SEQ ID N°685; SEQ ID N°687; SEQ ID
	N°699; SEQ ID N°700; SEQ ID N°708; SEQ ID N°716; SEQ ID
	N°719; SEQ ID N°725; SEQ ID N°747; SEQ ID N°749; SEQ ID
30	N°756; SEQ ID N°765; SEQ ID N°767; SEQ ID N°794; SEQ ID
	N°796; SEQ ID N°797; SEQ ID N°799; SEQ ID N°801; SEQ ID
	N°807; SEQ ID N°821; SEQ ID N°823; SEQ ID N°826; SEQ ID
	N°847; SEQ ID N°853; SEQ ID N°861; SEQ ID N°870; SEQ ID
	N°871; SEQ ID N°875; SEQ ID N°882; SEQ ID N°888; SEQ ID
35	N°889; SEQ ID N°898; SEQ ID N°902; SEQ ID N°903; SEQ ID
	N°911; SEQ ID N°916; SEQ ID N°931; SEQ ID N°939; SEQ ID
	N°975; SEQ ID N°976; SEQ ID N°978; SEQ ID N°983; SEQ ID

N°986; SEQ ID N°987; SEQ ID N°992; SEQ ID N°993; SEQ ID N°1000; SEQ ID N°1002; SEQ ID N°1008; SEQ ID N°1019; SEQ ID N°1022; SEQ ID N°1032; SEQ ID N°1034; SEQ ID N°1046; SEQ ID N°1054; SEQ ID N°1060; SEQ ID N°1071 et un de leurs
 5 fragments représentatifs.

34. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide transmembranaire de *Chlamydia trachomatis* ou un de ses
 10 fragments, présentant au moins 7 domaines transmembranaires, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°4; SEQ ID N°6; SEQ ID N°13; SEQ ID N°20; SEQ ID N°51; SEQ ID N°71; SEQ ID N°88; SEQ ID N°118; SEQ ID N°128;
 15 SEQ ID N°132; SEQ ID N°133; SEQ ID N°158; SEQ ID N°159; SEQ ID N°174; SEQ ID N°180; SEQ ID N°189; SEQ ID N°210; SEQ ID N°211; SEQ ID N°214; SEQ ID N°215; SEQ ID N°226; SEQ ID N°229; SEQ ID N°233; SEQ ID N°235; SEQ ID N°240; SEQ ID N°246; SEQ ID N°251; SEQ ID N°255; SEQ ID N°273; SEQ ID
 20 N°354; SEQ ID N°364; SEQ ID N°369; SEQ ID N°371; SEQ ID N°397; SEQ ID N°401; SEQ ID N°409; SEQ ID N°412; SEQ ID N°419; SEQ ID N°439; SEQ ID N°453; SEQ ID N°462; SEQ ID N°490; SEQ ID N°510; SEQ ID N°511; SEQ ID N°518; SEQ ID N°535; SEQ ID N°548; SEQ ID N°550; SEQ ID N°564; SEQ ID
 25 N°565; SEQ ID N°578; SEQ ID N°579; SEQ ID N°614; SEQ ID N°631; SEQ ID N°636; SEQ ID N°650; SEQ ID N°662; SEQ ID N°667; SEQ ID N°679; SEQ ID N°681; SEQ ID N°702; SEQ ID N°727; SEQ ID N°741; SEQ ID N°763; SEQ ID N°791; SEQ ID N°792; SEQ ID N°815; SEQ ID N°816; SEQ ID N°832; SEQ ID
 30 N°846; SEQ ID N°858; SEQ ID N°865; SEQ ID N°867; SEQ ID N°868; SEQ ID N°877; SEQ ID N°891; SEQ ID N°896; SEQ ID N°907; SEQ ID N°908; SEQ ID N°918; SEQ ID N°919; SEQ ID N°932; SEQ ID N°959; SEQ ID N°977; SEQ ID N°994; SEQ ID N°998; SEQ ID N°1024; SEQ ID N°1028; SEQ ID N°1042; SEQ ID
 35 N°1067; SEQ ID N°1070; SEQ ID N°1073 et un de leurs fragments représentatifs.

35. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme intermédiaire, notamment dans le métabolisme des sucres et/ou des cofacteurs, et en ce qu'il est choisi
5 parmi les polypeptides de séquences suivantes :

SEQ ID N°10; SEQ ID N°44; SEQ ID N°45; SEQ ID N°46; SEQ ID N°47; SEQ ID N°93; SEQ ID N°101; SEQ ID N°102; SEQ ID N°103; SEQ ID N°106; SEQ ID N°107; SEQ ID N°120; SEQ ID
10 N°121; SEQ ID N°130; SEQ ID N°135; SEQ ID N°140; SEQ ID N°143; SEQ ID N°144; SEQ ID N°145; SEQ ID N°158; SEQ ID N°159; SEQ ID N°160; SEQ ID N°161; SEQ ID N°192; SEQ ID N°193; SEQ ID N°196; SEQ ID N°196; SEQ ID N°197; SEQ ID N°198; SEQ ID N°199; SEQ ID N°227; SEQ ID N°229; SEQ ID
15 N°236; SEQ ID N°236; SEQ ID N°239; SEQ ID N°243; SEQ ID N°245; SEQ ID N°264; SEQ ID N°265; SEQ ID N°297; SEQ ID N°331; SEQ ID N°333; SEQ ID N°359; SEQ ID N°360; SEQ ID N°374; SEQ ID N°404; SEQ ID N°405; SEQ ID N°405; SEQ ID N°410; SEQ ID N°415; SEQ ID N°415; SEQ ID N°416; SEQ ID
20 N°417; SEQ ID N°432; SEQ ID N°460; SEQ ID N°461; SEQ ID N°462; SEQ ID N°495; SEQ ID N°513; SEQ ID N°515; SEQ ID N°566; SEQ ID N°566; SEQ ID N°566; SEQ ID N°589; SEQ ID N°613; SEQ ID N°645; SEQ ID N°646; SEQ ID N°647; SEQ ID N°652; SEQ ID N°653; SEQ ID N°654; SEQ ID N°672; SEQ ID
25 N°673; SEQ ID N°674; SEQ ID N°682; SEQ ID N°684; SEQ ID N°692; SEQ ID N°700; SEQ ID N°725; SEQ ID N°801; SEQ ID N°802; SEQ ID N°835; SEQ ID N°836; SEQ ID N°837; SEQ ID N°860; SEQ ID N°861; SEQ ID N°862; SEQ ID N°863; SEQ ID N°869; SEQ ID N°869; SEQ ID N°925; SEQ ID N°964; SEQ ID
30 N°983 et un de leurs fragments.

36. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des nucléotides, et en ce qu'il est choisi
35 parmi les polypeptides de séquences suivantes :

SEQ ID N°142; SEQ ID N°142; SEQ ID N°169; SEQ ID N°256; SEQ ID N°268; SEQ ID N°325; SEQ ID N°352; SEQ ID N°366; SEQ ID N°435; SEQ ID N°444; SEQ ID N°528; SEQ ID N°529; SEQ ID N°530; SEQ ID N°548; SEQ ID N°549; SEQ ID N°601; SEQ ID N°602; SEQ ID N°617; SEQ ID N°619; SEQ ID N°644; SEQ ID N°745; SEQ ID N°971; SEQ ID N°972; SEQ ID N°1023 et un de leurs fragments représentatifs.

37. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des acides nucléiques, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°5; SEQ ID N°12; SEQ ID N°82; SEQ ID N°96; SEQ ID N°97; SEQ ID N°98; SEQ ID N°99; SEQ ID N°100; SEQ ID N°105; SEQ ID N°118; SEQ ID N°136; SEQ ID N°137; SEQ ID N°163; SEQ ID N°190; SEQ ID N°204; SEQ ID N°259; SEQ ID N°260; SEQ ID N°262; SEQ ID N°290; SEQ ID N°300; SEQ ID N°301; SEQ ID N°302; SEQ ID N°387; SEQ ID N°427; SEQ ID N°434; SEQ ID N°441; SEQ ID N°444; SEQ ID N°471; SEQ ID N°595; SEQ ID N°596; SEQ ID N°597; SEQ ID N°599; SEQ ID N°600; SEQ ID N°605; SEQ ID N°612; SEQ ID N°624; SEQ ID N°625; SEQ ID N°650; SEQ ID N°657; SEQ ID N°658; SEQ ID N°702; SEQ ID N°703; SEQ ID N°704; SEQ ID N°708; SEQ ID N°719; SEQ ID N°766; SEQ ID N°767; SEQ ID N°775; SEQ ID N°779; SEQ ID N°787; SEQ ID N°788; SEQ ID N°794; SEQ ID N°841; SEQ ID N°842; SEQ ID N°883; SEQ ID N°884; SEQ ID N°907; SEQ ID N°918; SEQ ID N°924; SEQ ID N°928; SEQ ID N°929; SEQ ID N°962; SEQ ID N°962; SEQ ID N°963; SEQ ID N°969; SEQ ID N°970; SEQ ID N°975; SEQ ID N°979; SEQ ID N°995; SEQ ID N°1031; SEQ ID N°1032 et un de leurs fragments.

38. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des acides aminés, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°27; SEQ ID N°41; SEQ ID N°55; SEQ ID N°56; SEQ ID N°57; SEQ ID N°59; SEQ ID N°62; SEQ ID N°63; SEQ ID N°64; SEQ ID N°65; SEQ ID N°119; SEQ ID N°132; SEQ ID N°240; SEQ ID N°241; SEQ ID N°277; SEQ ID N°278; SEQ ID N°279; SEQ ID N°382; SEQ ID N°406; SEQ ID N°428; SEQ ID N°442; SEQ ID N°446; SEQ ID N°447; SEQ ID N°453; SEQ ID N°454; SEQ ID N°541; SEQ ID N°542; SEQ ID N°591; SEQ ID N°608; SEQ ID N°609; SEQ ID N°610; SEQ ID N°618; SEQ ID N°648; SEQ ID N°649; SEQ ID N°660; SEQ ID N°661; SEQ ID N°677; SEQ ID N°717; SEQ ID N°765; SEQ ID N°797; SEQ ID N°871; SEQ ID N°875; SEQ ID N°920; SEQ ID N°922; SEQ ID N°937; SEQ ID N°998; SEQ ID N°1020; SEQ ID N°1021; SEQ ID N°1034; SEQ ID N°1044; SEQ ID N°1046; SEQ ID N°1049 et un de leurs fragments.

15

39. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des polypeptides, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°21; SEQ ID N°21; SEQ ID N°22; SEQ ID N°23; SEQ ID N°24; SEQ ID N°25; SEQ ID N°26; SEQ ID N°75; SEQ ID N°84; SEQ ID N°84; SEQ ID N°86; SEQ ID N°92; SEQ ID N°133; SEQ ID N°151; SEQ ID N°152; SEQ ID N°157; SEQ ID N°179; SEQ ID N°209; SEQ ID N°307; SEQ ID N°326; SEQ ID N°343; SEQ ID N°344; SEQ ID N°345; SEQ ID N°371; SEQ ID N°429; SEQ ID N°519; SEQ ID N°557; SEQ ID N°586; SEQ ID N°587; SEQ ID N°630; SEQ ID N°656; SEQ ID N°706; SEQ ID N°707; SEQ ID N°730; SEQ ID N°751; SEQ ID N°752; SEQ ID N°786; SEQ ID N°847; SEQ ID N°885; SEQ ID N°923; SEQ ID N°978; SEQ ID N°1039; SEQ ID N°1048 et un de leurs fragments.

40. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des acides gras, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°4; SEQ ID N°15; SEQ ID N°16; SEQ ID N°141; SEQ ID N°173; SEQ ID N°205; SEQ ID N°205; SEQ ID N°206; SEQ ID N°207; SEQ ID N°208; SEQ ID N°312; SEQ ID N°355; SEQ ID N°415; SEQ ID N°550; SEQ ID N°558; SEQ ID N°560; SEQ ID N°561; SEQ ID N°574; SEQ ID N°574; SEQ ID N°577; SEQ ID N°578; SEQ ID N°590; SEQ ID N°614; SEQ ID N°772; SEQ ID N°808; SEQ ID N°809; SEQ ID N°904; SEQ ID N°905; SEQ ID N°905; SEQ ID N°933; SEQ ID N°934; SEQ ID N°934; SEQ ID N°936 et un de leurs fragments.

10

41. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans la synthèse de la paroi, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°87; SEQ ID N°196; SEQ ID N°242; SEQ ID N°269; SEQ ID N°628; SEQ ID N°629; SEQ ID N°634; SEQ ID N°635; SEQ ID N°637; SEQ ID N°638; SEQ ID N°1019 et un de leurs fragments.

20

42. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le processus de transcription, de traduction ou de maturation, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°112; SEQ ID N°113; SEQ ID N°332; SEQ ID N°212; SEQ ID N°213; SEQ ID N°350; SEQ ID N°362; SEQ ID N°363; SEQ ID N°364; SEQ ID N°407; SEQ ID N°451; SEQ ID N°546; SEQ ID N°643; SEQ ID N°744; SEQ ID N°746; SEQ ID N°833; SEQ ID N°868; SEQ ID N°981; SEQ ID N°982; SEQ ID N°1003; SEQ ID N°1011; SEQ ID N°1042 et un de leurs fragments.

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43. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide ribosomal de *Chlamydia trachomatis* ou un de ses fragments, et en ce

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qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°114; SEQ ID N°115; SEQ ID N°116; SEQ ID N°328; SEQ ID N°361; SEQ ID N°375; SEQ ID N°445; SEQ ID N°543; SEQ ID
 5 N°584; SEQ ID N°585; SEQ ID N°743; SEQ ID N°813; SEQ ID N°941; SEQ ID N°942; SEQ ID N°944; SEQ ID N°946; SEQ ID N°947; SEQ ID N°948; SEQ ID N°950; SEQ ID N°951; SEQ ID N°952; SEQ ID N°953; SEQ ID N°954; SEQ ID N°955; SEQ ID N°955; SEQ ID N°957; SEQ ID N°958; SEQ ID N°960; SEQ ID
 10 N°961; SEQ ID N°1040; SEQ ID N°1041; SEQ ID N°1043; SEQ ID N°1063; SEQ ID N°1064 et un de leurs fragments.

44. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de
 15 transport de *Chlamydia trachomatis* ou un de ses fragments, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°6; SEQ ID N°50; SEQ ID N°51; SEQ ID N°80; SEQ ID N°125; SEQ ID N°126; SEQ ID N°128; SEQ ID N°129; SEQ ID
 20 N°215; SEQ ID N°246; SEQ ID N°248; SEQ ID N°249; SEQ ID N°251; SEQ ID N°252; SEQ ID N°253; SEQ ID N°255; SEQ ID N°271; SEQ ID N°275; SEQ ID N°293; SEQ ID N°309; SEQ ID N°323; SEQ ID N°324; SEQ ID N°398; SEQ ID N°401; SEQ ID N°449; SEQ ID N°511; SEQ ID N°512; SEQ ID N°564; SEQ ID
 25 N°565; SEQ ID N°667; SEQ ID N°679; SEQ ID N°680; SEQ ID N°711; SEQ ID N°712; SEQ ID N°713; SEQ ID N°714; SEQ ID N°715; SEQ ID N°730; SEQ ID N°731; SEQ ID N°736; SEQ ID N°737; SEQ ID N°738; SEQ ID N°870; SEQ ID N°908; SEQ ID N°919; SEQ ID N°977; SEQ ID N°987; SEQ ID N°988; SEQ ID
 30 N°992; SEQ ID N°993; SEQ ID N°994; SEQ ID N°1028; SEQ ID N°1029 et un de leurs fragments.

45. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de
 35 *Chlamydia trachomatis* ou un de ses fragments impliqué dans le processus de virulence, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :

SEQ ID N°20; SEQ ID N°815; SEQ ID N°816; SEQ ID N°898; SEQ ID N°1059; SEQ ID N°1060 et un de leurs fragments.

5 46. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le système de sécrétion et/ou sécrété, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :
 10 SEQ ID N°758; SEQ ID N°888; SEQ ID N°889; SEQ ID N°890; SEQ ID N°891; SEQ ID N°896; SEQ ID N°897; SEQ ID N°898 et un de leurs fragments.

47. Polypeptide selon l'une des revendications 5 à 8, caractérisé en ce qu'il s'agit d'un polypeptide spécifique
 15 des *Chlamydiae* ou un de ses fragments, et en ce qu'il est choisi parmi les polypeptides de séquences suivantes :
 SEQ ID N°22; SEQ ID N°29; SEQ ID N°31; SEQ ID N°32; SEQ ID N°34; SEQ ID N°35; SEQ ID N°39; SEQ ID N°40; SEQ ID N°43; SEQ ID N°48; SEQ ID N°49; SEQ ID N°50; SEQ ID N°52; SEQ ID
 20 N°53; SEQ ID N°54; SEQ ID N°72; SEQ ID N°77; SEQ ID N°78; SEQ ID N°87; SEQ ID N°90; SEQ ID N°95; SEQ ID N°108; SEQ ID N°110; SEQ ID N°111; SEQ ID N°122; SEQ ID N°123; SEQ ID N°124; SEQ ID N°127; SEQ ID N°138; SEQ ID N°144; SEQ ID N°146; SEQ ID N°153; SEQ ID N°155; SEQ ID N°164; SEQ ID
 25 N°166; SEQ ID N°175; SEQ ID N°182; SEQ ID N°184; SEQ ID N°186; SEQ ID N°187; SEQ ID N°188; SEQ ID N°202; SEQ ID N°210; SEQ ID N°247; SEQ ID N°258; SEQ ID N°266; SEQ ID N°267; SEQ ID N°270; SEQ ID N°273; SEQ ID N°274; SEQ ID N°295; SEQ ID N°296; SEQ ID N°305; SEQ ID N°306; SEQ ID
 30 N°309; SEQ ID N°318; SEQ ID N°319; SEQ ID N°322; SEQ ID N°326; SEQ ID N°342; SEQ ID N°357; SEQ ID N°376; SEQ ID N°379; SEQ ID N°380; SEQ ID N°388; SEQ ID N°390; SEQ ID N°400; SEQ ID N°431; SEQ ID N°433; SEQ ID N°438; SEQ ID N°443; SEQ ID N°456; SEQ ID N°457; SEQ ID N°458; SEQ ID
 35 N°464; SEQ ID N°468; SEQ ID N°470; SEQ ID N°473; SEQ ID N°486; SEQ ID N°489; SEQ ID N°497; SEQ ID N°501; SEQ ID N°503; SEQ ID N°504; SEQ ID N°508; SEQ ID N°512; SEQ ID

N°521; SEQ ID N°522; SEQ ID N°523; SEQ ID N°524; SEQ ID
 N°533; SEQ ID N°535; SEQ ID N°536; SEQ ID N°537; SEQ ID
 N°538; SEQ ID N°539; SEQ ID N°540; SEQ ID N°554; SEQ ID
 N°563; SEQ ID N°572; SEQ ID N°579; SEQ ID N°595; SEQ ID
 5 N°603; SEQ ID N°604; SEQ ID N°606; SEQ ID N°607; SEQ ID
 N°615; SEQ ID N°616; SEQ ID N°622; SEQ ID N°641; SEQ ID
 N°642; SEQ ID N°659; SEQ ID N°668; SEQ ID N°670; SEQ ID
 N°693; SEQ ID N°695; SEQ ID N°696; SEQ ID N°699; SEQ ID
 N°703; SEQ ID N°704; SEQ ID N°716; SEQ ID N°726; SEQ ID
 10 N°728; SEQ ID N°739; SEQ ID N°742; SEQ ID N°747; SEQ ID
 N°750; SEQ ID N°751; SEQ ID N°755; SEQ ID N°757; SEQ ID
 N°759; SEQ ID N°761; SEQ ID N°762; SEQ ID N°763; SEQ ID
 N°764; SEQ ID N°773; SEQ ID N°780; SEQ ID N°781; SEQ ID
 N°789; SEQ ID N°800; SEQ ID N°803; SEQ ID N°804; SEQ ID
 15 N°818; SEQ ID N°820; SEQ ID N°822; SEQ ID N°823; SEQ ID
 N°824; SEQ ID N°827; SEQ ID N°828; SEQ ID N°839; SEQ ID
 N°849; SEQ ID N°850; SEQ ID N°851; SEQ ID N°852; SEQ ID
 N°855; SEQ ID N°856; SEQ ID N°857; SEQ ID N°858; SEQ ID
 N°859; SEQ ID N°860; SEQ ID N°861; SEQ ID N°862; SEQ ID
 20 N°863; SEQ ID N°865; SEQ ID N°868; SEQ ID N°869; SEQ ID
 N°870; SEQ ID N°871; SEQ ID N°872; SEQ ID N°873; SEQ ID
 N°874; SEQ ID N°875; SEQ ID N°877; SEQ ID N°878; SEQ ID
 N°880; SEQ ID N°882; SEQ ID N°884; SEQ ID N°886; SEQ ID
 N°893; SEQ ID N°901; SEQ ID N°906; SEQ ID N°910; SEQ ID
 25 N°912; SEQ ID N°915; SEQ ID N°916; SEQ ID N°917; SEQ ID
 N°926; SEQ ID N°929; SEQ ID N°933; SEQ ID N°965; SEQ ID
 N°967; SEQ ID N°968; SEQ ID N°984; SEQ ID N°986; SEQ ID
 N°989; SEQ ID N°990; SEQ ID N°996; SEQ ID N°997; SEQ ID
 N°1001; SEQ ID N°1002; SEQ ID N°1013; SEQ ID N°1016; SEQ ID
 30 N°1031; SEQ ID N°1033; SEQ ID N°1035; SEQ ID N°1049; SEQ ID
 N°1051; SEQ ID N°1052; SEQ ID N°1054; SEQ ID N°1056; SEQ ID
 N°1057; SEQ ID N°1058; SEQ ID N°1062; SEQ ID N°1070; SEQ ID
 N°1071; SEQ ID N°1073 et un de leurs fragments.

35 48. Séquence nucléotidique selon l'une des revendications 1
 à 4, et, 9 à 28 , et/ou séquence de polypeptide selon l'une
 des revendications 5 à 8, et, 29 à 47, caractérisée(s) en

ce que ladite ou lesdites séquences sont enregistrées sur un support d'enregistrement dont la forme et la nature facilitent la lecture, l'analyse et/ou l'exploitation de ladite ou lesdites séquences.

5

49. Séquence nucléotidique utilisable comme amorce, caractérisée en ce que ladite séquence est choisie parmi les séquences nucléotidiques selon l'une des revendications 2 à 4, et, 9 à 28.

10

50. Séquence nucléotidique utilisable comme sonde, caractérisée en ce que ladite séquence est choisie parmi les séquences nucléotidiques selon l'une des revendications 2 à 4, et, 9 à 28.

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51. Séquence nucléotidique selon l'une des revendications 49 et 50, caractérisée en ce qu'elle est marquée par un composé radioactif ou par un composé non radioactif.

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52. Séquence nucléotidique selon l'une des revendications 49 à 51, caractérisée en ce quelle est immobilisée sur un support, de manière covalente ou non-covalente.

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53. Séquence nucléotidique selon l'une des revendications 49 à 52, caractérisée en ce quelle est immobilisée sur un support d'une puce à ADN.

30

54. Séquence nucléotidique selon l'une des revendications 49 à 53 pour la détection et/ou l'amplification de séquences nucléiques.

35

55. Puce à ADN, caractérisée en ce qu'elle contient au moins une séquence nucléotidique selon la revendication 53.

56. Puce à ADN selon la revendication 55, caractérisée en ce qu'elle contient en outre au moins une séquence

nucléotidique de micro-organisme autre que *Chlamydia trachomatis*, immobilisée sur le support de ladite puce.

57. Puce à ADN selon la revendication 56, caractérisée en ce que le micro-organisme autre est choisi parmi un micro-organisme associé à *Chlamydia trachomatis*, une bactérie de la famille Chlamydia, et un variant de *Chlamydia trachomatis*.
58. Vecteur de clonage, et/ ou d'expression, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 2 à 5, et, 9 à 28.
59. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 10 à 12.
60. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 13 à 15.
61. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 16 à 21.
62. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 22 à 25.
63. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon la revendication 26.
64. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon la revendication 27.

65. Vecteur selon la revendication 58, caractérisé en ce qu'il contient une séquence nucléotidique selon la revendication 28.
- 5 66. Cellule hôte, caractérisée en ce qu'elle est transformée par un vecteur selon l'une des revendications 58 à 65.
- 10 67. Cellule hôte selon la revendication 66, caractérisée en ce qu'il s'agit d'une bactérie appartenant à la famille *Chlamydia*.
- 15 68. Cellule hôte selon la revendication 67, caractérisée en ce qu'il s'agit d'une bactérie appartenant à l'espèce *Chlamydia trachomatis*.
- 20 69. Cellule hôte selon la revendication 66, caractérisée en ce qu'il s'agit d'un micro-organisme associé à l'espèce *Chlamydia trachomatis*.
70. Animal, excepté l'Homme, comprenant une cellule transformée selon l'une des revendications 66 à 69.
- 25 71. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 58, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.
- 30 72. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 59, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.
- 35 73. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 60, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

74. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 61, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

75. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 62, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

76. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 63, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

77. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 64, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

78. Procédé de préparation d'un polypeptide, caractérisé en ce qu'il met en œuvre un vecteur selon la revendication 65, une cellule transformée par ledit vecteur et/ou un animal comprenant ladite cellule transformée.

79. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 71.

80. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 72.

81. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 73.

82. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 74.

83. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 75.
- 5 84. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 76.
85. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 77.
- 10 86. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 78.
- 15 87. Procédé de préparation d'un polypeptide synthétique, caractérisé en ce qu'il utilise une séquence d'acides aminés d'un polypeptide selon l'une des revendications 5 à 8, 29 à 47, et, 79 à 86.
- 20 88. Polypeptide synthétique obtenu par un procédé selon la revendication 87.
- 25 89. Polypeptide hybride, caractérisé en ce qu'il comporte au moins la séquence d'un polypeptide selon l'une des revendications 5 à 8, 29 à 47, et, 79 à 86, et 88, et une séquence d'un polypeptide susceptible d'induire une réponse immunitaire chez l'homme ou l'animal.
- 30 90. Polypeptide hybride selon la revendication 89, caractérisé en ce qu'il comporte au moins la séquence d'un polypeptide selon l'une des revendications 29 à 31, et 80, et une séquence d'un polypeptide susceptible d'induire une réponse immunitaire chez l'homme ou l'animal.
- 35 91. Polypeptide hybride selon l'une des revendications 89 et 90, caractérisé en ce que le polypeptide susceptible d'induire une réponse immunitaire contient au moins un

déterminant antigénique capable d'induire une réponse humorale et/ou cellulaire.

5 92. Séquence nucléotidique codant pour un polypeptide hybride selon l'une des revendications 89 à 91.

93. Vecteur caractérisé en ce qu'il contient une séquence nucléotidique selon la revendication 92.

10 94. Polypeptide hybride selon l'une des revendications 89 à 91, caractérisée en ce qu'il s'agit d'un polypeptide recombinant obtenu par la mise en œuvre d'un vecteur selon la revendication 93.

15 95. Procédé pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes :

20 a) mise en contact de l'échantillon biologique avec un polypeptide selon l'une des 5 à 8, 29 à 47, 79 à 86, et 88 ;

b) mise en évidence du complexe antigène-anticorps éventuellement formé.

25 96. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

a) un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88 ;

30 b) le cas échéant, les réactifs pour la constitution du milieu propice à la réaction immunologique ;

c) les réactifs permettant mise en évidence des complexes antigène-anticorps éventuellement formés entre le ou les polypeptides de l'invention et les anticorps ;

35 d) le cas échéant, un échantillon biologique de référence (témoin négatif) dépourvu d'anticorps reconnus par ledit polypeptide ;

e) le cas échéant, un échantillon biologique de référence (témoin positif) contenant une quantité prédéterminée d'anticorps reconnus par ledit polypeptide.

5 97. Anticorps mono- ou polyclonaux, leurs fragments, ou anticorps chimériques, caractérisés en ce qu'ils sont capables de reconnaître spécifiquement un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88.

10 98. Anticorps selon la revendication 97, caractérisé en ce qu'il s'agit d'un anticorps marqué.

99. Procédé pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes :

- a) mise en contact de l'échantillon biologique avec un anticorps selon l'une des revendications 97 et 98 ;
- b) mise en évidence du complexe antigène-anticorps formé.

20

100. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- 25 a) un anticorps polyclonal ou monoclonal selon l'une des revendications 97 et 98 ;
- b) le cas échéant, les réactifs pour la constitution du milieu propice à la réaction immunologique ;
- c) les réactifs permettant la mise en évidence des complexes antigène-anticorps produits par la réaction
- 30 immunologique.

101. Polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88, ou anticorps selon l'une des revendications 97 et 98, caractérisé en ce qu'il est immobilisé sur un support, notamment d'une puce à protéine.

35

102. Puce à protéine, caractérisée en ce qu'elle contient au moins un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88, ou au moins anticorps selon l'une des revendications 97 et 98, immobilisé sur le support de ladite puce.

103. Puce à protéine selon la revendication 102, caractérisée en ce qu'elle contient en outre au moins un polypeptide de micro-organisme autre que *Chlamydia trachomatis* ou au moins un anticorps dirigé contre un composé de micro-organisme autre que *Chlamydia trachomatis*, immobilisé sur le support de ladite puce.

104. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend une puce à protéine selon l'une des revendications 102 et 103.

105. Kit ou nécessaire pour la détection et/ou l'identification d'un micro-organisme, caractérisé en ce qu'il comprend une puce à protéine selon la revendication 103.

106. Procédé de détection et/ou d'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il met en œuvre une séquence nucléotidique selon l'une des revendications 1 à 4, 9 à 28, 49 à 54.

107. Procédé selon la revendication 106, caractérisé en ce qu'il comporte les étapes suivantes :

a) le cas échéant, isolement de l'ADN à partir de l'échantillon biologique à analyser, ou éventuellement obtention d'un ADNc à partir de l'ARN de l'échantillon biologique ;

- b) amplification spécifique de l'ADN de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé à l'aide d'au moins une amorce selon l'une des revendications 49 à 54;
- 5 c) mise en évidence des produits d'amplification.

108. Procédé selon la revendication 106, caractérisé en ce qu'il comprend les étapes suivantes :

- 10 a) mise en contact d'une sonde nucléotidique selon l'une des revendications 50 à 54, avec un échantillon biologique, l'ADN contenu dans l'échantillon biologique ayant, le cas échéant, préalablement été rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'ADN d'une bactérie appartenant à l'espèce
- 15 *Chlamydia trachomatis* ou à un micro-organisme associé ;
- b) mise en évidence de l'hybride éventuellement formé entre la sonde nucléotidique et l'ADN de l'échantillon biologique.

20 109. Procédé selon la revendication 106, caractérisé en ce qu'il comprend les étapes suivantes :

- a) mise en contact d'une sonde nucléotidique immobilisée sur un support selon la des revendications 52 avec un échantillon biologique, l'ADN de l'échantillon, ayant, le
- 25 cas échéant, été préalablement rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'ADN d'une bactérie appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé ;
- 30 b) mise en contact de l'hybride formé entre la sonde nucléotidique immobilisée sur un support et l'ADN contenu dans l'échantillon biologique, le cas échéant après élimination de l'ADN de l'échantillon biologique n'ayant pas hybridé avec la sonde, avec une sonde nucléotidique
- 35 marquée selon la revendication 51 ;
- c) mise en évidence du nouvel hybride formé à l'étape b).

110. Procédé selon la revendication 109, caractérisé en ce que, préalablement à l'étape a), l'ADN de l'échantillon biologique, ou l'ADNc obtenu éventuellement par transcription inverse de l'ARN de l'échantillon, est amplifié à l'aide d'au moins une amorce selon l'une des revendications 49 à 54.

111. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique selon l'une des revendications 50 à 54;
- b) le cas échéant, les réactifs nécessaires à la mise en œuvre d'une réaction d'hybridation ;
- c) le cas échéant, au moins une amorce selon l'une des revendications 49 à 54 ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

112. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique, dite sonde de capture, selon la revendication 52 ;
- b) une sonde oligonucléotidique, dite sonde de révélation, selon la revendication 51;
- c) le cas échéant, au moins une amorce selon l'une des revendications 49 à 54 ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

113. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) au moins une amorce selon l'une des revendications 49 à 54;

b) le cas échéant, les réactifs nécessaires pour effectuer une réaction d'amplification d'ADN ;

c) le cas échéant, un composant permettant de vérifier la séquence du fragment amplifié, plus particulièrement une sonde oligonucléotidique selon l'une des revendications 50 à 54.

114. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis* ou à un micro-organisme associé, caractérisé en ce qu'il comprend une puce à ADN selon la revendication 55.

115. Kit ou nécessaire pour la détection et/ou l'identification d'un micro-organisme, caractérisé en ce qu'il comprend une puce à ADN selon l'une des revendications 56 et 57.

116. Procédé ou kit ou nécessaire selon l'une des revendications 95, 96, 99, 100 et, 104 à 115 pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Chlamydia trachomatis*, caractérisé en ce que ladite amorce et/ou ladite sonde sont choisies parmi les séquences nucléotidiques selon l'une des revendications 2 à 4, 9 à 28, et, 49 à 54 spécifiques de l'espèce *Chlamydia trachomatis*, en ce que lesdits polypeptides sont choisies parmi les polypeptides selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, 88 et 101 spécifiques de l'espèce *Chlamydia trachomatis* et en ce que lesdits anticorps sont choisis parmi les anticorps selon l'une des revendications 97 et 98 dirigés contre les polypeptides choisies parmi les polypeptides selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, 88 et 101 spécifiques de l'espèce *Chlamydia trachomatis*.

117. Procédé ou kit ou nécessaire selon la revendication 116, caractérisé en ce que ladite amorce et/ou ladite sonde

sont choisies parmi les séquences nucléotidiques selon la revendication 28, en ce que lesdits polypeptides sont choisies parmi les polypeptides selon l'une des revendications 47 et 86, et en ce que lesdits anticorps
5 sont choisies parmi les anticorps selon l'une des revendications 97 et 98 dirigés contre les polypeptides selon l'une des revendications 47 et 86 selon la revendication.

10 118. Procédé ou kit ou nécessaire selon l'une des revendications 95, 96, 99, 100, et, 104 à 117, pour le diagnostic de prédispositions à des maladies génitales, induites ou aggravées par une infection par *Chlamydia trachomatis*.

15 119. Procédé ou kit ou nécessaire selon l'une des revendications 95, 96, 99, 100, et, 104 à 117, pour le diagnostic de prédispositions à, ou d'affections par, des maladies oculaires induites ou aggravées par une infection
20 par *Chlamydia trachomatis*.

120. Procédé ou kit ou nécessaire selon l'une des revendications 95, 96, 99, 100, et, 104 à 117, pour le diagnostic de prédispositions à, ou d'affections par, des
25 maladies systémiques, notamment du système lymphatique, induites ou aggravées par une infection par *Chlamydia trachomatis*.

121. Utilisation de polypeptide selon l'une des
30 revendications 5 à 8, 29 à 47, 79 à 86, et 88, une cellule transformée selon l'une des revendications 66 à 69 et/ou un animal selon la revendication 70, pour la biosynthèse ou la biodégradation de composé d'intérêt.

35 122. Procédé de biosynthèse ou de biodégradation de composé d'intérêt, caractérisé en ce qu'il met en œuvre un polypeptide selon l'une des revendications 5 à 8, 29 à 47,

79 à 86, et 88, une cellule transformée selon l'une des revendications 66 à 69 et/ou un animal selon la revendication 70.

- 5 123. Utilisation d'une séquence nucléotidique selon l'une des revendications 2 à 4, et, 9 à 28, d'un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88, d'un anticorps selon l'une des revendications 97 et 98, d'une cellule selon l'une des revendications 66 à 69, 10 et/ou d'un animal transformé selon la revendication 70 pour la sélection de composé organique ou inorganique capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la réplication cellulaire de cellules eucaryotes ou procaryotes ou 15 capables d'induire, d'inhiber ou d'aggraver chez un organisme animal ou humain les pathologies liées à une infection par *Chlamydia trachomatis* ou par un micro-organisme associé.
- 20 124. Méthode de sélection de composé capable de se lier à un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, et 88, capable de se lier à une séquence nucléotidique selon l'une des revendications 2 à 4, et, 9 à 28, ou capable de reconnaître un anticorps selon l'une des 25 revendications 97 et 98, et/ou capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la réplication cellulaire de cellules eucaryotes ou procaryotes, ou capables d'induire, d'inhiber ou d'aggraver chez un organisme animal ou humain les 30 pathologies liées à une infection par *Chlamydia trachomatis*, caractérisée en ce qu'elle comprend les étapes suivantes :
- a) mise en contact dudit composé avec ledit polypeptide, ladite séquence nucléotidique, avec une cellule transformée 35 selon l'une des revendications 66 à 69 , et/ou administration dudit composé à un animal transformé selon la revendication 70;

b) détermination de la capacité dudit composé à se lier avec ledit polypeptide ou ladite séquence nucléotidique, ou de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, ou de moduler la croissance ou la réplication cellulaire, ou d'induire, d'inhiber ou d'aggraver chez
 5 ledit organisme animal ou humain les pathologies liées à une infection par *Chlamydia trachomatis* ou par un micro-organisme associé.

10 125. Composé susceptible d'être sélectionné par une méthode selon la revendication 124.

126. Composition pharmaceutique comprenant un composé choisi

15 parmi les composés suivants :

a) une séquence nucléotidique selon l'une des revendications 2 à 4, 9 à 28 ;

b) un polypeptide selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, 88 à 91, et 94 ;

20 c) un vecteur selon l'une des revendications 58 à 65, et 93 ;

d) un anticorps selon la revendication 97 ; et

e) un composé selon la revendication 125.

25 127. Composition selon la revendication 126, éventuellement en association avec un véhicule pharmaceutiquement acceptable.

30 128. Composition pharmaceutique selon l'une des revendications 126 et 127 pour la prévention ou le traitement d'une infection par une bactérie appartenant à l'espèce *Chlamydia trachomatis* ou par un micro-organisme associé.

35 129. Composition vaccinale, caractérisée en ce qu'elle comprend un ou plusieurs polypeptides selon l'une des revendications 5 à 8, 29 à 47, 79 à 86, 88, et/ou un ou

plusieurs polypeptides hybrides selon l'une des revendications 89 à 91 et 94.

5 130. Utilisation d'une cellule selon l'une des revendications 66 à 69, pour la préparation d'une composition vaccinale.

10 131. Composition vaccinale, caractérisée en ce qu'elle contient un vecteur selon l'une des revendications 58 à 65, et 93, et/ou une cellule selon l'une des revendications 66 à 69.

15 132. Composition vaccinale selon l'une des revendications 129 et 131, pour la prévention ou le traitement d'une infection par une bactérie appartenant à l'espèce *Chlamydia trachomatis* ou par un micro-organisme associé.

20 133. Composition vaccinale selon l'une des revendications 129, 131 à 132, en association avec un véhicule pharmaceutiquement acceptable et, le cas échéant un ou plusieurs adjuvants de l'immunité appropriés.

25 134. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour le traitement et/ou la prévention de maladies génitales induites ou aggravées par *Chlamydia trachomatis*.

30 135. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour le traitement et/ou la prévention de maladies oculaires induites ou aggravées par *Chlamydia trachomatis*.

35 136. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour le traitement et/ou la prévention de maladies systémiques induites ou aggravées par la présence de *Chlamydia trachomatis*.

137. Utilisation selon la revendication 136, caractérisée en ce que la maladie systémique affecte le système lymphatique.

impliqué dans le métabolisme des acides nucléiques, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

5 ORF5; ORF12; ORF82; ORF96; ORF97; ORF98; ORF99; ORF100;
ORF105; ORF118; ORF136; ORF137; ORF163; ORF190; ORF204;
ORF259; ORF260; ORF262; ORF290; ORF300; ORF301; ORF302;
ORF387; ORF427; ORF434; ORF441; ORF444; ORF471; ORF595;
ORF596; ORF597; ORF599; ORF600; ORF605; ORF612; ORF624;
ORF625; ORF650; ORF657; ORF658; ORF702; ORF703; ORF704;
10 ORF708; ORF719; ORF766; ORF767; ORF775; ORF779; ORF787;
ORF788; ORF794; ORF841; ORF842; ORF883; ORF884; ORF907;
ORF918; ORF924; ORF928; ORF929; ORF962; ORF962; ORF963;
ORF969; ORF970; ORF975; ORF979; ORF995; ORF1031; ORF1032 et
un de leurs fragments représentatifs.

15

19. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des acides aminés, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

20 ORF27; ORF41; ORF55; ORF56; ORF57; ORF59; ORF62; ORF63;
ORF64; ORF65; ORF119; ORF132; ORF240; ORF241; ORF277;
ORF278; ORF279; ORF382; ORF406; ORF428; ORF442; ORF446;
25 ORF447; ORF453; ORF454; ORF541; ORF542; ORF591; ORF608;
ORF609; ORF610; ORF618; ORF648; ORF649; ORF660; ORF661;
ORF677; ORF717; ORF765; ORF797; ORF871; ORF875; ORF920;
ORF922; ORF937; ORF998; ORF1020; ORF1021; ORF1034; ORF1044;
ORF1046; ORF1049 et un de leurs fragments représentatifs.

30

20. Séquence nucléotidique selon l'une des revendications 2 à 4, et 9, caractérisée en ce qu'elle code pour un polypeptide de *Chlamydia trachomatis* ou un de ses fragments impliqué dans le métabolisme des polypeptides, et en ce qu'elle comprend une séquence nucléotidique choisie parmi les séquences suivantes :

35

plusieurs polypeptides hybrides selon l'une des revendications 89 à 91 et 94.

5 130. Utilisation d'une cellule selon l'une des revendications 66 à 69, pour la préparation d'une composition vaccinale.

10 131. Composition vaccinale, caractérisée en ce qu'elle contient un vecteur selon l'une des revendications 58 à 65, et 93, et/ou une cellule selon l'une des revendications 66 à 69.

132. Composition vaccinale selon l'une des revendications 129 et 131, pour la prévention ou le traitement d'une infection par une bactérie appartenant à l'espèce *Chlamydia trachomatis* ou par un micro-organisme associé.

15 133. Composition vaccinale selon l'une des revendications 129, 131 à 132, en association avec un véhicule pharmaceutiquement acceptable et, le cas échéant un ou plusieurs adjuvants de l'immunité appropriés.

20 134. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour la préparation d'un médicament destiné au traitement et/ou à la prévention de maladies génitales induites ou aggravées par *Chlamydia trachomatis*.

25 135. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour la préparation d'un médicament destiné au traitement et/ou à la prévention de maladies oculaires induites ou aggravées par *Chlamydia trachomatis*.

30 136. Utilisation d'une composition selon l'une des revendications 126 à 129, et, 131 à 133, pour la préparation d'un médicament destiné au traitement et/ou à la prévention de maladies systémiques induites ou aggravées par la présence de *Chlamydia trachomatis*.

Figure 1.

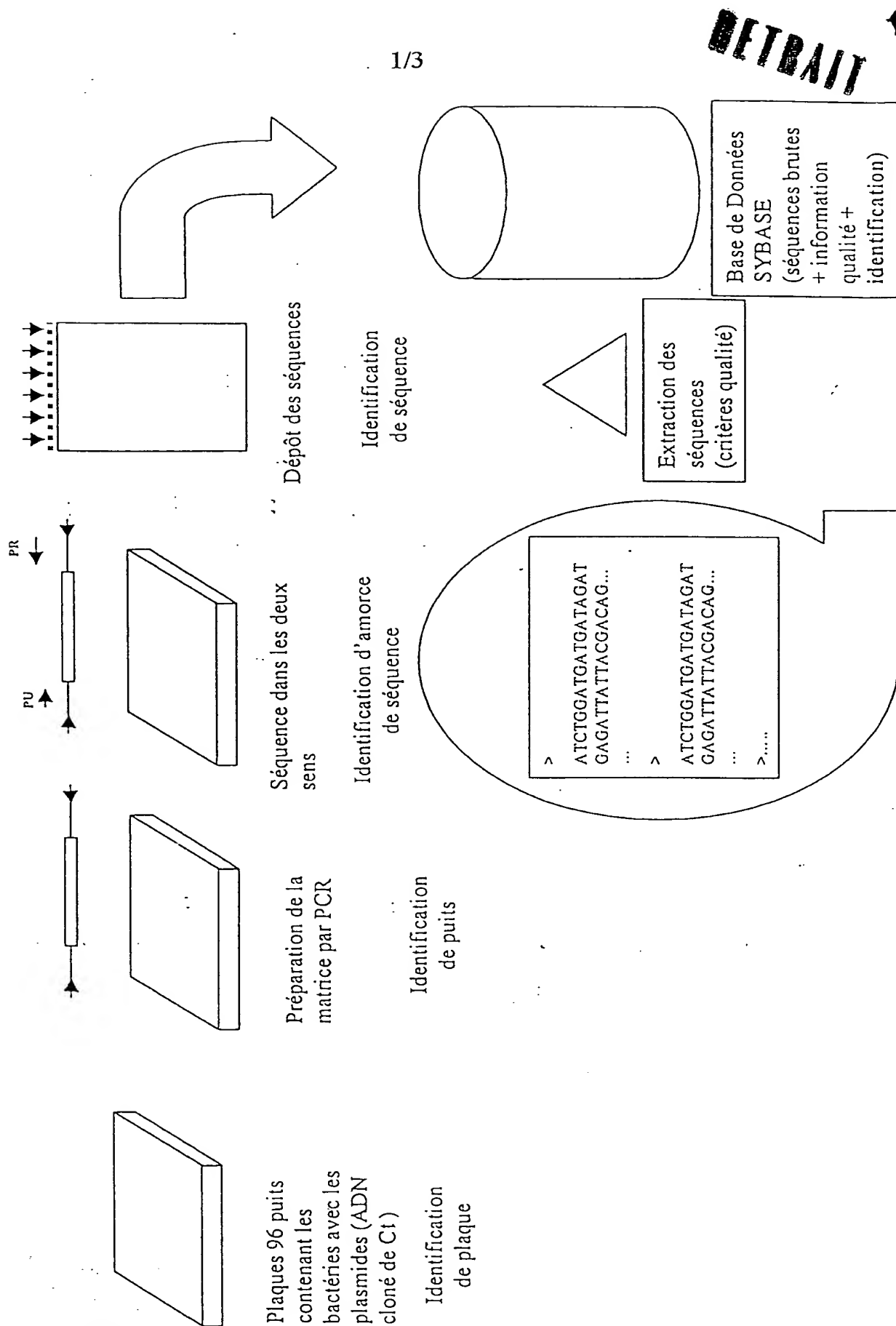
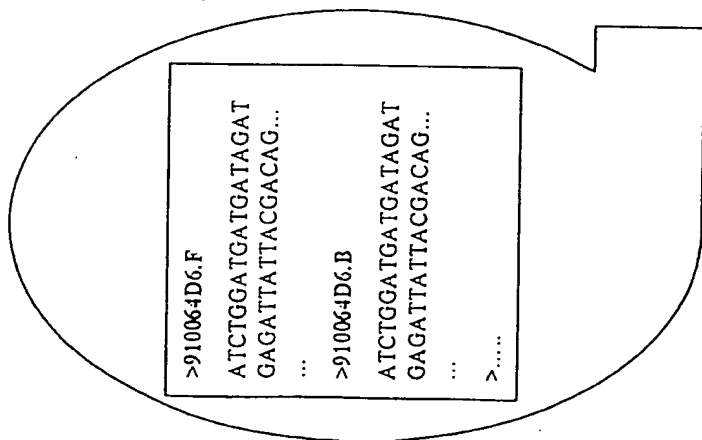


Figure 2.



STADEN Package
 Sun Solaris

TIGR Asmg
 Sun Solaris

Comparaison
 des résultats

PC/Windows NT :

Fabrication carte d'assemblage :

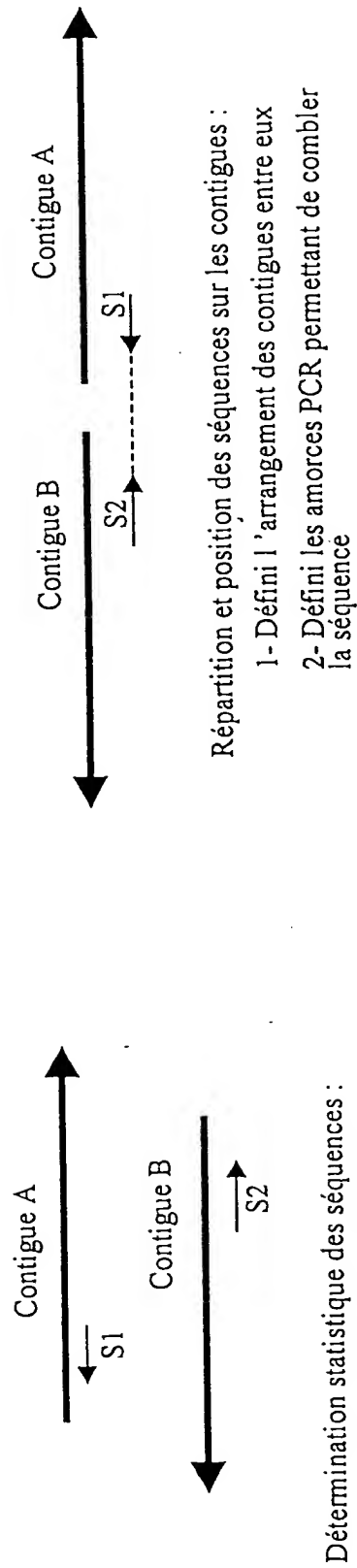
- Relation et orientation des « contigues » entre eux.
- Détermination des clones utiles pour obtenir les séquences manquantes entre les « contigues »
- Choix des amorces PCR et de séquence pour obtenir les séquences manquantes entre les « contigues »
- Détermination des extrémités de « contigues » n'ayant pas de relation avec d'autres « contigues » (extrémités orphelines)
- Choix des amorces PCR permettant d'étudier la relation entre elles des extrémités orphelines

Figure 3a

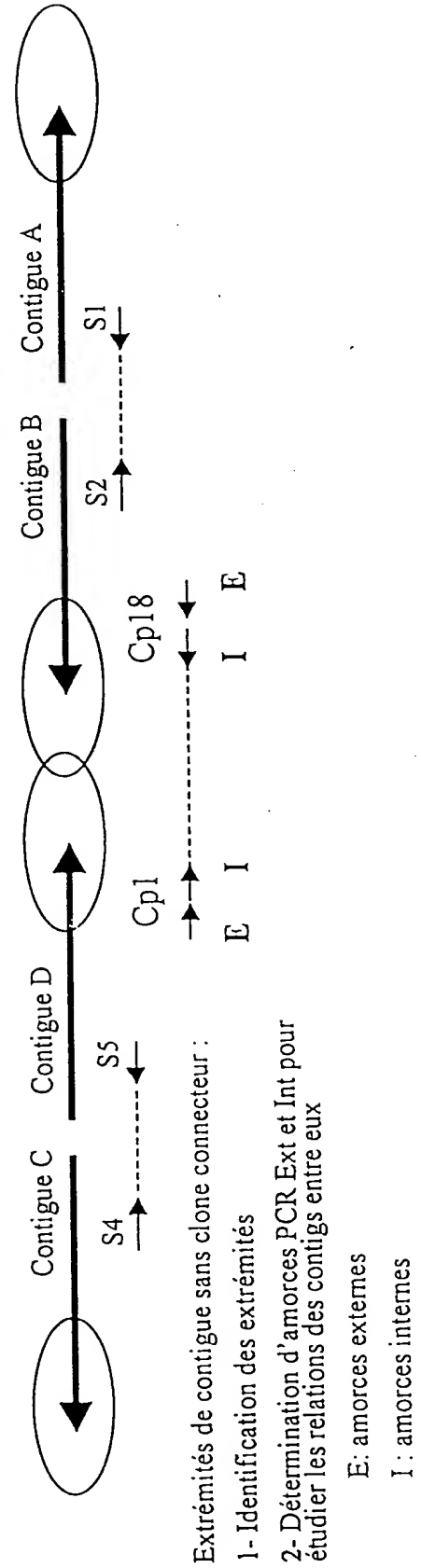
Figure 3b

Figure 3.

a.



b.



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